ttctcacaga agactggtga aagcttctgt gaagcatggg agcgtttcaa gggttacacc 480 aaccaatgcc ctcatcatga ttttactaaa gcctctctac tcagcactct ttacagagga 540 gtcctaccac gcatcagaat gcttctggat accgccagca atgggaattt ttag

- (2) INFORMATION FOR SEQ ID NO:433:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..197
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Met Ala Glu Glu Gln Asn Gln Gln Asn Gly Pro Val Asn Ile Gly Ala 1 5 10 15

Arg Asp Ala Pro Arg Asp His Arg Gln Arg Lys Gly Ile Ala Pro Pro 20 25 30

Ala Ile Leu Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ser Met 35 40 45

Ile Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp 50 55

His Leu Asn Glu Phe Asp Arg Leu Cys Asn Leu Thr Lys Ile Asn Gly 65 70 75 80

Val Ser Glu Asp Gly Phe Lys Leu Cys Leu Phe Pro Phe Ser Leu Gly
85 90 95

Asp Lys Ala His Ile Trp Glu Lys Asn Leu Pro His Asp Ser Ile Thr 100 105 110

Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ser Lys Phe Phe Ser Asn 115 120 125

Ala Ile Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Ser Gln Lys
130 135 140

Thr Gly Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Thr 145 150 155 160

Asn Gln Cys Pro His His Asp Phe Thr Lys Ala Ser Leu Leu Ser Thr 165 170 175 Leu Tyr Arg Gly Val Leu Pro Arg Ile Arg Met Leu Leu Asp Thr Ala

Leu Tyr Arg Gly Val Leu Pro Arg Ile Arg Met Leu Leu Asp Thr Ala 180 190

Ser Asn Gly Asn Phe 195

- (2) INFORMATION FOR SEQ ID NO:434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..150
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Ile Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu
1 10 15

Asp His Leu Asn Glu Phe Asp Arg Leu Cys Asn Leu Thr Lys Ile Asn 20 25 30

Gly Val Ser Glu Asp Gly Phe Lys Leu Cys Leu Phe Pro Phe Ser Leu 35 40 45

Gly Asp Lys Ala His Ile Trp Glu Lys Asn Leu Pro His Asp Ser Ile 50 55 60

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Thr Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ser Lys Phe Phe Ser
                                         75
                    70
Asn Ala Ile Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Ser Gln
                                    90
                85
Lys Thr Gly Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr
                                                     110
                                105
Thr Asn Gln Cys Pro His His Asp Phe Thr Lys Ala Ser Leu Leu Ser
                                                 125
                            120
Thr Leu Tyr Arg Gly Val Leu Pro Arg Ile Arg Met Leu Leu Asp Thr
                        135
    130
Ala Ser Asn Gly Asn Phe
                    150
145
(2) INFORMATION FOR SEQ ID NO:435:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 690 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..690
           (D) OTHER INFORMATION: / Ceres Seq. ID 1585636
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:
gaagttgttg ctgagagcac tggaggcatt ggaggaggg cgggcggcgg attgacgatt
                                                                        60
aaggatagcg atgagcagac gattgggtta gaggcggttt cgggtttggt ttggaggtgt
                                                                        120
ttgacgatgg agaacactgg tattattgga ttatatggtg tggaaggtgt tggaaagacg
                                                                        180
                                                                        240
actqttttga ctcaggttaa taacaggttg cttcaacaga aagcaaatgg gtttgatttt
                                                                        300
gttttgtggg tgtttgtatc caagaacctg aatcttcaga agattcaaga tacgattagg
                                                                        360
gagaagattg ggttcttgga taggacttgg acgagtaagt ccgaggaaga gaaagctgcg
                                                                        420
aagatetttg agatettgag taagagaegg ttegetttgt ttettgatga tgtttgggag
                                                                        480
aaagttgatc ttgtgaaagc tggagttccg ccaccggatg cgcagaaccg gtcgaagata
gtgttcacga catgttccga agaagtttgt aaggagatga gtgcacagac aaagatcaaa
                                                                        540
                                                                        600
gtagagaaat tggcatggga acgagcttgg gacttgttta agaagaatgt tggagaagat
                                                                        660
actataaaga gccacccaga catagccaaa gtggctcaag aggttgcagc caggtgcgac
ggtcttcctc tagctttggt caccattgga
 (2) INFORMATION FOR SEQ ID NO:436:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 230 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..230
           (D) OTHER INFORMATION: / Ceres Seq. ID 1585637
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:
 Glu Val Val Ala Glu Ser Thr Gly Gly Ile Gly Gly Gly Ala Gly Gly
                                      10
 Gly Leu Thr Ile Lys Asp Ser Asp Glu Gln Thr Ile Gly Leu Glu Ala
                                                      30
                                  25
             20
 Val Ser Gly Leu Val Trp Arg Cys Leu Thr Met Glu Asn Thr Gly Ile
                              40
 Ile Gly Leu Tyr Gly Val Glu Gly Val Gly Lys Thr Thr Val Leu Thr
                                              60
· Gln Val Asn Asn Arg Leu Leu Gln Gln Lys Ala Asn Gly Phe Asp Phe
                                          75
                     7.0
```

Val Leu Trp Val Phe Val Ser Lys Asn Leu Asn Leu Gln Lys Ile Gln

Asp Thr Ile Arg Glu Lys Ile Gly Phe Leu Asp Arg Thr Trp Thr Ser

8.5

```
105
                                         110
Lys Ser Glu Glu Glu Lys Ala Ala Lys Ile Phe Glu Ile Leu Ser Lys
 115 120 125
Arg Arg Phe Ala Leu Phe Leu Asp Asp Val Trp Glu Lys Val Asp Leu
130 135 140
Val Lys Ala Gly Val Pro Pro Pro Asp Ala Gln Asn Arg Ser Lys Ile
                               155 160
145 150
Val Phe Thr Thr Cys Ser Glu Glu Val Cys Lys Glu Met Ser Ala Gln
          165 	 170 	 175
Thr Lys Ile Lys Val Glu Lys Leu Ala Trp Glu Arg Ala Trp Asp Leu
                         185
Phe Lys Lys Asn Val Gly Glu Asp Thr Ile Lys Ser His Pro Asp Ile
    195 200
Ala Lys Val Ala Gln Glu Val Ala Ala Arg Cys Asp Gly Leu Pro Leu
 210 215
Ala Leu Val Thr Ile Gly
225 230
(2) INFORMATION FOR SEQ ID NO:437:
   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 188 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..188
        (D) OTHER INFORMATION: / Ceres Seq. ID 1585638
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:
Met Glu Asn Thr Gly Ile Ile Gly Leu Tyr Gly Val Glu Gly Val Gly
                          10
Lys Thr Thr Val Leu Thr Gln Val Asn Asn Arg Leu Leu Gln Gln Lys
 20
                          25
Ala Asn Gly Phe Asp Phe Val Leu Trp Val Phe Val Ser Lys Asn Leu
 35
                      4.0
Asn Leu Gln Lys Ile Gln Asp Thr Ile Arg Glu Lys Ile Gly Phe Leu
                   55
Asp Arg Thr Trp Thr Ser Lys Ser Glu Glu Glu Lys Ala Ala Lys Ile
                70
                                75
Phe Glu Ile Leu Ser Lys Arg Arg Phe Ala Leu Phe Leu Asp Asp Val
                            90
            85
Trp Glu Lys Val Asp Leu Val Lys Ala Gly Val Pro Pro Pro Asp Ala
         100
                       105
Gln Asn Arg Ser Lys Ile Val Phe Thr Thr Cys Ser Glu Glu Val Cys
                      120
 115
Lys Glu Met Ser Ala Gln Thr Lys Ile Lys Val Glu Lys Leu Ala Trp
  130 135
                                    140
Glu Arg Ala Trp Asp Leu Phe Lys Lys Asn Val Gly Glu Asp Thr Ile
145 150 155
Lys Ser His Pro Asp Ile Ala Lys Val Ala Gln Glu Val Ala Ala Arg
       165 170
Cys Asp Gly Leu Pro Leu Ala Leu Val Thr Ile Gly
         180 185
(2) INFORMATION FOR SEQ ID NO:438:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 698 base pairs
         (B) TYPE: nucleic acid
```

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..698
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438: gtgctcctct cgttgatggt ttgaagattc agaacaaaaa cggtgctgtg atgaatcggc 60 gtgccttcgg tgacatcgga aatcttgttt ctgttcccat taatcgaccc attactcgaa 120 gtttccgtga ccagttatta gcgaatgccc aactcaaaag aaagcccatc aatggagaca 180 240 acaagaagaa gaatctagtg gttaagcaac agacgaagcc tgttgaagtg atcgagacga agagggaggt gactaaaaac gaagtagcga tgtcacctaa gaataagaaa gtgacgtact 300 360 cgtctgtact tagtgctcgg agcaaagctg cttgtggtat tgatgaatct gacaaagata 420 atcatctggc tgcagtggag tatgttgatg atatgtactc gttctataaa gaagttgaga 480 aggagagtca gcctaagatg catattcaaa ctaagatgaa tgagaagatc agagcgatct tgattgattg gttactagaa gttcacatca agtttgagct taaccttgga actctttacc 540 tcactgttaa ccttgatcga ttcctctctg tgaaagttgt taccaaaaga gagttgcagc 600 660 tagtgggaat cagtgtcttc caaatatgca ggtacttcac gttcaaaaga aaaatcttca agctgcaaag acaaaaagtt tcagcataca agggttga
- (2) INFORMATION FOR SEQ ID NO:439:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..231
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585643
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:
- Ala Pro Leu Val Asp Gly Leu Lys Ile Gln Asn Lys Asn Gly Ala Val 1 5 10 15
- Met Asn Arg Arg Ala Phe Gly Asp Ile Gly Asn Leu Val Ser Val Pro 20 25 30
- Ile Asn Arg Pro Ile Thr Arg Ser Phe Arg Asp Gln Leu Leu Ala Asn 35 40 45
- Ala Gln Leu Lys Arg Lys Pro Ile Asn Gly Asp Asn Lys Lys Lys Asn 50 55 60
- Leu Val Val Lys Gln Gln Thr Lys Pro Val Glu Val Ile Glu Thr Lys 65 70 75 80
- Arg Glu Val Thr Lys Asn Glu Val Ala Met Ser Pro Lys Asn Lys Lys 85 90 95 Val Thr Tyr Ser Ser Val Leu Ser Ala Arg Ser Lys Ala Ala Cys Gly
- 100 105 110

 Ile Asp Glu Ser Asp Lys Asp Asn His Leu Ala Ala Val Glu Tyr Val
- 115 120 125
 Asp Asp Met Tyr Ser Phe Tyr Lys Glu Val Glu Lys Glu Ser Gln Pro
 130 135 140
- Lys Met His Ile Gln Thr Lys Met Asn Glu Lys Ile Arg Ala Ile Leu 145 150 155 160
- Ile Asp Trp Leu Leu Glu Val His Ile Lys Phe Glu Leu Asn Leu Gly
 165 170 175
- Thr Leu Tyr Leu Thr Val Asn Leu Asp Arg Phe Leu Ser Val Lys Val
- Val Thr Lys Arg Glu Leu Gln Leu Val Gly Ile Ser Val Phe Gln Ile 195 200 205
- Cys Arg Tyr Phe Thr Phe Lys Arg Lys Ile Phe Lys Leu Gln Arg Gln 210 215 220
- Lys Val Ser Ala Tyr Lys Gly
- 225 230
- (2) INFORMATION FOR SEQ ID NO:440:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..215
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585644
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:
- Met Asn Arg Arg Ala Phe Gly Asp Ile Gly Asn Leu Val Ser Val Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$
- Ile Asn Arg Pro Ile Thr Arg Ser Phe Arg Asp Gln Leu Leu Ala Asn 20 25 30
- Ala Gln Leu Lys Arg Lys Pro Ile Asn Gly Asp Asn Lys Lys Asn 35 40 45
- Leu Val Val Lys Gln Gln Thr Lys Pro Val Glu Val Ile Glu Thr Lys
 50 55 60
- Arg Glu Val Thr Lys Asn Glu Val Ala Met Ser Pro Lys Asn Lys Lys 65 70 75 80
- Val Thr Tyr Ser Ser Val Leu Ser Ala Arg Ser Lys Ala Ala Cys Gly 85 90 95
- Ile Asp Glu Ser Asp Lys Asp Asn His Leu Ala Ala Val Glu Tyr Val
- Asp Asp Met Tyr Ser Phe Tyr Lys Glu Val Glu Lys Glu Ser Gln Pro 115 120 125
- Lys Met His Ile Gln Thr Lys Met Asn Glu Lys Ile Arg Ala Ile Leu 130 135 140
- Ile Asp Trp Leu Leu Glu Val His Ile Lys Phe Glu Leu Asn Leu Gly 145 150 155 160
- Thr Leu Tyr Leu Thr Val Asn Leu Asp Arg Phe Leu Ser Val Lys Val
 165 170 175
- Val Thr Lys Arg Glu Leu Gln Leu Val Gly Ile Ser Val Phe Gln Ile 180 185 190
- Cys Arg Tyr Phe Thr Phe Lys Arg Lys Ile Phe Lys Leu Gln Arg Gln 195 200 205
- Lys Val Ser Ala Tyr Lys Gly 210 215
- (2) INFORMATION FOR SEQ ID NO:441:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:
- Met Ser Pro Lys Asn Lys Lys Val Thr Tyr Ser Ser Val Leu Ser Ala 1 5 10 15
- Arg Ser Lys Ala Ala Cys Gly Ile Asp Glu Ser Asp Lys Asp Asn His
 20 25 30
- Leu Ala Ala Val Glu Tyr Val Asp Asp Met Tyr Ser Phe Tyr Lys Glu 35 40 45
- Val Glu Lys Glu Ser Gln Pro Lys Met His Ile Gln Thr Lys Met Asn 50 55 60
- Glu Lys Ile Arg Ala Ile Leu Ile Asp Trp Leu Leu Glu Val His Ile 65 70 75 80
- Lys Phe Glu Leu Asn Leu Gly Thr Leu Tyr Leu Thr Val Asn Leu Asp

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Client Docket No. 80146.003
Arg Phe Leu Ser Val Lys Val Val Thr Lys Arg Glu Leu Gln Leu Val
                               105
            100
Gly Ile Ser Val Phe Gln Ile Cys Arg Tyr Phe Thr Phe Lys Arg Lys
                                                125
                           120
       115
Ile Phe Lys Leu Gln Arg Gln Lys Val Ser Ala Tyr Lys Gly
                       135
(2) INFORMATION FOR SEQ ID NO:442:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1284 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
```

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1284
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442: atgcagacat tttcttccgc cgccgctctc acctccatcc tccgtcgtac aacgatctat 60 120 cacqqcqqat ttqqaactqq tctccqaatc cqccqcaqct tttattttct ctcaqcqata cgacaagaga accctaatgt cactaaaaat ccccacccga acaagactat tetcagatce 180 ttcttagctc cggttctccc gttagacgaa aaacctaacc tcgttgagct tcaagccatc 240 ggtacaatcg ccaccgctca agctgactac atgcgcgtca ttgttcaaga tgtacctgag 300 agtgataatg gagaggatga taagattggc gttgatttgc tttgtgtggt gagaaagtta 360 ctgaagaaga taggtacgac tgttcttgtt ggtgataaag ttctcgttga taaagttgat 420 tgggttgatc ggagagctaa gattatcaat gtgtttgatc gagtctcgga ggttttggat 480 540 ccaccggttg cgaatgttga tcacttagtg attctgtttt ctcttgatca acctaagatt 600 gatccattta cacttactag gttcttggtg gaagctgaat ctattggaat tcgaatcaca 660 gttgctttga acaaatgtga actcgtcact caagagggat tgattagaga catgataaga 720 ttgcgtagtt ggaactatga accattgatc tgtagtgtgg gaactaaagt cggacttgat gagattgcgt ttaacctgag aaatcagact tctgtcattg ttggacctag tggtgttgga 780 840 aagtccagct taatcaatat attgagaagt agctatggtg gtgacattaa acacgaagaa gtgtttaagc ctagtgtagg ggaagtttca catagaaatg gaagaggtaa acatacaacc 900 cgaaatgtaa cgctacttcc tctttgtgga ggtggatacc ttgctgatac ttctggcttt 960 aacaagcata agttgctgaa agtaacaaag caaaaacttc ccttgtgttt tcctgagata 1020 cggaaaatgg tcgagggagg aaaatgtggt tgggaaaggt atgattactt tttacaactg 1080 cttgatgaga tcaaaatcga tgaggagtgt caacttaaga agtatggaac caaaagggaa 1140 ggtggtgtta gttgccacat gggagagaag ggtgtggaac aagctaaacc acggatagat 1200 cccaagaagt ataggagaga atcgaggaag acgatgaaag atgaaagagc tatattaaga 1260 cagcatagag aacaattaac ctaa
- (2) INFORMATION FOR SEQ ID NO:443:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..427
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585651
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Gln Thr Phe Ser Ser Ala Ala Ala Leu Thr Ser Ile Leu Arg Arg 10 Thr Thr Ile Tyr His Gly Gly Phe Gly Thr Gly Leu Arg Ile Arg Arg 25

Ser Phe Tyr Phe Leu Ser Ala Ile Arg Gln Glu Asn Pro Asn Val Thr 45 40

Lys Asn Pro His Pro Asn Lys Thr Ile Leu Arg Ser Phe Leu Ala Pro 60 50 55 Val Leu Pro Leu Asp Glu Lys Pro Asn Leu Val Glu Leu Gln Ala Ile

75 70 65 Gly Thr Ile Ala Thr Ala Gln Ala Asp Tyr Met Arg Val Ile Val Gln 85 90 Asp Val Pro Glu Ser Asp Asn Gly Glu Asp Asp Lys Ile Gly Val Asp 100 105 110 Leu Leu Cys Val Val Arg Lys Leu Leu Lys Lys Ile Gly Thr Thr Val 115 120 125 Leu Val Gly Asp Lys Val Leu Val Asp Lys Val Asp Trp Val Asp Arg 130 135 140 Arg Ala Lys Ile Ile Asn Val Phe Asp Arg Val Ser Glu Val Leu Asp 145 150 155 160 Pro Pro Val Ala Asn Val Asp His Leu Val Ile Leu Phe Ser Leu Asp 165 170 175 Gln Pro Lys Ile Asp Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala 180 185 190 Glu Ser Ile Gly Ile Arg Ile Thr Val Ala Leu Asn Lys Cys Glu Leu 195 200 205 Val Thr Gln Glu Gly Leu Ile Arg Asp Met Ile Arg Leu Arg Ser Trp 210 215 Asn Tyr Glu Pro Leu Ile Cys Ser Val Gly Thr Lys Val Gly Leu Asp 230 235 Glu Ile Ala Phe Asn Leu Arg Asn Gln Thr Ser Val Ile Val Gly Pro 245 250 255 Ser Gly Val Gly Lys Ser Ser Leu Ile Asn Ile Leu Arg Ser Ser Tyr 260 265 Gly Gly Asp Ile Lys His Glu Glu Val Phe Lys Pro Ser Val Gly Glu 275 280 285 Val Ser His Arg Asn Gly Arg Gly Lys His Thr Thr Arg Asn Val Thr 300 295 Leu Leu Pro Leu Cys Gly Gly Gly Tyr Leu Ala Asp Thr Ser Gly Phe 315 310 Asn Lys His Lys Leu Leu Lys Val Thr Lys Gln Lys Leu Pro Leu Cys 325 330 Phe Pro Glu Ile Arg Lys Met Val Glu Gly Gly Lys Cys Gly Trp Glu 345 Arg Tyr Asp Tyr Phe Leu Gln Leu Leu Asp Glu Ile Lys Ile Asp Glu 360 Glu Cys Gln Leu Lys Lys Tyr Gly Thr Lys Arg Glu Gly Gly Val Ser 375 380 Cys His Met Gly Glu Lys Gly Val Glu Gln Ala Lys Pro Arg Ile Asp 385 390 395 400 Pro Lys Lys Tyr Arg Arg Glu Ser Arg Lys Thr Met Lys Asp Glu Arg 405 410 Ala Ile Leu Arg Gln His Arg Glu Gln Leu Thr 420 425

- (2) INFORMATION FOR SEQ ID NO:444:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..337
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585653
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Met Arg Val Ile Val Gln Asp Val Pro Glu Ser Asp Asn Gly Glu Asp 1 5 10 15
Asp Lys Ile Gly Val Asp Leu Leu Cys Val Val Arg Lys Leu Leu Lys

20 25 30

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Lys Ile Gly Thr Thr Val Leu Val Gly Asp Lys Val Leu Val Asp Lys
                           4.0
Val Asp Trp Val Asp Arg Arg Ala Lys Ile Ile Asn Val Phe Asp Arg
                       55
Val Ser Glu Val Leu Asp Pro Pro Val Ala Asn Val Asp His Leu Val
                   70
                                       75
Ile Leu Phe Ser Leu Asp Gln Pro Lys Ile Asp Pro Phe Thr Leu Thr
                                   90
               85
Arg Phe Leu Val Glu Ala Glu Ser Ile Gly Ile Arg Ile Thr Val Ala
          100
                               105
Leu Asn Lys Cys Glu Leu Val Thr Gln Glu Gly Leu Ile Arg Asp Met
                                              125
                           120
Ile Arg Leu Arg Ser Trp Asn Tyr Glu Pro Leu Ile Cys Ser Val Gly
                                          140
                       135
Thr Lys Val Gly Leu Asp Glu Ile Ala Phe Asn Leu Arg Asn Gln Thr
                   150
                                      155
Ser Val Ile Val Gly Pro Ser Gly Val Gly Lys Ser Ser Leu Ile Asn
                                  170
               165
Ile Leu Arg Ser Ser Tyr Gly Gly Asp Ile Lys His Glu Glu Val Phe
                               185
Lys Pro Ser Val Gly Glu Val Ser His Arg Asn Gly Arg Gly Lys His
                           200
                                               205
Thr Thr Arg Asn Val Thr Leu Leu Pro Leu Cys Gly Gly Tyr Leu
                       215
                                          220
Ala Asp Thr Ser Gly Phe Asn Lys His Lys Leu Leu Lys Val Thr Lys
                   230
                                       235
Gln Lys Leu Pro Leu Cys Phe Pro Glu Ile Arg Lys Met Val Glu Gly
               245
                                   250
Gly Lys Cys Gly Trp Glu Arg Tyr Asp Tyr Phe Leu Gln Leu Leu Asp
           260
                               265
Glu Ile Lys Ile Asp Glu Glu Cys Gln Leu Lys Lys Tyr Gly Thr Lys
                                              285
                           280
Arg Glu Gly Gly Val Ser Cys His Met Gly Glu Lys Gly Val Glu Gln
                       295
Ala Lys Pro Arg Ile Asp Pro Lys Lys Tyr Arg Arg Glu Ser Arg Lys
                310
                                   315
Thr Met Lys Asp Glu Arg Ala Ile Leu Arg Gln His Arg Glu Gln Leu
                                   330
```

- (2) INFORMATION FOR SEQ ID NO:445:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..642
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585658
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

, ,	~					
tgggagctgg	atacggatca	cgatttcctg	attgacaaag	aaaatcttat	gagatatgga	60
aaccatqctc	ttacctaccg	gattgtcgac	agaatattct	cccaggttgc	taggaagttc	120
actagcaaag	ttgaagggaa	gatggggtat	gaagactttg	tctatttcat	tcttgcggaa	180
gaagataaat	catcaatacc	tagcctagaa	tattggttta	agtgcataga	cttggatgca	240
aatgggatta	taacgcgaaa	tgagatgcaa	ttcttttatg	aagagcagtt	gcatagaatg	300
		tgttcttttc				360
		ccatataacg				420
		ttttaatcta				480
		gcgcgagaac				540

catagagagt atattcggct atcaatggaa gaagatgttg aagatgcatc caatggaagt 600 gctgaggttt gggatgactc gtcactggag gctcccttct ga

- (2) INFORMATION FOR SEQ ID NO: 446:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..213
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585659
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Trp Glu Leu Asp Thr Asp His Asp Phe Leu Ile Asp Lys Glu Asn Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Met Arg Tyr Gly Asn His Ala Leu Thr Tyr Arg Ile Val Asp Arg Ile 20 25 30

Phe Ser Gln Val Ala Arg Lys Phe Thr Ser Lys Val Glu Gly Lys Met

Gly Tyr Glu Asp Phe Val Tyr Phe Ile Leu Ala Glu Glu Asp Lys Ser 50 55 60

Ser Val Pro Ser Leu Glu Tyr Trp Phe Lys Cys Ile Asp Leu Asp Ala 70 75 80

Asn Gly Ile Ile Thr Arg Asn Glu Met Gln Phe Phe Tyr Glu Glu Gln
85 90 95

Leu His Arg Met Glu Cys Met Ala Gln Glu Ala Val Leu Phe Glu Asp 100 105 110

Ile Leu Cys Gln Met Ile Asp Met Ile Gly Pro Glu Asn Glu Ser His 115 120 125

Ile Thr Leu His Glu Leu Lys Gly Ser Lys Leu Ser Gly Asn Val Phe 130 135 140

Asn Ile Leu Phe Asn Leu Asn Lys Phe Met Ala Phe Glu Thr Arg Asp 145 150 155 160

Pro Phe Leu Ile Arg Glu Arg Glu Asn Pro Thr Leu Thr Asp Trp
165 170 175

Asp Arg Phe Ala His Arg Glu Tyr Ile Arg Leu Ser Met Glu Glu Asp 180 185 190

Val Glu Asp Ala Ser Asn Gly Ser Ala Glu Val Trp Asp Asp Ser Ser 195 200 205

Leu Glu Ala Pro Phe 210

- (2) INFORMATION FOR SEQ ID NO:447:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..197
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585660
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Met Arg Tyr Gly Asn His Ala Leu Thr Tyr Arg Ile Val Asp Arg Ile 1 10 15

Phe Ser Gln Val Ala Arg Lys Phe Thr Ser Lys Val Glu Gly Lys Met 20 25 30

Gly Tyr Glu Asp Phe Val Tyr Phe Ile Leu Ala Glu Glu Asp Lys Ser

Ser Val Pro Ser Leu Glu Tyr Trp Phe Lys Cys Ile Asp Leu Asp Ala

60 50 55 Asn Gly Ile Ile Thr Arg Asn Glu Met Gln Phe Phe Tyr Glu Glu Gln 70 75 Leu His Arg Met Glu Cys Met Ala Gln Glu Ala Val Leu Phe Glu Asp 90 85 Ile Leu Cys Gln Met Ile Asp Met Ile Gly Pro Glu Asn Glu Ser His 100 105 110 Ile Thr Leu His Glu Leu Lys Gly Ser Lys Leu Ser Gly Asn Val Phe 115 120 125 Asn Ile Leu Phe Asn Leu Asn Lys Phe Met Ala Phe Glu Thr Arg Asp 130 135 140 Pro Phe Leu Ile Arg Gln Glu Arg Glu Asn Pro Thr Leu Thr Asp Trp 155 160 Asp Arg Phe Ala His Arg Glu Tyr Ile Arg Leu Ser Met Glu Glu Asp 170 175 Val Glu Asp Ala Ser Asn Gly Ser Ala Glu Val Trp Asp Asp Ser Ser 180 185 Leu Glu Ala Pro Phe 195

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585661
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Gly Tyr Glu Asp Phe Val Tyr Phe Ile Leu Ala Glu Glu Asp Lys
1 5 10 15

Ser Ser Val Pro Ser Leu Glu Tyr Trp Phe Lys Cys Ile Asp Leu Asp 20 25 30

Ala Asn Gly Ile Ile Thr Arg Asn Glu Met Gln Phe Phe Tyr Glu Glu
35 40 45

Gln Leu His Arg Met Glu Cys Met Ala Gln Glu Ala Val Leu Phe Glu 50 55 60

Asp Ile Leu Cys Gln Met Ile Asp Met Ile Gly Pro Glu Asn Glu Ser 65 70 75 80

His Ile Thr Leu His Glu Leu Lys Gly Ser Lys Leu Ser Gly Asn Val 85 90 95

Phe Asn Ile Leu Phe Asn Leu Asn Lys Phe Met Ala Phe Glu Thr Arg 100 105 110

Asp Pro Phe Leu Ile Arg Gln Glu Arg Glu Asn Pro Thr Leu Thr Asp 115 120 125

Trp Asp Arg Phe Ala His Arg Glu Tyr Ile Arg Leu Ser Met Glu Glu 130 135 140

Asp Val Glu Asp Ala Ser Asn Gly Ser Ala Glu Val Trp Asp Asp Ser 145 150 155 160

Ser Leu Glu Ala Pro Phe

- (2) INFORMATION FOR SEQ ID NO:449:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..987
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585675
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449: atgcttctgg ataccgccag caatgggaat ttccagaaca aagatgttga agaaggctgg 60 120 gaattggttg agaaccttgc tcaatcagat ggcaattaca acgaagactg tgataggacc 180 gtcaaaggaa cagctgactc tgatgacaaa cacaggaaga agatcaaagc gctgaatgac 240 aagctggaca ggattattct cggccagcag aagcatgtgc acttccttgt tgatgacgag 300 caqtatcaag tcanagacgg ggagggtaac cagttggaag aagtcagcta catcaacaac aaccagggtg gctacaaaag atacaacaac ttcaaaacca acaatcccaa cctctcttac 360 cgcagcacca acgttgctaa ccctcaggat caagtgtatc ctccacagca acaacaaagt 420 480 ttcgttccta agcagcagtt ccaggggaac taccagcaac caccaccacc tgggtttgca cctcagcaaa cccaaggtcc tgctgctcct gatgctgaaa tgaaacagat ggtcaagcag 540 ctgctacagg gacaagcatc tagctcaatg gaaatggcta aaaaattatc taaattgcac 600 cataagctgg actgcagcta caatgacctg aatgccaaag tggaggcatt gaataccaaa 660 gtcagatact tggaaggcca atcagtatct acctctgtac caaaagttac aggacttcca 720 gggaagtcca tacagaatcc aaaagagtat gcaaccgctc acgccatcac catctgccat 780 gatcgagagc tgccaactcg acctgtcctt gatttcatca ctggggacaa tgatgttcaa 840 gaagggaagg cttctactca ggttgtagtc tctgttgttg aattcaacca ttccgctggt 900 960 tctcgccatc tcactcaatc catctcggaa gaaaaggccg ccataatcga gagaatgcat ttaaggtgtc aatccaaatg ggtgtaa
- (2) INFORMATION FOR SEQ ID NO:450:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..328
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585676
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450: Met Leu Leu Asp Thr Ala Ser Asn Gly Asn Phe Gln Asn Lys Asp Val 10 Glu Glu Gly Trp Glu Leu Val Glu Asn Leu Ala Gln Ser Asp Gly Asn 25 20 Tyr Asn Glu Asp Cys Asp Arg Thr Val Lys Gly Thr Ala Asp Ser Asp 40 Asp Lys His Arg Lys Lys Ile Lys Ala Leu Asn Asp Lys Leu Asp Arg 55 Ile Ile Leu Gly Gln Gln Lys His Val His Phe Leu Val Asp Asp Glu 7.5 70 Gln Tyr Gln Val Xaa Asp Gly Glu Gly Asn Gln Leu Glu Glu Val Ser 90 Tyr Ile Asn Asn Asn Gln Gly Gly Tyr Lys Arg Tyr Asn Asn Phe Lys 105 Thr Asn Asn Pro Asn Leu Ser Tyr Arg Ser Thr Asn Val Ala Asn Pro 120 125 Gln Asp Gln Val Tyr Pro Pro Gln Gln Gln Gln Ser Phe Val Pro Lys 140 135 Gln Gln Phe Gln Gly Asn Tyr Gln Gln Pro Pro Pro Gly Phe Ala 155 150 Pro Gln Gln Thr Gln Gly Pro Ala Ala Pro Asp Ala Glu Met Lys Gln 170 165 Met Val Lys Gln Leu Leu Gln Gly Gln Ala Ser Ser Ser Met Glu Met 190 185 180 Ala Lys Lys Leu Ser Lys Leu His His Lys Leu Asp Cys Ser Tyr Asn 200 205 Asp Leu Asn Ala Lys Val Glu Ala Leu Asn Thr Lys Val Arg Tyr Leu

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Glu Gly Gln Ser Val Ser Thr Ser Val Pro Lys Val Thr Gly Leu Pro
                    230
                                        235
Gly Lys Ser Ile Gln Asn Pro Lys Glu Tyr Ala Thr Ala His Ala Ile
                245
                                    250
Thr Ile Cys His Asp Arg Glu Leu Pro Thr Arg Pro Val Leu Asp Phe
                                                    270
                                265
Ile Thr Gly Asp Asn Asp Val Gln Glu Gly Lys Ala Ser Thr Gln Val
                                                285
                            280
Val Val Ser Val Val Glu Phe Asn His Ser Ala Gly Ser Arg His Leu
                                            300
                        295
Thr Gln Ser Ile Ser Glu Glu Lys Ala Ala Ile Ile Glu Arg Met His
                                        315
                    310
Leu Arg Cys Gln Ser Lys Trp Val
                325
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- (2) INFORMATION FOR SEQ ID NO:451:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1365
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585682
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451: 60 atgcttctgg ataccgccag caatgggaat ttccagaaca aagatgttga agaaggctgg 120 gaattggttg agaaccttgc tcaatcagat ggcaattaca acgaagactg tgataggacc gtcaaaggaa cagctgactc tgatgacaaa cacaggaaga agatcaaagc gctgaatgac 180 aagctggaca ggattattct cggccagcag aagcatgtgc acttccttgt tgatgacgag 240 300 cagtatcaag tcanagacgg ggagggtaac cagttggaag aagtcagcta catcaacaac 360 aaccagggtg gctacaaaag atacaacaac ttcaaaaacca acaatcccaa cctctcttac 420 cgcagcacca acgttgctaa ccctcaggat caagtgtatc ctccacagca acaacaaagt 480 ttcqttccta agcagcagtt ccaggggaac taccagcaac caccaccacc tgggtttgca cctcagcaaa cccaaggtcc tgctgctcct gatgctgaaa tgaaacagat ggtcaagcag 540 600 ctgctacagg gacaagcatc tagctcaatg gaaatggcta aaaaattatc taaattgcac 660 cataagctgg actgcagcta caatgacctg aatgccaaag tggaggcatt gaataccaaa 720 gtcagatact tggaaggcca atcagtatct acctctgtac caaaagttac aggacttcca 780 gggaagtcca tacagaatcc aaaagagtat gcaaccgctc acgccatcac catctgccat 840 gatcgagagc tgccaactcg acctgtcctt gatttcatca ctggggacaa tgatgttcaa gaagggaagg cttctactca ggttgtagtc tctgttgttg aattcaacca ttccgctggt 900 960 tctcgccatc tcactcaatc catctcggaa gaaaaggccg ccataatcga gagaatggta aaacgattca aacctactcc actaccctca cgtgctcttc cttggacatt caggaaagca 1020 1080 tggatggaga gatacaagtc tgttgcagag aagcagctag acgagattga agcagtgatg ccattgatgg aagttctcaa cctgattccc gatcctcaca aagatgtgag aaatttgata 1140 ctggaaagaa tcaagatgta tcacgattca gatgatgaaa gtgatgccac tccgtctcta 1200 gctgctgata agaggattgt tcaagagaag ttagaagatc ctggattgat acaaagggtt 1260 ttctgtgtca attccctaaa tgcatcttat gtcattgcag catttaaggt gtcaatccaa 1320 atgggtgtaa ttgctatcaa tcaggatatg atcaaagaat actaa
- (2) INFORMATION FOR SEQ ID NO:452:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..454
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585683
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met Leu Leu Asp Thr Ala Ser Asn Gly Asn Phe Gln Asn Lys Asp Val 10 Glu Glu Gly Trp Glu Leu Val Glu Asn Leu Ala Gln Ser Asp Gly Asn 25 Tyr Asn Glu Asp Cys Asp Arg Thr Val Lys Gly Thr Ala Asp Ser Asp 40 Asp Lys His Arg Lys Lys Ile Lys Ala Leu Asn Asp Lys Leu Asp Arg 55 Ile Ile Leu Gly Gln Gln Lys His Val His Phe Leu Val Asp Asp Glu 70 Gln Tyr Gln Val Xaa Asp Gly Glu Gly Asn Gln Leu Glu Glu Val Ser 85 90 Tyr Ile Asn Asn Asn Gln Gly Gly Tyr Lys Arg Tyr Asn Asn Phe Lys 105 Thr Asn Asn Pro Asn Leu Ser Tyr Arg Ser Thr Asn Val Ala Asn Pro 120 Gln Asp Gln Val Tyr Pro Pro Gln Gln Gln Ser Phe Val Pro Lys 135 Gln Gln Phe Gln Gly Asn Tyr Gln Gln Pro Pro Pro Gly Phe Ala 155 150 Pro Gln Gln Thr Gln Gly Pro Ala Ala Pro Asp Ala Glu Met Lys Gln 170 165 Met Val Lys Gln Leu Gln Gly Gln Ala Ser Ser Met Glu Met 185 Ala Lys Lys Leu Ser Lys Leu His His Lys Leu Asp Cys Ser Tyr Asn 200 Asp Leu Asn Ala Lys Val Glu Ala Leu Asn Thr Lys Val Arg Tyr Leu 220 215 Glu Gly Gln Ser Val Ser Thr Ser Val Pro Lys Val Thr Gly Leu Pro 230 235 Gly Lys Ser Ile Gln Asn Pro Lys Glu Tyr Ala Thr Ala His Ala Ile 250 245 Thr Ile Cys His Asp Arg Glu Leu Pro Thr Arg Pro Val Leu Asp Phe 265 260 Ile Thr Gly Asp Asn Asp Val Gln Glu Gly Lys Ala Ser Thr Gln Val 280 275 Val Val Ser Val Val Glu Phe Asn His Ser Ala Gly Ser Arg His Leu 300 295 Thr Gln Ser Ile Ser Glu Glu Lys Ala Ala Ile Ile Glu Arg Met Val 315 310 Lys Arg Phe Lys Pro Thr Pro Leu Pro Ser Arg Ala Leu Pro Trp Thr 325 330 Phe Arg Lys Ala Trp Met Glu Arg Tyr Lys Ser Val Ala Glu Lys Gln 340 345 Leu Asp Glu Ile Glu Ala Val Met Pro Leu Met Glu Val Leu Asn Leu 360 365 Ile Pro Asp Pro His Lys Asp Val Arg Asn Leu Ile Leu Glu Arg Ile 375 380 Lys Met Tyr His Asp Ser Asp Asp Glu Ser Asp Ala Thr Pro Ser Leu 390 395 Ala Ala Asp Lys Arg Ile Val Gln Glu Lys Leu Glu Asp Pro Gly Leu 405 410 Ile Gln Arg Val Phe Cys Val Asn Ser Leu Asn Ala Ser Tyr Val Ile 425 430 420 Ala Ala Phe Lys Val Ser Ile Gln Met Gly Val Ile Ala Ile Asn Gln 440 445 435 Asp Met Ile Lys Glu Tyr

450

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..281
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:
- Met Lys Gln Met Val Lys Gln Leu Leu Gln Gly Gln Ala Ser Ser 1 10 15
- Met Glu Met Ala Lys Lys Leu Ser Lys Leu His His Lys Leu Asp Cys 20 25 30
- Ser Tyr Asn Asp Leu Asn Ala Lys Val Glu Ala Leu Asn Thr Lys Val 35 40 45
- Arg Tyr Leu Glu Gly Gln Ser Val Ser Thr Ser Val Pro Lys Val Thr 50 60
- Gly Leu Pro Gly Lys Ser Ile Gln Asn Pro Lys Glu Tyr Ala Thr Ala 65 70 75 80
- His Ala Ile Thr Ile Cys His Asp Arg Glu Leu Pro Thr Arg Pro Val 85 90 95
- Leu Asp Phe Ile Thr Gly Asp Asn Asp Val Gln Glu Gly Lys Ala Ser 100 105 110
- Thr Gln Val Val Ser Val Val Glu Phe Asn His Ser Ala Gly Ser 115 120 125
- Arg His Leu Thr Gln Ser Ile Ser Glu Glu Lys Ala Ala Ile Ile Glu 130 135 140
- Pro Trp Thr Phe Arg Lys Ala Trp Met Glu Arg Tyr Lys Ser Val Ala 165 170 175
- Glu Lys Gln Leu Asp Glu Ile Glu Ala Val Met Pro Leu Met Glu Val 180 185 190
- Leu Asn Leu Ile Pro Asp Pro His Lys Asp Val Arg Asn Leu Ile Leu 195 200 205
- Glu Arg Ile Lys Met Tyr His Asp Ser Asp Asp Glu Ser Asp Ala Thr 210 215 220
- Pro Ser Leu Ala Ala Asp Lys Arg Ile Val Gln Glu Lys Leu Glu Asp 225 230 235 240
- Pro Gly Leu Ile Gln Arg Val Phe Cys Val Asn Ser Leu Asn Ala Ser 245 250 255
- Tyr Val Ile Ala Ala Phe Lys Val Ser Ile Gln Met Gly Val Ile Ala 260 265 270
- Ile Asn Gln Asp Met Ile Lys Glu Tyr 275 280
- (2) INFORMATION FOR SEQ ID NO:454:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 825 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..825
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585695
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

atggtgaaag aaactcgtct tggaatcact gcaaagaaag atgaagattt tgggaagtgg agaaagacca cactcaaggg tttgctccag aggttgcttg ggttacaaga gctggtggat aagaggacac agggacctcc ctttgaagcc gcgtgtatga ctcatggaga tgacaaaggt ttagtattcc ctcctaaagt ggcacctgtt caagttgttg taatccatgt tcccatcaaa

60 120

ggcgctgctg attatcaaga actttgtgat gcttgtgaag ctgttgaatc caccttgctt 300 ggggctggaa tccgtgctga agcagatata cgcgacaact attcttqcqq atggaaqtat 360 gcggatcaag aactaacggg tgttcctttg agaattgaaa ctggacctag agatttggcc 420 aatgatcagg tgaggatagt gacgcgtgac aatggagcta agatggatgt caagagaggg 480 gatttgattg aacaagttaa ggacttgcta gagaaaatcc agagtaacct ctatgatgtg 540 gcaaagagaa aggttgaaga atgtactcaa aaggttgaaa cttgggatga atttgtggaa 600 660 qctttgagcc aaaagaaact gattttagct ccatggtgtg ataaggttga agtggagaag qatqtgaaga ggcgtaccag aggtgatgaa acaggaggag gaggaggagg aggagctaag 720 actctatgta ctcctcttga gcagcctaaa ctaggagaag agactctatg ctttgcatca 780 ggaaagccag ccaagaagtg gagctactgg ggaagaagtt actaa

- (2) INFORMATION FOR SEQ ID NO:455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (B) TYPE: amino acid

(A) LENGTH: 274 amino acids

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..274
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585696 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455: Met Val Lys Glu Thr Arg Leu Gly Ile Thr Ala Lys Lys Asp Glu Asp 10 Phe Gly Lys Trp Arg Lys Thr Thr Leu Lys Gly Leu Leu Gln Arg Leu 20 25 Leu Gly Leu Gln Glu Leu Val Asp Lys Arg Thr Gln Gly Pro Pro Phe 40 Glu Ala Ala Cys Met Thr His Gly Asp Asp Lys Gly Leu Val Phe Pro 55 60 Pro Lys Val Ala Pro Val Gln Val Val Val Ile His Val Pro Ile Lys 75 Gly Ala Ala Asp Tyr Gln Glu Leu Cys Asp Ala Cys Glu Ala Val Glu 90 Ser Thr Leu Leu Gly Ala Gly Ile Arg Ala Glu Ala Asp Ile Arg Asp 105 110 Asn Tyr Ser Cys Gly Trp Lys Tyr Ala Asp Gln Glu Leu Thr Gly Val 120 125 115 Pro Leu Arg Ile Glu Thr Gly Pro Arg Asp Leu Ala Asn Asp Gln Val 135 140 130 Arg Ile Val Thr Arg Asp Asn Gly Ala Lys Met Asp Val Lys Arg Gly 155 150 Asp Leu Ile Glu Gln Val Lys Asp Leu Leu Glu Lys Ile Gln Ser Asn 165 170 Leu Tyr Asp Val Ala Lys Arg Lys Val Glu Glu Cys Thr Gln Lys Val 185 190 180 Glu Thr Trp Asp Glu Phe Val Glu Ala Leu Ser Gln Lys Lys Leu Ile 200 205 195 Leu Ala Pro Trp Cys Asp Lys Val Glu Val Glu Lys Asp Val Lys Arg 215 Arg Thr Arg Gly Asp Glu Thr Gly Gly Gly Gly Gly Gly Ala Lys 235 230 Thr Leu Cys Thr Pro Leu Glu Gln Pro Lys Leu Gly Glu Glu Thr Leu 250 245 Cys Phe Ala Ser Gly Lys Pro Ala Lys Lys Trp Ser Tyr Trp Gly Arg 270 265
- (2) INFORMATION FOR SEQ ID NO:456:

Ser Tyr

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..222
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585698
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:
- Met Thr His Gly Asp Asp Lys Gly Leu Val Phe Pro Pro Lys Val Ala 1 5 10 15
- Pro Val Gln Val Val Val Ile His Val Pro Ile Lys Gly Ala Ala Asp 20 25 30
- Tyr Gln Glu Leu Cys Asp Ala Cys Glu Ala Val Glu Ser Thr Leu Leu 35 40 45
- Gly Ala Gly Ile Arg Ala Glu Ala Asp Ile Arg Asp Asn Tyr Ser Cys
 50 55 60
- Gly Trp Lys Tyr Ala Asp Gln Glu Leu Thr Gly Val Pro Leu Arg Ile 65 70 75 80
- Glu Thr Gly Pro Arg Asp Leu Ala Asn Asp Gln Val Arg Ile Val Thr 85 90 95
- Arg Asp Asn Gly Ala Lys Met Asp Val Lys Arg Gly Asp Leu Ile Glu 100 105 110
- Gln Val Lys Asp Leu Leu Glu Lys Ile Gln Ser Asn Leu Tyr Asp Val 115 120 125
- Ala Lys Arg Lys Val Glu Glu Cys Thr Gln Lys Val Glu Thr Trp Asp 130 135 140
- Glu Phe Val Glu Ala Leu Ser Gln Lys Lys Leu Ile Leu Ala Pro Trp 145 150 155 160
- Cys Asp Lys Val Glu Val Glu Lys Asp Val Lys Arg Arg Thr Arg Gly 165 170 175
- Asp Glu Thr Gly Gly Gly Gly Gly Gly Ala Lys Thr Leu Cys Thr 180 185 190
- Pro Leu Glu Gln Pro Lys Leu Gly Glu Glu Thr Leu Cys Phe Ala Ser 195 200 205
- Gly Lys Pro Ala Lys Lys Trp Ser Tyr Trp Gly Arg Ser Tyr 210 215 220
- (2) INFORMATION FOR SEQ ID NO:457:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..357
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585732
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:
- (2) INFORMATION FOR SEQ ID NO:458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585733
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:
- Val Ala Glu Arg Ala Leu Phe Leu Trp Asn Asn Glu His Ile Val Gly
 1 5 10 15
- Leu Ile Ala Gln Asn Arg Ser Val Ile Leu Pro Ile Ile Tyr Pro Thr
 20 25 30
- Leu Glu Lys Asn Ile Gln Ser His Trp Asn Gln Ala Val His Gly Leu $35 \hspace{1cm} 40 \hspace{1cm} 45$
- Thr Thr Asn Ile Lys Lys Met Phe Met Glu Met Asp Pro Glu Leu Phe 50 60
- Glu Glu Cys Gln Arg Gln Tyr Glu Glu Lys Gln Ala Lys Ser Lys Glu 65 70 75 80
- Val Glu Glu Gln Pro Ile Tyr Met Glu Glu Ile Ser Arg Ser Ser Gly 85 90 95
- Gly Ala Arg Trp Arg Arg Arg Arg Arg Ser Tyr Asp His Phe Leu $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Asp Arg Ser Lys Arg Val

- (2) INFORMATION FOR SEQ ID NO:459:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585734
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:
- Met Phe Met Glu Met Asp Pro Glu Leu Phe Glu Glu Cys Gln Arg Gln 1 5 10 15
- Tyr Glu Glu Lys Gln Ala Lys Ser Lys Glu Val Glu Glu Gln Pro Ile
 20 25 30
- Tyr Met Glu Glu Ile Ser Arg Ser Ser Gly Gly Ala Arg Trp Arg Arg 35 40 45
- Arg Arg Arg Ser Tyr Asp His Phe Leu Asp Arg Ser Lys Arg Val 50 55 60
- (2) INFORMATION FOR SEQ ID NO:460:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585735
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:
- Met Glu Met Asp Pro Glu Leu Phe Glu Glu Cys Gln Arg Gln Tyr Glu 1 5 10 15
- Glu Lys Gln Ala Lys Ser Lys Glu Val Glu Glu Gln Pro Ile Tyr Met
 20 25 30
- Glu Glu Ile Ser Arg Ser Ser Gly Gly Ala Arg Trp Arg Arg Arg

Client Docket No. 80146.003 40 35 Arg Arg Ser Tyr Asp His Phe Leu Asp Arg Ser Lys Arg Val 55 (2) INFORMATION FOR SEQ ID NO:461: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 818 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..818 (D) OTHER INFORMATION: / Ceres Seq. ID 1585740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461: ctttagcttt cactaacctt cttccttcac agtgaatcaa tggcgtcttc ttctccaatc aactetttge ageteaactt ettettet acateceaac tecaaactet cacattetet

120 ttcagctaaa ttatcctcca aagcaaatgt ttccgtccaa tttctgggaa agaaacagtc 180 tecgettete tecteaacte egagatttet caetgttate geeatggete caectaaace 240 300 cggaggcaaa gctaaaaaag ttgtgggagt tatcaaactt gctttagagg cgggaaaagc 360 aactccggca ccaccggttg gtccggcgct tggttctaag ggagttaaca ttatggcttt ttgcaaggat tataatgcaa gaactgctga taaagctggt tatatcattc ctgttgaaat 420 cactgtette gatgataaga getteaegtt tatteteaag acceegeetg etteggtttt 480 540 gttgcttaaa gctgcaggtg ttgagaaggg atcaaaagat ccacagcaag ataaagttgg 600 ggtgataaca atagaccagc tacgcacaat tgcagcagag aagctacccg acctgaactg 660 cacgaccatt gaatccgcta tgagaatcat tgcaggaact gcagctaaca tggggataga 720 cattgaccct ccgattcttg aacccaaaaa gaaagcagtt ttattgtaaa agcctggttg 780 gtagtttcta ttccataatg ccttattcgt ttcaaagtgt aattttccaa catgacgctt aagagagttc gatataatga tgcaacatgt atgtgttt

- (2) INFORMATION FOR SEQ ID NO:462:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

150

- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462: Met Ala Pro Pro Lys Pro Gly Gly Lys Ala Lys Lys Val Val Gly Val 10 5 Ile Lys Leu Ala Leu Glu Ala Gly Lys Ala Thr Pro Ala Pro Pro Val 25 Gly Pro Ala Leu Gly Ser Lys Gly Val Asn Ile Met Ala Phe Cys Lys 45 40 Asp Tyr Asn Ala Arg Thr Ala Asp Lys Ala Gly Tyr Ile Ile Pro Val 60 55 Glu Ile Thr Val Phe Asp Asp Lys Ser Phe Thr Phe Ile Leu Lys Thr 75 70 Pro Pro Ala Ser Val Leu Leu Leu Lys Ala Ala Gly Val Glu Lys Gly 90 Ser Lys Asp Pro Gln Gln Asp Lys Val Gly Val Ile Thr Ile Asp Gln 110 105 100 Leu Arg Thr Ile Ala Ala Glu Lys Leu Pro Asp Leu Asn Cys Thr Thr 125 120 115 Ile Glu Ser Ala Met Arg Ile Ile Ala Gly Thr Ala Ala Asn Met Gly 140 135 Ile Asp Ile Asp Pro Pro Ile Leu Glu Pro Lys Lys Ala Val Leu

Leu

- (2) INFORMATION FOR SEQ ID NO:463:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585742
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met Ala Phe Cys Lys Asp Tyr Asn Ala Arg Thr Ala Asp Lys Ala Gly $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Tyr Ile Ile Pro Val Glu Ile Thr Val Phe Asp Asp Lys Ser Phe Thr 20 25 30

Phe Ile Leu Lys Thr Pro Pro Ala Ser Val Leu Leu Leu Lys Ala Ala 35 40 45

Gly Val Glu Lys Gly Ser Lys Asp Pro Gln Gln Asp Lys Val Gly Val 50 60

Ile Thr Ile Asp Gln Leu Arg Thr Ile Ala Ala Glu Lys Leu Pro Asp 65 70 75 80

Leu Asn Cys Thr Thr Ile Glu Ser Ala Met Arg Ile Ile Ala Gly Thr 85 90 95

Lys Lys Ala Val Leu Leu

115

- (2) INFORMATION FOR SEQ ID NO:464:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 866 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..866
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585784
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

gactagaaga agtgatggat tttcttgaag aagcatttcc agatattgac attgctatgg cacatggaaa gcaatactcg aaacaactag aggaaaccat ggagagattt gcgcaaggaa 120 agatcaaaat cctcatatgt actaatattg ttgaaagcgg acttgatatt caaaatgcaa 180 240 ataccataat cattcaggat gttcaacaat ttgggctcgc tcagttgtac cagttgcgtg gaagggttgg tcgggcagat aaagaagctc atgcctacct attttatccc gataaatcgc 300 tgctctctga tcaagcactg gaaaggctta gcgctcttga agagtgccgt gaacttggac 360 420 aaggetteca acttgeagag aaggatatgg gtataagagg ttttgggaca atetttggag aacaacagac gggggatgtt ggaaatgtcg gtatcgatct cttctttgaa atgctttttg 480 agagtetete caaggtggag gaacteegta tttttteggt tecatatgae etegtgaaga 540 ttgacataaa tataaatccc cggctaccct cggagtatgt aaattacctg gaaaatccga 600 tggagatcat tcatgaagct gaaaaagcag cagagaaaga tatgtggagt ctaatgcaat 660 720 ttacaqaqaa cctqcqtcgc caatatggga aagagcctta ctccatggaa atcattttaa agaagctgta tgtgagacgc atggcggctg atcttggagt aaacagaatt tatgcatcag 780 gcaagatggt tgtcatgaaa acaaatatga gtaagaaggt gttcaagctg atcacagatt 840 ccatgacttg tgacgtttac cgaaga

- (2) INFORMATION FOR SEQ ID NO:465:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..288
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585785
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:
- Leu Glu Glu Val Met Asp Phe Leu Glu Glu Ala Phe Pro Asp Ile Asp

 1 10 15
- Ile Ala Met Ala His Gly Lys Gln Tyr Ser Lys Gln Leu Glu Glu Thr 20 25 30
- Met Glu Arg Phe Ala Gln Gly Lys Ile Lys Ile Leu Ile Cys Thr Asn 35 40 45
- Ile Val Glu Ser Gly Leu Asp Ile Gln Asn Ala Asn Thr Ile Ile Ile 50 55
- Gln Asp Val Gln Gln Phe Gly Leu Ala Gln Leu Tyr Gln Leu Arg Gly 65 70 75 80
- Arg Val Gly Arg Ala Asp Lys Glu Ala His Ala Tyr Leu Phe Tyr Pro
- Asp Lys Ser Leu Leu Ser Asp Gln Ala Leu Glu Arg Leu Ser Ala Leu
- 100 105 110 Glu Glu Cys Arg Glu Leu Gly Gln Gly Phe Gln Leu Ala Glu Lys Asp
- 115 120 125

 Met Gly Ile Arg Gly Phe Gly Thr Ile Phe Gly Glu Gln Gln Thr Gly
- 130 135 140
 Asp Val Gly Asn Val Gly Ile Asp Leu Phe Phe Glu Met Leu Phe Glu
- 145 150 155 160 Ser Leu Ser Lys Val Glu Glu Leu Arg Ile Phe Ser Val Pro Tyr Asp
- 165 170 175 Leu Val Lys Ile Asp Ile Asn Ile Asn Pro Arg Leu Pro Ser Glu Tyr
- 180 185 190
 Val Asn Tyr Leu Glu Asn Pro Met Glu Ile Ile His Glu Ala Glu Lys
- 195 200 205 Ala Ala Glu Lys Asp Met Trp Ser Leu Met Gln Phe Thr Glu Asn Leu
- 210 215 220
 Arg Arg Gln Tyr Gly Lys Glu Pro Tyr Ser Met Glu Ile Ile Leu Lys
- 225 230 235 240 Lys Leu Tyr Val Arg Arg Met Ala Ala Asp Leu Gly Val Asn Arg Ile
- 245 250 255

 Tyr Ala Ser Gly Lys Met Val Val Met Lys Thr Asn Met Ser Lys Lys 260 265 270
- Val Phe Lys Leu Ile Thr Asp Ser Met Thr Cys Asp Val Tyr Arg Arg 275 280 285
- (2) INFORMATION FOR SEQ ID NO:466:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..284
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585786
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:
- Met Asp Phe Leu Glu Glu Ala Phe Pro Asp Ile Asp Ile Ala Met Ala 1 5 10 15 His Gly Lys Gln Tyr Ser Lys Gln Leu Glu Glu Thr Met Glu Arg Phe

25 20 Ala Gln Gly Lys Ile Lys Ile Leu Ile Cys Thr Asn Ile Val Glu Ser 40 Gly Leu Asp Ile Gln Asn Ala Asn Thr Ile Ile Ile Gln Asp Val Gln 55 Gln Phe Gly Leu Ala Gln Leu Tyr Gln Leu Arg Gly Arg Val Gly Arg 70 Ala Asp Lys Glu Ala His Ala Tyr Leu Phe Tyr Pro Asp Lys Ser Leu 90 Leu Ser Asp Gln Ala Leu Glu Arg Leu Ser Ala Leu Glu Glu Cys Arg 100 105 Glu Leu Gly Gln Gly Phe Gln Leu Ala Glu Lys Asp Met Gly Ile Arg 120 Gly Phe Gly Thr Ile Phe Gly Glu Gln Gln Thr Gly Asp Val Gly Asn 140 135 Val Gly Ile Asp Leu Phe Phe Glu Met Leu Phe Glu Ser Leu Ser Lys 150 155 Val Glu Glu Leu Arg Ile Phe Ser Val Pro Tyr Asp Leu Val Lys Ile 170 165 Asp Ile Asn Ile Asn Pro Arg Leu Pro Ser Glu Tyr Val Asn Tyr Leu 180 185 Glu Asn Pro Met Glu Ile Ile His Glu Ala Glu Lys Ala Ala Glu Lys 195 200 Asp Met Trp Ser Leu Met Gln Phe Thr Glu Asn Leu Arg Arg Gln Tyr 215 220 Gly Lys Glu Pro Tyr Ser Met Glu Ile Ile Leu Lys Lys Leu Tyr Val 235 230 Arg Arg Met Ala Ala Asp Leu Gly Val Asn Arg Ile Tyr Ala Ser Gly 245 250 Lys Met Val Val Met Lys Thr Asn Met Ser Lys Lys Val Phe Lys Leu 260 265 Ile Thr Asp Ser Met Thr Cys Asp Val Tyr Arg Arg 275 280

- (2) INFORMATION FOR SEQ ID NO:467:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..270
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585787
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:
- Met Ala His Gly Lys Gln Tyr Ser Lys Gln Leu Glu Glu Thr Met Glu

 1 5 10 15
- Arg Phe Ala Gln Gly Lys Ile Lys Ile Leu Ile Cys Thr Asn Ile Val 20 25 30
- Glu Ser Gly Leu Asp Ile Gln Asn Ala Asn Thr Ile Ile Ile Gln Asp 35 40 45
- Val Gln Gln Phe Gly Leu Ala Gln Leu Tyr Gln Leu Arg Gly Arg Val 50 60
- Gly Arg Ala Asp Lys Glu Ala His Ala Tyr Leu Phe Tyr Pro Asp Lys 65 70 75 80
- Ser Leu Leu Ser Asp Gln Ala Leu Glu Arg Leu Ser Ala Leu Glu Glu 85 90 95
- Cys Arg Glu Leu Gly Gln Gly Phe Gln Leu Ala Glu Lys Asp Met Gly $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$
- Ile Arg Gly Phe Gly Thr Ile Phe Gly Glu Gln Gln Thr Gly Asp Val

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Gly Asn Val Gly Ile Asp Leu Phe Phe Glu Met Leu Phe Glu Ser Leu
                       135
                                            140
Ser Lys Val Glu Glu Leu Arg Ile Phe Ser Val Pro Tyr Asp Leu Val
                   150
                                       155
Lys Ile Asp Ile Asn Ile Asn Pro Arg Leu Pro Ser Glu Tyr Val Asn
               165
                                   170
Tyr Leu Glu Asn Pro Met Glu Ile Ile His Glu Ala Glu Lys Ala Ala
                               185
           180
Glu Lys Asp Met Trp Ser Leu Met Gln Phe Thr Glu Asn Leu Arg Arg
                           200
       195
Gln Tyr Gly Lys Glu Pro Tyr Ser Met Glu Ile Ile Leu Lys Lys Leu
                                           220
                       215
   210
Tyr Val Arg Arg Met Ala Ala Asp Leu Gly Val Asn Arg Ile Tyr Ala
                                       235
                   230
Ser Gly Lys Met Val Val Met Lys Thr Asn Met Ser Lys Lys Val Phe
                                   250
               245
Lys Leu Ile Thr Asp Ser Met Thr Cys Asp Val Tyr Arg Arg
                              265
           260
(2) INFORMATION FOR SEQ ID NO:468:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 519 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..519
          (D) OTHER INFORMATION: / Ceres Seq. ID 1585887
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:
atgcctttcc tacctccact aaagcctcca accgagttgt atctaggaat ccaattgcca
                                                                      120
aaccccataa gcatacttgt caactacctc ccagtcagcc aaactcccat agagacgcta
                                                                      180
gggaacttag tctacacttg tgacatcaac acccttgcaa ttgatgaatt catgacgtgg
                                                                      240
ccqactttqc tccaaccgga ttctaccttc cgcccttact tcgagctgct gctagaacgt
                                                                      300
ggaccaatcc cggcggttta ccttgaaggt gttcgccaag cgagcaactt cgtcacagta
gctcagggcc ttttgctcat gacaacggtc gcattttctg atccctttgc ttgctttgcc
                                                                      360
                                                                      420
accggtttgt tccttacgtg taccggtaat cacttggatt tcctcccaat cagcgagaag
                                                                      480
ttctqqqaaa tqacactcac ccttqaagca ggccacacgg ttagagagat ggtgatgtat
cacatcagcc agettcacac taaggetget egecactag
(2) INFORMATION FOR SEQ ID NO:469:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 172 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..172
          (D) OTHER INFORMATION: / Ceres Seq. ID 1585888
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:
Met Pro Phe Leu Pro Pro Leu Lys Pro Pro Thr Glu Leu Tyr Leu Gly
               5
                                    10
Ile Gln Leu Pro Asn Pro Ile Ser Ile Leu Val Asn Tyr Leu Pro Val
                                25
            20
Ser Gln Thr Pro Ile Glu Thr Leu Gly Asn Leu Val Tyr Thr Cys Asp
                            40
Ile Asn Thr Leu Ala Ile Asp Glu Phe Met Thr Trp Pro Thr Leu Leu
                                            60
                        5.5
Gln Pro Asp Ser Thr Phe Arg Pro Tyr Phe Glu Leu Leu Glu Arg
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420

480

540

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Page 293
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Gly Pro Ile Pro Ala Val Tyr Leu Glu Gly Val Arg Gln Ala Ser Asn
Phe Val Thr Val Ala Gln Gly Leu Leu Leu Met Thr Thr Val Ala Phe
                                105
                                                    110
            100
Ser Asp Pro Phe Ala Cys Phe Ala Thr Gly Leu Phe Leu Thr Cys Thr
                            120
        115
Gly Asn His Leu Asp Phe Leu Pro Ile Ser Glu Lys Phe Trp Glu Met
                                            140
                        135
Thr Leu Thr Leu Glu Ala Gly His Thr Val Arg Glu Met Val Met Tyr
                   150
                                        155
His Ile Ser Gln Leu His Thr Lys Ala Ala Arg His
                                    170
               165
(2) INFORMATION FOR SEQ ID NO:470:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 115 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..115
          (D) OTHER INFORMATION: / Ceres Seq. ID 1585890
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:
Met Thr Trp Pro Thr Leu Leu Gln Pro Asp Ser Thr Phe Arg Pro Tyr
                                    10
Phe Glu Leu Leu Glu Arg Gly Pro Ile Pro Ala Val Tyr Leu Glu
            20
                                25
                                                     30
Gly Val Arg Gln Ala Ser Asn Phe Val Thr Val Ala Gln Gly Leu Leu
                                                 45
                            40
Leu Met Thr Thr Val Ala Phe Ser Asp Pro Phe Ala Cys Phe Ala Thr
                                             60
                        55
Gly Leu Phe Leu Thr Cys Thr Gly Asn His Leu Asp Phe Leu Pro Ile
                                        75
                    70
Ser Glu Lys Phe Trp Glu Met Thr Leu Thr Leu Glu Ala Gly His Thr
                                    90
                8.5
Val Arg Glu Met Val Met Tyr His Ile Ser Gln Leu His Thr Lys Ala
                                105
                                                     110
Ala Arg His
        115
(2) INFORMATION FOR SEQ ID NO:471:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 678 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..678
           (D) OTHER INFORMATION: / Ceres Seq. ID 1585950
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:
gaagacttaa aatctttgcg tgcaaaaatc gctatgctgg aggaggaatt gcgtaaatct
                                                                        60
                                                                        120
cgacaagatt cttctgagta tcaccacctt gtcaggaatc ttgagaatga ggtaaaagat
ctgaaagatc aggaacaaca agggaagcaa aagacaacta aagtaatctc ggaccttctc
                                                                        180
atatctgttt ccaaaactga gagacaagaa gcaagaacga aagtcagaaa tgaatctttg
                                                                        240
cgattaggca gtgttggtgt tctcaggaca ggaacgatca tagctgagac atgggaggac
                                                                        300
```

ggacaaatgt taaaagatct gaatgctcaa cttagacaat tgctggaaac caaggaggct

attgagagac aaagaaagtt acttaagaaa cgacaaaatg gtgataagaa tgacggaact

gacacagaat caggagcaca ggaggaagat atcatccctg acgaggttta caagtctcgt

cttactagta ttaagcggga agaggaagct gttttgcgtg agagagaaag gtacacatta

gagaaggggc tacttatgag ggagatgaaa cgcatacgag atgaagatgg ttctcgtttc 600 aaccatttcc cagttttgaa tagccgctat gctcttctaa atcttcttgg taaaggcgga 660 tttagtgaag tctataag

- (2) INFORMATION FOR SEQ ID NO:472:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..226
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585951
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Glu Asp Leu Lys Ser Leu Arg Ala Lys Ile Ala Met Leu Glu Glu Glu 1 5 10 15

Leu Arg Lys Ser Arg Gln Asp Ser Ser Glu Tyr His His Leu Val Arg 20 25 30

Asn Leu Glu Asn Glu Val Lys Asp Leu Lys Asp Gln Glu Gln Gly 35 40 45

Lys Gln Lys Thr Thr Lys Val Ile Ser Asp Leu Leu Ile Ser Val Ser 50 55 60

Lys Thr Glu Arg Gln Glu Ala Arg Thr Lys Val Arg Asn Glu Ser Leu 65 70 75 80

Arg Leu Gly Ser Val Gly Val Leu Arg Thr Gly Thr Ile Ile Ala Glu 85 90 95

Thr Trp Glu Asp Gly Gln Met Leu Lys Asp Leu Asn Ala Gln Leu Arg 100 105 110

Gln Leu Leu Glu Thr Lys Glu Ala Ile Glu Arg Gln Arg Lys Leu Leu 115 120 125

Lys Lys Arg Gln Asn Gly Asp Lys Asn Asp Gly Thr Asp Thr Glu Ser 130 135 140

Gly Ala Gln Glu Glu Asp Ile Ile Pro Asp Glu Val Tyr Lys Ser Arg 145 150 155 160

Leu Thr Ser Ile Lys Arg Glu Glu Glu Ala Val Leu Arg Glu Arg Glu 165 170 175

Arg Tyr Thr Leu Glu Lys Gly Leu Leu Met Arg Glu Met Lys Arg Ile 180 185 190

Arg Asp Glu Asp Gly Ser Arg Phe Asn His Phe Pro Val Leu Asn Ser 195 200 205

Arg Tyr Ala Leu Leu Asn Leu Leu Gly Lys Gly Gly Phe Ser Glu Val 210 215 220

Tyr Lys 225

- (2) INFORMATION FOR SEQ ID NO:473:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..215
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met Leu Glu Glu Glu Leu Arg Lys Ser Arg Gln Asp Ser Ser Glu Tyr 1 5 10 15

His His Leu Val Arg Asn Leu Glu Asn Glu Val Lys Asp Leu Lys Asp 20 25 30

Gln Glu Gln Gln Gly Lys Gln Lys Thr Thr Lys Val Ile Ser Asp Leu Leu Ile Ser Val Ser Lys Thr Glu Arg Gln Glu Ala Arg Thr Lys Val 55 Arg Asn Glu Ser Leu Arg Leu Gly Ser Val Gly Val Leu Arg Thr Gly 70 Thr Ile Ile Ala Glu Thr Trp Glu Asp Gly Gln Met Leu Lys Asp Leu 90 Asn Ala Gln Leu Arg Gln Leu Leu Glu Thr Lys Glu Ala Ile Glu Arg 105 Gln Arg Lys Leu Leu Lys Lys Arg Gln Asn Gly Asp Lys Asn Asp Gly 120 Thr Asp Thr Glu Ser Gly Ala Gln Glu Glu Asp Ile Ile Pro Asp Glu 135 140 Val Tyr Lys Ser Arg Leu Thr Ser Ile Lys Arg Glu Glu Glu Ala Val 155 150 Leu Arg Glu Arg Glu Arg Tyr Thr Leu Glu Lys Gly Leu Leu Met Arg 170 165 Glu Met Lys Arg Ile Arg Asp Glu Asp Gly Ser Arg Phe Asn His Phe 185 180 Pro Val Leu Asn Ser Arg Tyr Ala Leu Leu Asn Leu Leu Gly Lys Gly 195 200

Gly Phe Ser Glu Val Tyr Lys 210 215

- (2) INFORMATION FOR SEQ ID NO: 474:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585953
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Leu Lys Asp Leu Asn Ala Gln Leu Arg Gln Leu Leu Glu Thr Lys

1 10 15

Glu Ala Ile Glu Arg Gln Arg Lys Leu Leu Lys Lys Arg Gln Asn Gly 20 25 30

Asp Lys Asn Asp Gly Thr Asp Thr Glu Ser Gly Ala Gln Glu Glu Asp 35 40 45

Ile Ile Pro Asp Glu Val Tyr Lys Ser Arg Leu Thr Ser Ile Lys Arg 50 55 60

Glu Glu Glu Ala Val Leu Arg Glu Arg Glu Arg Tyr Thr Leu Glu Lys 70 75 80 Gly Leu Leu Met Arg Glu Met Lys Arg Ile Arg Asp Glu Asp Gly Ser

85 90 95
Arg Phe Asn His Phe Pro Val Leu Asn Ser Arg Tyr Ala Leu Leu Asn

Leu Leu Gly Lys Gly Gly Phe Ser Glu Val Tyr Lys
115 120

- (2) INFORMATION FOR SEQ ID NO:475:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

(B) LOCATION: 1..1596

(D) OTHER INFORMATION: / Ceres Seq. ID 1586052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475: atgtcgaaag cttggggtgg aattggaatt ggagcttggg ctgatgaagc agagcgtgcc 60 gatgaagaac aagcggcgga agctactgct gcgacggcgg atacacagag ttttcctagc 120 ctgagagagg ctgctgctgc gactgcgact agtggtaagt ctaggaagat gaagaagatg 180 240 agtttatctq agtttactac aggtgcttat acagcacctg gaggtagaaa ctctgttgga 300 ttgactcagc aagagattct tcaattacct actggtccta gacaacgttc cgaggaggaa 360 atgcaacctq qtcqtttaqq cqqtqqqttt tcatcttatq qtqqtcqttc tggtggaaga 420 attqqqaqaq atcqaqatqa ttctqatqgc tcttqqaqtq gtqqtqqtqq tqgtqqtana 480 agragacett atggtggtgg atttgatgat gataggaggg ggaatcagte tagggttteg 540 gattttcctc aaccttctag agctgatgag gttgatgatt gggggaaaga gaagaaacca 600 cttccctctt ttgatcaagg acgacaaggt cgttacagtg gcggtggtgg tggttttgga 660 ggtggtggaa gtggttttgg aggcggtggt ggtggaggtg gaggattatc tagagctgat gatgttgata attggggtgc agggaaaagg caagcaccgg ttagatcatc tacatttggg 720 780 tcgagttttg gtgattcagg tcaggaagaa cgtcgtcgtt tggttttgga accacggaag gttgagtcag gagggagtga gactccacct gttgttgaga agacgagtaa gccgaatcca 840 900 tttggggcag ctagaccgag ggaggatgtt ttggcggaga aaggtttgga ttggaagaag 960 attgactcag atattgaggc taagaaagga agttctcaaa caagtaggcc aacgagtgca 1020 cattctagta gaccttctag tgctcaatct aacaggtctg agagttcagg attgaataat qtqqtqaaac cqaqaccaaa qqtqaatcct tttqqcgatq caaagcctcg agaagtgttg 1080 ttagaggaac aagggaagga ttggcgtaag atggatttgg aactcgagca tcgcagggtt 1140 qacaqqcctq aaacaqaaqa agagaagatg ttgaaagaag agattgaaga gctaaggaaa 1200 aaactcqaqa aqqaatccat tgctccagag atcaaggaat ctgatcaaga acctggcagt 1260 1320 aataataatc acaatgatgt accagaaata atacgtggga aagagaaaga tctggaaata 1380 ctaacccgtg aattggacga caaagtcagg ttcaggcaga aaccagttga gaggcccggg 1440 tctggtgcag gtagaaccgg aacatattca gaaagaacac attcccgggc tggctcaatt 1500 gatgaaacca ggagttttga atctacagag agacccagat cacgtggtgc cgtcgatgcc

- (2) INFORMATION FOR SEQ ID NO: 476:
 - (i) SEQUENCE CHARACTERISTICS:

ttcagcaaca ggtcttcctc tagggaagga tggtaa

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..531
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586053

tgggttagac cagccgatga gcagcgaaga aactttcaag gaagcaaaga gcgcggattc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476: Met Ser Lys Ala Trp Gly Gly Ile Gly Ile Gly Ala Trp Ala Asp Glu

1 5 10 15
Ala Glu Arg Ala Asp Glu Glu Gln Ala Ala Glu Ala Thr Ala Ala Thr
20 25 30

Ala Asp Thr Gln Ser Phe Pro Ser Leu Arg Glu Ala Ala Ala Thr 35 40 45

Ala Thr Ser Gly Lys Ser Arg Lys Met Lys Lys Met Ser Leu Ser Glu 50 60

Phe Thr Thr Gly Ala Tyr Thr Ala Pro Gly Gly Arg Asn Ser Val Gly 65 70 75 80

Leu Thr Gln Gln Glu Ile Leu Gln Leu Pro Thr Gly Pro Arg Gln Arg 85 90 95 Ser Glu Glu Glu Met Gln Pro Gly Arg Leu Gly Gly Gly Phe Ser Ser

100 105 110

Tyr Gly Gly Arg Ser Gly Gly Arg Ile Gly Arg Asp Arg Asp Ser
115 120 125

Asp Gly Ser Trp Ser Gly Gly Gly Gly Gly Kaa Xaa Arg Pro Tyr 130 135 140 Gly Gly Gly Phe Asp Asp Asp Arg Gly Asn Gln Ser Arg Val Ser

155 145 150 Asp Phe Pro Gln Pro Ser Arg Ala Asp Glu Val Asp Asp Trp Gly Lys 165 170 175 Glu Lys Lys Pro Leu Pro Ser Phe Asp Gln Gly Arg Gln Gly Arg Tyr 185 180 Ser Gly Gly Gly Gly Phe Gly Gly Gly Gly Ser Gly Phe Gly Gly 200 Gly Gly Gly Gly Gly Gly Leu Ser Arg Ala Asp Asp Val Asp Asn 215 Trp Gly Ala Gly Lys Arg Gln Ala Pro Val Arg Ser Ser Thr Phe Gly 235 240 230 Ser Ser Phe Gly Asp Ser Gly Gln Glu Glu Arg Arg Leu Val Leu 250 255 245 Glu Pro Arg Lys Val Glu Ser Gly Gly Ser Glu Thr Pro Pro Val Val 265 260 Glu Lys Thr Ser Lys Pro Asn Pro Phe Gly Ala Ala Arg Pro Arg Glu 280 275 Asp Val Leu Ala Glu Lys Gly Leu Asp Trp Lys Lys Ile Asp Ser Asp 300 290 295 Ile Glu Ala Lys Lys Gly Ser Ser Gln Thr Ser Arg Pro Thr Ser Ala 310 315 His Ser Ser Arg Pro Ser Ser Ala Gln Ser Asn Arg Ser Glu Ser Ser 325 330 Gly Leu Asn Asn Val Val Lys Pro Arg Pro Lys Val Asn Pro Phe Gly 345 Asp Ala Lys Pro Arg Glu Val Leu Leu Glu Glu Gln Gly Lys Asp Trp 360 365 Arg Lys Met Asp Leu Glu Leu Glu His Arg Arg Val Asp Arg Pro Glu 375 380 Thr Glu Glu Glu Lys Met Leu Lys Glu Glu Ile Glu Glu Leu Arg Lys 395 400 390 Lys Leu Glu Lys Glu Ser Ile Ala Pro Glu Ile Lys Glu Ser Asp Gln 405 410 415 Glu Pro Gly Ser Asn Asn His Asn Asp Val Pro Glu Ile Ile Arg 420 425 Gly Lys Glu Lys Asp Leu Glu Ile Leu Thr Arg Glu Leu Asp Asp Lys 435 440 Val Arg Phe Arg Gln Lys Pro Val Glu Arg Pro Gly Ser Gly Ala Gly 450 455 460 Arg Thr Gly Thr Tyr Ser Glu Arg Thr His Ser Arg Ala Gly Ser Ile 470 475 Asp Glu Thr Arg Ser Phe Glu Ser Thr Glu Arg Pro Arg Ser Arg Gly 485 490 495 Ala Val Asp Ala Trp Val Arg Pro Ala Asp Glu Gln Arg Asp Phe 500 505 510 Gln Gly Ser Lys Glu Arg Gly Phe Phe Ser Asn Arg Ser Ser Ser Arg 520 515 Glu Gly Trp 530

- (2) INFORMATION FOR SEQ ID NO:477:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..475
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586055
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Lys Lys Met Ser Leu Ser Glu Phe Thr Thr Gly Ala Tyr Thr Ala 10 Pro Gly Gly Arg Asn Ser Val Gly Leu Thr Gln Glu Ile Leu Gln Leu Pro Thr Gly Pro Arg Gln Arg Ser Glu Glu Met Gln Pro Gly 40 Arg Leu Gly Gly Gly Phe Ser Ser Tyr Gly Gly Arg Ser Gly Gly Arg 55 Ile Gly Arg Asp Arg Asp Asp Ser Asp Gly Ser Trp Ser Gly Gly Gly Gly Gly Xaa Xaa Arg Pro Tyr Gly Gly Gly Phe Asp Asp Asp Arg 8.5 Arg Gly Asn Gln Ser Arg Val Ser Asp Phe Pro Gln Pro Ser Arg Ala 105 100 Asp Glu Val Asp Asp Trp Gly Lys Glu Lys Lys Pro Leu Pro Ser Phe 120 115 Asp Gln Gly Arg Gln Gly Arg Tyr Ser Gly Gly Gly Gly Phe Gly 135 Gly Gly Gly Ser Gly Phe Gly Gly Gly Gly Gly Gly Gly Gly Leu 150 155 Ser Arg Ala Asp Asp Val Asp Asn Trp Gly Ala Gly Lys Arg Gln Ala 170 165 Pro Val Arg Ser Ser Thr Phe Gly Ser Ser Phe Gly Asp Ser Gly Gln 185 180 Glu Glu Arg Arg Arg Leu Val Leu Glu Pro Arg Lys Val Glu Ser Gly 200 Gly Ser Glu Thr Pro Pro Val Val Glu Lys Thr Ser Lys Pro Asn Pro 220 215 Phe Gly Ala Ala Arg Pro Arg Glu Asp Val Leu Ala Glu Lys Gly Leu 230 235 Asp Trp Lys Lys Ile Asp Ser Asp Ile Glu Ala Lys Lys Gly Ser Ser 250 Gln Thr Ser Arg Pro Thr Ser Ala His Ser Ser Arg Pro Ser Ser Ala 265 Gln Ser Asn Arg Ser Glu Ser Ser Gly Leu Asn Asn Val Val Lys Pro 280 285 Arg Pro Lys Val Asn Pro Phe Gly Asp Ala Lys Pro Arg Glu Val Leu 300 295 Leu Glu Glu Gln Gly Lys Asp Trp Arg Lys Met Asp Leu Glu Leu Glu 310 315 His Arg Arg Val Asp Arg Pro Glu Thr Glu Glu Lys Met Leu Lys 325 330 Glu Glu Ile Glu Glu Leu Arg Lys Lys Leu Glu Lys Glu Ser Ile Ala 340 345 Pro Glu Ile Lys Glu Ser Asp Gln Glu Pro Gly Ser Asn Asn Asn His 360 Asn Asp Val Pro Glu Ile Ile Arg Gly Lys Glu Lys Asp Leu Glu Ile 375 Leu Thr Arg Glu Leu Asp Asp Lys Val Arg Phe Arg Gln Lys Pro Val 390 395 Glu Arg Pro Gly Ser Gly Ala Gly Arg Thr Gly Thr Tyr Ser Glu Arg 410 405 Thr His Ser Arg Ala Gly Ser Ile Asp Glu Thr Arg Ser Phe Glu Ser 425 420 Thr Glu Arg Pro Arg Ser Arg Gly Ala Val Asp Ala Trp Val Arg Pro 440 445 Ala Asp Glu Gln Arg Arg Asn Phe Gln Gly Ser Lys Glu Arg Gly Phe 455 Phe Ser Asn Arg Ser Ser Ser Arg Glu Gly Trp 470 (2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..495
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586145
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

gtttctttgt	tctttaccga	gtccccaaca	aatccatttc	ttcgatgtgt	agatattaag	60
ttagtttcaa	aaatctgtca	tagaagagga	actcttgttt	gtatagacgc	taccattgca	120
acacctatca	atcaaaagac	acttgctctt	ggtgctgatc	ttgttcacca	ttctgctact	180
	gaggccacaa					240
gtttccaaga	ttcgcaattt	gcataagctt	ttgggaggca	cgcttaatcc	gaacgctgca	300
tatttactca	tacgaggcat	gaagacgatg	catcttcgtg	taagacaaca	gaattcaacc	360
ggtatgaaga	tggcccaagt	gttagaagca	catcccaagg	tgagtcgcgt	ttactatcta	420
ggccttccga	gtcatcccga	acatttaata	gccaagcgac	aaatgactgg	tattggtggc	480
ctgatctctt	tcgag					

- (2) INFORMATION FOR SEQ ID NO: 479:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..165
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586146
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Val Ser Leu Phe Phe Thr Glu Ser Pro Thr Asn Pro Phe Leu Arg Cys
1 10 15

Val Asp Ile Lys Leu Val Ser Lys Ile Cys His Arg Arg Gly Thr Leu 20 25 30

Val Cys Ile Asp Ala Thr Ile Ala Thr Pro Ile Asn Gln Lys Thr Leu $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Ala Leu Gly Ala Asp Leu Val His His Ser Ala Thr Lys Tyr Ile Gly 50 55 60

Gly His Asn Asp Phe Leu Ala Gly Ser Ile Ser Gly Ser Met Glu Leu 65 70 75 80

Val Ser Lys Ile Arg Asn Leu His Lys Leu Leu Gly Gly Thr Leu Asn 85 90 95

Pro Asn Ala Ala Tyr Leu Leu Ile Arg Gly Met Lys Thr Met His Leu
100 105 110

Arg Val Arg Gln Gln Asn Ser Thr Gly Met Lys Met Ala Gln Val Leu 115 120 125

Glu Ala His Pro Lys Val Ser Arg Val Tyr Tyr Leu Gly Leu Pro Ser 130 135 140

His Pro Glu His Leu Ile Ala Lys Arg Gln Met Thr Gly Ile Gly Gly 145 150 155 160

Leu Ile Ser Phe Glu

- (2) INFORMATION FOR SEQ ID NO:480:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586147
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:
- Met Glu Leu Val Ser Lys Ile Arg Asn Leu His Lys Leu Leu Gly Gly 1 5 10 15
- Thr Leu Asn Pro Asn Ala Ala Tyr Leu Leu Ile Arg Gly Met Lys Thr 20 25 30
- Met His Leu Arg Val Arg Gln Gln Asn Ser Thr Gly Met Lys Met Ala 35 40 45
- Gln Val Leu Glu Ala His Pro Lys Val Ser Arg Val Tyr Tyr Leu Gly 50 55 60
- Leu Pro Ser His Pro Glu His Leu Ile Ala Lys Arg Gln Met Thr Gly 65 70 75 80
- Ile Gly Gly Leu Ile Ser Phe Glu 85
- (2) INFORMATION FOR SEQ ID NO:481:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..372
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586148
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

 aatactggag atttcctaat ccgagcaaat acaaaaaagc gccagaaagt tcaagaatct 60

 aacaacttca gtgttgttga tcatgttgag ccacaagagg cagcatatga tggaaggaaa 120

 aatgatgctg agtccaagac aggccttgat gtaagtaaga agaaacaagg tcgaggtcgg 180

 gcttcgtcaa caggtagagg gcgtggttct aaaactaata acgatgtgac aaaatctcag 240

 tttgtggttg caccagtatc agctgccagt caactggatg cctctgatca aaaggttagt 300

 attgtttacc tcatcggacc ttacatggaa ccactcttct catcatcgag gatttacata 360

 tatgagactt aa
- (2) INFORMATION FOR SEQ ID NO:482:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586149
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:
- Asn Thr Gly Asp Phe Leu Ile Arg Ala Asn Thr Lys Lys Arg Gln Lys 1 10 15
- Val Gln Glu Ser Asn Asn Phe Ser Val Val Asp His Val Glu Pro Gln
 20 25 30
- Glu Ala Ala Tyr Asp Gly Arg Lys Asn Asp Ala Glu Ser Lys Thr Gly 35 40 45
- Leu Asp Val Ser Lys Lys Gln Gly Arg Gly Arg Ala Ser Ser Thr 50 55 60
- Gly Arg Gly Arg Gly Ser Lys Thr Asn Asn Asp Val Thr Lys Ser Gln 65 70 75 80
- Phe Val Val Ala Pro Val Ser Ala Ala Ser Gln Leu Asp Ala Ser Asp 85 90 95
 Gln Lys Val Ser Ile Val Tyr Leu Ile Gly Pro Tyr Met Glu Pro Leu

100 105 110 Phe Ser Ser Arg Ile Tyr Ile Tyr Glu Thr 115 120 (2) INFORMATION FOR SEQ ID NO:483: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 807 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..807 (D) OTHER INFORMATION: / Ceres Seq. ID 1586187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:483: 60 atggatttta agcaggcata tgatttggtg gaccatagat atgttgcgtg caagcttcat ggtttaaatg ctcagtggag tgaagaaaag aagcaaagtt acatccgcca tgccaacagg 120 180 gaatgtgaga tccataaaag tcttgtgcat caccacattg ttcggctttg ggataaattt catatcgaca tgcatacatt ctgcaccgtt ctggaatatt gtagtgggaa agaccttgat 240 300 gctgtattaa aggcaacatc taatcttcct gagaaagaag caaggattat cattgtgcaa 360 ataqttcaaq qccttgtata tctgaacaaa aagtcacaga agataatcca ctatgatctg 420 aagcctggta atgttctctt tgatgagttt ggagtagcaa aagtaactga ttttggtcta agcaagatag tggaggacaa tgttggttct caaggaatgg agcttacatc acagggagct 480 qqaacatact qqtacttqcc cccaqaatqc tttgagctta acaaaactcc tatgatctca 540 600 tcaaaqqttq atqtatqqtc aqttqqtqtt ttqttttacc aaatgctgtt tggaaagcga ccttttggac atgaccaaag ccaagaacgg atactaagag aagacacaat cattaaagcc 660 aaaaaggttg agttcccagt aacaagacct gccatctcaa atgaagcgaa ggatttgatt 720 780 cgacggtgtc taacatataa ccaagaagat aggccggatg ttctaacaat ggcacaggat ccatatcttg cctactctaa gaagtga (2) INFORMATION FOR SEQ ID NO:484: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 268 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..268 (D) OTHER INFORMATION: / Ceres Seq. ID 1586188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484: Met Asp Phe Lys Gln Ala Tyr Asp Leu Val Asp His Arg Tyr Val Ala 10 Cys Lys Leu His Gly Leu Asn Ala Gln Trp Ser Glu Glu Lys Lys Gln 25 Ser Tyr Ile Arg His Ala Asn Arg Glu Cys Glu Ile His Lys Ser Leu 4.0 Val His His His Ile Val Arg Leu Trp Asp Lys Phe His Ile Asp Met His Thr Phe Cys Thr Val Leu Glu Tyr Cys Ser Gly Lys Asp Leu Asp 70 Ala Val Leu Lys Ala Thr Ser Asn Leu Pro Glu Lys Glu Ala Arg Ile 90 85 Ile Ile Val Gln Ile Val Gln Gly Leu Val Tyr Leu Asn Lys Lys Ser 100 105 Gln Lys Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Val Leu Phe Asp 120 125 115 Glu Phe Gly Val Ala Lys Val Thr Asp Phe Gly Leu Ser Lys Ile Val

135

150

Glu Asp Asn Val Gly Ser Gln Gly Met Glu Leu Thr Ser Gln Gly Ala

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Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Glu Leu Asn Lys Thr
                               170
Pro Met Ile Ser Ser Lys Val Asp Val Trp Ser Val Gly Val Leu Phe
                  185
         180
Tyr Gln Met Leu Phe Gly Lys Arg Pro Phe Gly His Asp Gln Ser Gln
                       200
Glu Arg Ile Leu Arg Glu Asp Thr Ile Ile Lys Ala Lys Lys Val Glu
                                      220
  210 215
Phe Pro Val Thr Arg Pro Ala Ile Ser Asn Glu Ala Lys Asp Leu Ile
                               235
                230
Arg Arg Cys Leu Thr Tyr Asn Gln Glu Asp Arg Pro Asp Val Leu Thr
          245 250
Met Ala Gln Asp Pro Tyr Leu Ala Tyr Ser Lys Lys
```

- (2) INFORMATION FOR SEQ ID NO:485:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..205
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586190
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Met His Thr Phe Cys Thr Val Leu Glu Tyr Cys Ser Gly Lys Asp Leu 10

Asp Ala Val Leu Lys Ala Thr Ser Asn Leu Pro Glu Lys Glu Ala Arg 20 25

Ile Ile Ile Val Gln Ile Val Gln Gly Leu Val Tyr Leu Asn Lys Lys

Ser Gln Lys Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Val Leu Phe 55

Asp Glu Phe Gly Val Ala Lys Val Thr Asp Phe Gly Leu Ser Lys Ile 70 75

Val Glu Asp Asn Val Gly Ser Gln Gly Met Glu Leu Thr Ser Gln Gly 85 90

Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Glu Leu Asn Lys 100 105

Thr Pro Met Ile Ser Ser Lys Val Asp Val Trp Ser Val Gly Val Leu 120 125

Phe Tyr Gln Met Leu Phe Gly Lys Arg Pro Phe Gly His Asp Gln Ser 130 135 140

Gln Glu Arg Ile Leu Arg Glu Asp Thr Ile Ile Lys Ala Lys Lys Val 155 150 Glu Phe Pro Val Thr Arg Pro Ala Ile Ser Asn Glu Ala Lys Asp Leu

165 170 Ile Arg Arg Cys Leu Thr Tyr Asn Gln Glu Asp Arg Pro Asp Val Leu

180 185 Thr Met Ala Gln Asp Pro Tyr Leu Ala Tyr Ser Lys Lys 195 200

- (2) INFORMATION FOR SEQ ID NO:486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

- (B) LOCATION: 1..760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586191
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486: atggatttta agcaggcata tgatttggtg gaccatagat atgttgcgtg caagcttcat 60 ggtttaaatg ctcagtggag tgaagaaaag aagcaaagtt acatccgcca tgccaacagg 120 gaatgtgaga tccataaaag tcttgtgcat caccacattg ttcggctttg ggataaattt 180 240 catatogaca tgcatacatt ctgcaccgtt ctggaatatt gtagtgggaa agaccttgat 300 qctqtattaa aqqcaacatc taatcttcct gagaaagaag caaggattat cattgtgcaa 360 atagttcaag gccttgtata tctgaacaaa aagtcacaga agataatcca ctatgatctg 420 aaqcctqqta atgttctctt tgatgagttt ggagtagcaa aagtaactga ttttggtcta 480 aqcaaqataq tqqaqqacaa tqttqqttct caaqqaatqq aqcttacatc acaqqqaqct 540 qqaacatact qqtacttqcc cccaqaatqc tttgagctta acaaaactcc tatgatctca 600 tcaaaqqttq atqtatqqtc agttggtqtt ttgttttacc aaatgctgtt tggaaagcga 660 ccttttggac atgaccaaag ccaagaacgg atactaagag aagacacaat cattaaagcc 720 aaaaaqqttq aqttcccaqt aacaagacct gccatctcaa atgaagcgaa gaagaaagct
- (2) INFORMATION FOR SEQ ID NO:487:
 - (i) SEQUENCE CHARACTERISTICS:

gaaagttgga aacaggcccc aaatcgttct tgcttctcag

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..253
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487: Met Asp Phe Lys Gln Ala Tyr Asp Leu Val Asp His Arg Tyr Val Ala 10 Cys Lys Leu His Gly Leu Asn Ala Gln Trp Ser Glu Glu Lys Lys Gln 25 2.0 Ser Tyr Ile Arg His Ala Asn Arg Glu Cys Glu Ile His Lys Ser Leu 4.0 45 Val His His His Ile Val Arg Leu Trp Asp Lys Phe His Ile Asp Met 55 His Thr Phe Cys Thr Val Leu Glu Tyr Cys Ser Gly Lys Asp Leu Asp 75 70 Ala Val Leu Lys Ala Thr Ser Asn Leu Pro Glu Lys Glu Ala Arg Ile 90 8.5 Ile Ile Val Gln Ile Val Gln Gly Leu Val Tyr Leu Asn Lys Lys Ser 105 110 100 Gln Lys Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Val Leu Phe Asp 125 120 Glu Phe Gly Val Ala Lys Val Thr Asp Phe Gly Leu Ser Lys Ile Val 135 140 Glu Asp Asn Val Gly Ser Gln Gly Met Glu Leu Thr Ser Gln Gly Ala 155 150 Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Glu Leu Asn Lys Thr 170 165 Pro Met Ile Ser Ser Lys Val Asp Val Trp Ser Val Gly Val Leu Phe 180 185 Tyr Gln Met Leu Phe Gly Lys Arg Pro Phe Gly His Asp Gln Ser Gln 205 200 Glu Arg Ile Leu Arg Glu Asp Thr Ile Ile Lys Ala Lys Lys Val Glu 215 220 Phe Pro Val Thr Arg Pro Ala Ile Ser Asn Glu Ala Lys Lys Lys Ala 230 235 Glu Ser Trp Lys Gln Ala Pro Asn Arg Ser Cys Phe Ser

250

(2) INFORMATION FOR SEQ ID NO:488:

660

720

780

Page 304 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 190 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..190 (D) OTHER INFORMATION: / Ceres Seq. ID 1586194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488: Met His Thr Phe Cys Thr Val Leu Glu Tyr Cys Ser Gly Lys Asp Leu 5 10 Asp Ala Val Leu Lys Ala Thr Ser Asn Leu Pro Glu Lys Glu Ala Arg 25 Ile Ile Ile Val Gln Ile Val Gln Gly Leu Val Tyr Leu Asn Lys Lys 40 Ser Gln Lys Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Val Leu Phe 55 Asp Glu Phe Gly Val Ala Lys Val Thr Asp Phe Gly Leu Ser Lys Ile 70 75 Val Glu Asp Asn Val Gly Ser Gln Gly Met Glu Leu Thr Ser Gln Gly 90 85 Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Glu Leu Asn Lys 105 100 Thr Pro Met Ile Ser Ser Lys Val Asp Val Trp Ser Val Gly Val Leu 120 125 Phe Tyr Gln Met Leu Phe Gly Lys Arg Pro Phe Gly His Asp Gln Ser 135 140 Gln Glu Arg Ile Leu Arg Glu Asp Thr Ile Ile Lys Ala Lys Lys Val 150 155 Glu Phe Pro Val Thr Arg Pro Ala Ile Ser Asn Glu Ala Lys Lys 170 165 Ala Glu Ser Trp Lys Gln Ala Pro Asn Arg Ser Cys Phe Ser 180 185 (2) INFORMATION FOR SEQ ID NO:489: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..782 (D) OTHER INFORMATION: / Ceres Seq. ID 1586195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:489: getttgttet taacatttta caaaggeeca caaatateaa aeteteaete teaeteteae ggtggggctt cccacaacaa caacgatcaa gacaaggcca ataattggct tcttggatgt 120 ctttatttaa ccataggaac agtgttgcta tctctatgga tgttgtttca agggacttta 180 agtattaagt accettgeaa atactegage acttgtetta tgteaatttt egeggeattt 240 300 caatgtgctc tcttgagcct ttacaagagc agagacgtta atgattggat catagatgat agattcgtta tcaccgtcat catatacgct ggagtggtag gacaagcaat gacgacggtt 360 gcaacaacat gggggattaa aaaattagga gctgtgttcg catcggcgtt tttcccactt 420 actotcattt cggctactot atttgatttc ctcattttac acactccttt ataccttgga 480

agtgtgattg gatcactagt gaccataacg ggtctctaca tgttcttgtg ggggaagaac aaagaaacgg aatcatcaac tgcattgtct tcaggaatgg ataacgaagc tcaatatact actoctaata aggataacga ctctaagtcg cccgtttaat ttaattatat tgttgttaat

gtatgtttca aataactgtt atgtcctagt taatgtttaa ggagaggtaa tgagagataa

aattttataa ttccaaacat caacgtagag atttgtgaaa tatttaaatc cggtttgttt

- (2) INFORMATION FOR SEQ ID NO:490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..212
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586196
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Ala Leu Phe Leu Thr Phe Tyr Lys Gly Pro Gln Ile Ser Asn Ser His 1 5 10 15

Ser His Ser His Gly Gly Ala Ser His Asn Asn Asn Asp Gln Asp Lys 20 25 30

Ala Asn Asn Trp Leu Leu Gly Cys Leu Tyr Leu Thr Ile Gly Thr Val

Leu Leu Ser Leu Trp Met Leu Phe Gln Gly Thr Leu Ser Ile Lys Tyr 50 60

Pro Cys Lys Tyr Ser Ser Thr Cys Leu Met Ser Ile Phe Ala Ala Phe
70 75 80

Gln Cys Ala Leu Leu Ser Leu Tyr Lys Ser Arg Asp Val Asn Asp Trp
85 90 95

Ile Ile Asp Asp Arg Phe Val Ile Thr Val Ile Ile Tyr Ala Gly Val 100 105 110

Val Gly Gln Ala Met Thr Thr Val Ala Thr Thr Trp Gly Ile Lys Lys 115 120 125

Leu Gly Ala Val Phe Ala Ser Ala Phe Phe Pro Leu Thr Leu Ile Ser 130 135 140

Ala Thr Leu Phe Asp Phe Leu Ile Leu His Thr Pro Leu Tyr Leu Gly 145 150 155 160

Ser Val Ile Gly Ser Leu Val Thr Ile Thr Gly Leu Tyr Met Phe Leu
165 170 175

Trp Gly Lys Asn Lys Glu Thr Glu Ser Ser Thr Ala Leu Ser Ser Gly
180
185
190

Met Asp Asn Glu Ala Gln Tyr Thr Thr Pro Asn Lys Asp Asn Asp Ser 195 200 205

Lys Ser Pro Val 210

- (2) INFORMATION FOR SEQ ID NO:491:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586197
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

Met Leu Phe Gln Gly Thr Leu Ser Ile Lys Tyr Pro Cys Lys Tyr Ser 1 5 10 15

Ser Thr Cys Leu Met Ser Ile Phe Ala Ala Phe Gln Cys Ala Leu Leu 20 25 30

Ser Leu Tyr Lys Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg 35 40 45

Phe Val Ile Thr Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met 50 55 60 Thr Thr Val Ala Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe

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65
                   70
                                      75
Ala Ser Ala Phe Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp
                                 90
Phe Leu Ile Leu His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser
                             105
Leu Val Thr Ile Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys
                         120 125
Glu Thr Glu Ser Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala
                    135
Gln Tyr Thr Thr Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Val
            150
(2) INFORMATION FOR SEQ ID NO:492:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 139 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..139
          (D) OTHER INFORMATION: / Ceres Seq. ID 1586198
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:
Met Ser Ile Phe Ala Ala Phe Gln Cys Ala Leu Leu Ser Leu Tyr Lys
                                  10
Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg Phe Val Ile Thr
                              25
          20
Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met Thr Thr Val Ala
                           40
Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe Ala Ser Ala Phe
                       55
Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp Phe Leu Ile Leu
                                      75
                   70
His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser Leu Val Thr Ile
                                  90
               85
Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys Glu Thr Glu Ser
                              105
                                                 110
           100
Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala Gln Tyr Thr Thr
                          120
      115
Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Val
                      135
(2) INFORMATION FOR SEQ ID NO:493:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1008 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..1008
          (D) OTHER INFORMATION: / Ceres Seq. ID 1586199
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

getttgttet taacattta caaaggeca caaatatcaa actetcacte teactetac 60
ggtggggett eccacaacaa caacgatcaa gacaaggeca ataattgget tettggatgt 120
etttatttaa ecataggaac agtgttgeta tetetatgga tgttgttea agggaeetta agtattaagt accettgeaa ataetegage acttgtetta tgteaattt egeggeattt eaatgtgete tettgageet ttaeaagage agagaegtta atgattggat eatagatgat 300
agattegtta teacegteat eatataeget ggagtggtag gacaageaat gacgaeggtt 360
geaacaacat gggggattaa aaaattagga getgtgtteg eateggegtt ttteecaett 420
acteteattt eggetaetet atttgatte eteatttae acaeteettt ataeettgga 480

agtgtgattg gatcactagt gaccataacg ggtctctaca tgttcttgtg ggggaagaac 540 aaagaaacgg aatcatcaac tgcattgtct tcaggaatgg ataacgaagc tcaatatact 600 660 actoctaata aggataacga ototaagtog ocoggagtto coggtgagat gataagtoag 720 attgcatact tgtctcctcc atggctactc tcaaggagag gatttgaagc agcgaatagc tgcaacggtc ctgttatgga tactaataca tctggagaag aattattagc taaggcaaga 780 840 aagccatata caataacaaa gcagcgagag cgatggactg aggatgagca tgagaggttt ctagaagcct tgaggcttta tggaagagct tggcaacgaa ttgaaggagt gtctttatct 900 cctcttgatt gggagattcc ttcttttctt ttcattttgt gtgcagaaca tattgggaca 960 aagactgctg ttcagatcag aagtcatgca caaaagttct tcacaaag

- (2) INFORMATION FOR SEQ ID NO:494:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 amino acids
 - (B) TYPE: amino acid (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..336
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494: Ala Leu Phe Leu Thr Phe Tyr Lys Gly Pro Gln Ile Ser Asn Ser His 10 Ser His Ser His Gly Gly Ala Ser His Asn Asn Asn Asp Gln Asp Lys 25 Ala Asn Asn Trp Leu Leu Gly Cys Leu Tyr Leu Thr Ile Gly Thr Val 40 Leu Leu Ser Leu Trp Met Leu Phe Gln Gly Thr Leu Ser Ile Lys Tyr 55 Pro Cys Lys Tyr Ser Ser Thr Cys Leu Met Ser Ile Phe Ala Ala Phe 75 70 Gln Cys Ala Leu Leu Ser Leu Tyr Lys Ser Arg Asp Val Asn Asp Trp 90 Ile Ile Asp Asp Arg Phe Val Ile Thr Val Ile Ile Tyr Ala Gly Val 105 Val Gly Gln Ala Met Thr Thr Val Ala Thr Thr Trp Gly Ile Lys Lys 125 120 115 Leu Gly Ala Val Phe Ala Ser Ala Phe Phe Pro Leu Thr Leu Ile Ser 140 135 Ala Thr Leu Phe Asp Phe Leu Ile Leu His Thr Pro Leu Tyr Leu Gly 155 160 150 Ser Val Ile Gly Ser Leu Val Thr Ile Thr Gly Leu Tyr Met Phe Leu 170 165 Trp Gly Lys Asn Lys Glu Thr Glu Ser Ser Thr Ala Leu Ser Ser Gly 190 180 185 Met Asp Asn Glu Ala Gln Tyr Thr Thr Pro Asn Lys Asp Asn Asp Ser 205 200 Lys Ser Pro Gly Val Pro Gly Glu Met Ile Ser Gln Ile Ala Tyr Leu 220 215 Ser Pro Pro Trp Leu Leu Ser Arg Gly Phe Glu Ala Ala Asn Ser 235 230 Cys Asn Gly Pro Val Met Asp Thr Asn Thr Ser Gly Glu Glu Leu Leu 250 245 Ala Lys Ala Arg Lys Pro Tyr Thr Ile Thr Lys Gln Arg Glu Arg Trp 265 270 Thr Glu Asp Glu His Glu Arg Phe Leu Glu Ala Leu Arg Leu Tyr Gly 280 Arg Ala Trp Gln Arg Ile Glu Gly Val Ser Leu Ser Pro Leu Asp Trp 295 300 Glu Ile Pro Ser Phe Leu Phe Ile Leu Cys Ala Glu His Ile Gly Thr 310 315

Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe Phe Thr Lys 325 330 335

- (2) INFORMATION FOR SEQ ID NO:495:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..283
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:
- Met Leu Phe Gln Gly Thr Leu Ser Ile Lys Tyr Pro Cys Lys Tyr Ser 1 5 10 15
- Ser Thr Cys Leu Met Ser Ile Phe Ala Ala Phe Gln Cys Ala Leu Leu 20 25 30
- Ser Leu Tyr Lys Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg 35 40 45
- Phe Val Ile Thr Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met
- Thr Thr Val Ala Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe 65 70 75 80
- Ala Ser Ala Phe Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp
 85 90 95
- Phe Leu Ile Leu His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser 100 105 110
- Leu Val Thr Ile Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys
 115 120 125
- Glu Thr Glu Ser Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala 130 135 140
- Gln Tyr Thr Thr Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Gly Val 145 150 155 160
- Pro Gly Glu Met Ile Ser Gln Ile Ala Tyr Leu Ser Pro Pro Trp Leu 165 170 175
- Leu Ser Arg Arg Gly Phe Glu Ala Ala Asn Ser Cys Asn Gly Pro Val
- Met Asp Thr Asn Thr Ser Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys
 195 200 205
- Pro Tyr Thr Ile Thr Lys Gln Arg Glu Arg Trp Thr Glu Asp Glu His 210 215 220
- Glu Arg Phe Leu Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg 225 230 235 240 Ile Glu Gly Val Ser Leu Ser Pro Leu Asp Trp Glu Ile Pro Ser Phe
- 245 250 255 Leu Phe Ile Leu Cys Ala Glu His Ile Gly Thr Lys Thr Ala Val Gln

265

- Ile Arg Ser His Ala Gln Lys Phe Phe Thr Lys
- (2) INFORMATION FOR SEQ ID NO:496:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..263 (D) OTHER INFORMATION: / Ceres Seq. ID 1586202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496: Met Ser Ile Phe Ala Ala Phe Gln Cys Ala Leu Leu Ser Leu Tyr Lys 10 Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg Phe Val Ile Thr 25 Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met Thr Thr Val Ala 40 Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe Ala Ser Ala Phe 55 Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp Phe Leu Ile Leu 7.5 70 His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser Leu Val Thr Ile 90 85 Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys Glu Thr Glu Ser 100 105 110 Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala Gln Tyr Thr Thr 120 125 Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Gly Val Pro Gly Glu Met 135 140 Ile Ser Gln Ile Ala Tyr Leu Ser Pro Pro Trp Leu Leu Ser Arg Arg 155 150 Gly Phe Glu Ala Ala Asn Ser Cys Asn Gly Pro Val Met Asp Thr Asn 175 165 170 Thr Ser Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys Pro Tyr Thr Ile 185 190 180 Thr Lys Gln Arg Glu Arg Trp Thr Glu Asp Glu His Glu Arg Phe Leu 200 205 195 Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg Ile Glu Gly Val 220 215 210 Ser Leu Ser Pro Leu Asp Trp Glu Ile Pro Ser Phe Leu Phe Ile Leu 230 235 Cys Ala Glu His Ile Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His 245 250 Ala Gln Lys Phe Phe Thr Lys 260

- (2) INFORMATION FOR SEQ ID NO:497:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 721 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..721
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497: atggatectg actteacteg teatggttet teeteegaeg gegattttgg attegetttt aatgacagta acttetetga tegettgett eggategaga teatgggtgg acetteggat 120 tctaggtccg aagttgaagg gtgtacgagt atcgctgatt gggctcgtca tcgcaagaga 180 agaagagaag atatcaagaa ggaatctggt gtcacgattt cagacattgt ggcgtgtcct 240 gaggagcaga ttttaactga tgaacaacct gacatggatg gatgtcctgg tggtgagaat 300 cctgatgatg aaggaggaga ggcaatggtt gaagaagctt tatcaggtga tgaagaggaa acgtctagtg agccaaactg gggaatggat tgttctacag ttgttagggt taaagaactt catattagtt ctcctatttt agctgccaaa agccctttct tttacaagtt gttctccaat ggaatgaggg aatctgagca aaggcatgtc accettagga ttaatgcatc agaggaagct gctttgatgg agcttttaaa ctttatgtat agcaatgcgg tatctgtcac cacagcacct gccttattag atgtgttgat ggctgctgat aagtttgaag ttgcctcttg tatgaggtac 660 tqcaqtaqac ttctccgtaa tatgcctatg actccagagt ctgccctgct ctatctcgag

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..240
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586208
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Asp Pro Asp Phe Thr Arg His Gly Ser Ser Ser Asp Gly Asp Phe 1 5 10 15

Gly Phe Ala Phe Asn Asp Ser Asn Phe Ser Asp Arg Leu Leu Arg Ile 20 25 30

Glu Ile Met Gly Gly Pro Ser Asp Ser Arg Ser Glu Val Glu Gly Cys
35 40 45

Thr Ser Ile Ala Asp Trp Ala Arg His Arg Lys Arg Arg Arg Glu Asp 50 55

Ile Lys Lys Glu Ser Gly Val Thr Ile Ser Asp Ile Val Ala Cys Pro 65 70 75 80

Glu Glu Gln Ile Leu Thr Asp Glu Gln Pro Asp Met Asp Gly Cys Pro 85 90 95

Gly Gly Glu As
n Pro Asp Asp Glu Gly Gly Glu Ala Met Val Glu Glu 100 105 110

Ala Leu Ser Gly Asp Glu Glu Glu Thr Ser Ser Glu Pro Asn Trp Gly 115 120 125

Met Asp Cys Ser Thr Val Val Arg Val Lys Glu Leu His Ile Ser Ser 130 135 140

Pro Ile Leu Ala Ala Lys Ser Pro Phe Phe Tyr Lys Leu Phe Ser Asn 145 150 155 160

Gly Met Arg Glu Ser Glu Gln Arg His Val Thr Leu Arg Ile Asn Ala 165 170 175

Ser Glu Glu Ala Ala Leu Met Glu Leu Leu Asn Phe Met Tyr Ser Asn 180 185 190

Ala Val Ser Val Thr Thr Ala Pro Ala Leu Leu Asp Val Leu Met Ala 195 200 205

Ala Asp Lys Phe Glu Val Ala Ser Cys Met Arg Tyr Cys Ser Arg Leu 210 215 220

Leu Arg Asn Met Pro Met Thr Pro Glu Ser Ala Leu Leu Tyr Leu Glu 225 230 235 240

- (2) INFORMATION FOR SEQ ID NO:499:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..206
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586210
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Met Gly Gly Pro Ser Asp Ser Arg Ser Glu Val Glu Gly Cys Thr Ser 1 10 15

Ile Ala Asp Trp Ala Arg His Arg Lys Arg Arg Arg Glu Asp Ile Lys
20 25 30

```
Lys Glu Ser Gly Val Thr Ile Ser Asp Ile Val Ala Cys Pro Glu Glu
                           40
Gln Ile Leu Thr Asp Glu Gln Pro Asp Met Asp Gly Cys Pro Gly Gly
                       55
                                          60
Glu Asn Pro Asp Asp Glu Gly Gly Glu Ala Met Val Glu Glu Ala Leu
                                       75
                   70
Ser Gly Asp Glu Glu Glu Thr Ser Ser Glu Pro Asn Trp Gly Met Asp
                                   90
               8.5
Cys Ser Thr Val Val Arg Val Lys Glu Leu His Ile Ser Ser Pro Ile
                              105
           100
Leu Ala Ala Lys Ser Pro Phe Phe Tyr Lys Leu Phe Ser Asn Gly Met
                          120
Arg Glu Ser Glu Gln Arg His Val Thr Leu Arg Ile Asn Ala Ser Glu
                                          140
                       135
Glu Ala Ala Leu Met Glu Leu Leu Asn Phe Met Tyr Ser Asn Ala Val
                                      155
                   150
Ser Val Thr Thr Ala Pro Ala Leu Leu Asp Val Leu Met Ala Ala Asp
                                  170
               165
Lys Phe Glu Val Ala Ser Cys Met Arg Tyr Cys Ser Arg Leu Leu Arg
                              185
           180
Asn Met Pro Met Thr Pro Glu Ser Ala Leu Leu Tyr Leu Glu
       195
                           200
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- (2) INFORMATION FOR SEQ ID NO:500:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..729
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586296
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500: aggttttccg gggaatgtga cggtgaaagt gacgtacatg ttgatcggag aaaacaaact 60 120 cggtgtaaaa atggaagcaa agccactcaa caaacctaca ccaatcaact tagctctcca 180 cacttactgg aacctccaca gccacaactc cgggaacatc ctctcccaca aaattcaact 240 cctcgccgga aaaatcactc ccgtcgacga caaactcatc cccaccggcg aaatcacctc 300 cattgccgga actccttacg attttctcga gcctcgcgag atcggaagcc ggatccacga attacccgga ggttacgaca tcaattacgt gatcgatgga ccgatcggga aacatctgag 360 420 gaaaactgcg gttgtgacgg aggaagtcac cggaaggaag atggagctgt ggacgaatca gcctggtgtt cagttttaca cgagtaatat gatgaaacgt gtcgtcggta aggtaaagcc 480 gtttatgaga aatacggtgg cttgtgtttg gagactcaag gcttcccaga ttccgtcaat 540 cacaagaact ttccgtcgca gattgttaat cccggcgaga gttatttgca tgttatgctc 600 660 tttttccgaa tactcgccaa cgtcgttgta atgcaaaatt gcaaatgcca ataaaaatat tcgactttt
- (2) INFORMATION FOR SEQ ID NO:501:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..229
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586297
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:
- Gly Phe Pro Gly Asn Val Thr Val Lys Val Thr Tyr Met Leu Ile Gly
 1 5 10 15

Glu Asn Lys Leu Gly Val Lys Met Glu Ala Lys Pro Leu Asn Lys Pro 25 Thr Pro Ile Asn Leu Ala Leu His Thr Tyr Trp Asn Leu His Ser His 40 Asn Ser Gly Asn Ile Leu Ser His Lys Ile Gln Leu Leu Ala Gly Lys 55 Ile Thr Pro Val Asp Asp Lys Leu Ile Pro Thr Gly Glu Ile Thr Ser 75 70 Ile Ala Gly Thr Pro Tyr Asp Phe Leu Glu Pro Arg Glu Ile Gly Ser 90 85 Arg Ile His Glu Leu Pro Gly Gly Tyr Asp Ile Asn Tyr Val Ile Asp 105 Gly Pro Ile Gly Lys His Leu Arg Lys Thr Ala Val Val Thr Glu Glu 125 120 115 Val Thr Gly Arg Lys Met Glu Leu Trp Thr Asn Gln Pro Gly Val Gln 135 140 Phe Tyr Thr Ser Asn Met Met Lys Arg Val Val Gly Lys Val Lys Pro 155 150 Phe Met Arg Asn Thr Val Ala Cys Val Trp Arg Leu Lys Ala Ser Gln 170 165 Ile Pro Ser Ile Thr Arg Thr Phe Arg Arg Arg Leu Leu Ile Pro Ala 190 180 185 Arg Val Ile Cys Met Leu Cys Ser Ser Asp Ser Leu Leu Thr Asn Arg 205 200 Val Gly Ser Gly Arg Val Gly Phe Leu Gly Phe Asn Phe Ser Glu Tyr 220 215 210 Ser Pro Thr Ser Leu

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..217
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586298
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:
- Met Leu Ile Gly Glu Asn Lys Leu Gly Val Lys Met Glu Ala Lys Pro 1 5 10 15
- Leu Asn Lys Pro Thr Pro Ile Asn Leu Ala Leu His Thr Tyr Trp Asn 20 25 30
- Leu His Ser His Asn Ser Gly Asn Ile Leu Ser His Lys Ile Gln Leu 35 40 45
- Leu Ala Gly Lys Ile Thr Pro Val Asp Asp Lys Leu Ile Pro Thr Gly 50 55 60
- Glu Ile Thr Ser Ile Ala Gly Thr Pro Tyr Asp Phe Leu Glu Pro Arg 65 70 75 80
- Glu Ile Gly Ser Arg Ile His Glu Leu Pro Gly Gly Tyr Asp Ile Asn 85 90 95
- Tyr Val Ile Asp Gly Pro Ile Gly Lys His Leu Arg Lys Thr Ala Val
- Val Thr Glu Glu Val Thr Gly Arg Lys Met Glu Leu Trp Thr Asn Gln
 115 120 125
- Pro Gly Val Gln Phe Tyr Thr Ser Asn Met Met Lys Arg Val Val Gly 130 135 140
- Lys Val Lys Pro Phe Met Arg Asn Thr Val Ala Cys Val Trp Arg Leu 145 150 155 160
- Lys Ala Ser Gln Ile Pro Ser Ile Thr Arg Thr Phe Arg Arg Arg Leu

120

180

240

170 175 165 Leu Ile Pro Ala Arg Val Ile Cys Met Leu Cys Ser Ser Asp Ser Leu 185 190 180 Leu Thr Asn Arg Val Gly Ser Gly Arg Val Gly Phe Leu Gly Phe Asn 200 Phe Ser Glu Tyr Ser Pro Thr Ser Leu 215 210 (2) INFORMATION FOR SEQ ID NO:503: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..206 (D) OTHER INFORMATION: / Ceres Seq. ID 1586299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503: Met Glu Ala Lys Pro Leu Asn Lys Pro Thr Pro Ile Asn Leu Ala Leu 10 His Thr Tyr Trp Asn Leu His Ser His Asn Ser Gly Asn Ile Leu Ser 25 His Lys Ile Gln Leu Leu Ala Gly Lys Ile Thr Pro Val Asp Asp Lys 40 Leu Ile Pro Thr Gly Glu Ile Thr Ser Ile Ala Gly Thr Pro Tyr Asp 60 55 Phe Leu Glu Pro Arg Glu Ile Gly Ser Arg Ile His Glu Leu Pro Gly 75 70 Gly Tyr Asp Ile Asn Tyr Val Ile Asp Gly Pro Ile Gly Lys His Leu 8.5 Arg Lys Thr Ala Val Val Thr Glu Glu Val Thr Gly Arg Lys Met Glu 100 105 Leu Trp Thr Asn Gln Pro Gly Val Gln Phe Tyr Thr Ser Asn Met Met 120 125 Lys Arg Val Val Gly Lys Val Lys Pro Phe Met Arg Asn Thr Val Ala 140 135 Cys Val Trp Arg Leu Lys Ala Ser Gln Ile Pro Ser Ile Thr Arg Thr 155 150 Phe Arg Arg Leu Leu Ile Pro Ala Arg Val Ile Cys Met Leu Cys 165 170 Ser Ser Asp Ser Leu Leu Thr Asn Arg Val Gly Ser Gly Arg Val Gly 180 185 Phe Leu Gly Phe Asn Phe Ser Glu Tyr Ser Pro Thr Ser Leu 200 (2) INFORMATION FOR SEQ ID NO:504: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..451 (D) OTHER INFORMATION: / Ceres Seq. ID 1586345 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504: agagettage taagatgaeg aagaactaee caacegtgag egaagattae aagaaggetg ttgagaagtg caggaggaag ctcagaggtt tgatcgctga gaagaactgt gcacccatca

tggtccgact cgcatggcac tctgctggaa ctttcgattg tcaatcaagg actggaggtc cattcggaac aatgaggttt gacgctgagc aagctcatgg agccaacagt ggtatccaca

ttgctcttag gttgttggac cccatcaggg agcaattccc taccatctct tttgctgatt 300 tccatcagct tgctggtgtt gtggccgttg aagttactgg tggccctgac attcctttcc 360 accctggaag agaggacaag ccccaaccac ctccagaggg tcgtcttcct gatgctgtt 420 gctgatgctt aagctgtgac gtatgctctg t

- (2) INFORMATION FOR SEQ ID NO:505:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids(B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586346
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Ser Leu Ala Lys Met Thr Lys Asn Tyr Pro Thr Val Ser Glu Asp Tyr

1 10 15

Lys Lys Ala Val Glu Lys Cys Arg Arg Lys Leu Arg Gly Leu Ile Ala 20 25 30

Glu Lys Asn Cys Ala Pro Ile Met Val Arg Leu Ala Trp His Ser Ala 35 40 45

Gly Thr Phe Asp Cys Gln Ser Arg Thr Gly Gly Pro Phe Gly Thr Met

Arg Phe Asp Ala Glu Gln Ala His Gly Ala Asn Ser Gly Ile His Ile
65 70 75 80

Ala Leu Arg Leu Leu Asp Pro Ile Arg Glu Gln Phe Pro Thr Ile Ser 85 90 95

Phe Ala Asp Phe His Gln Leu Ala Gly Val Val Ala Val Glu Val Thr

Gly Gly Pro Asp Ile Pro Phe His Pro Gly Arg Glu Asp Lys Pro Gln
115 120 125

Pro Pro Pro Glu Gly Arg Leu Pro Asp Ala Val Cys 130 135 140

- (2) INFORMATION FOR SEQ ID NO:506:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586347
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Met Thr Lys Asn Tyr Pro Thr Val Ser Glu Asp Tyr Lys Lys Ala Val 1 5 10 15

Glu Lys Cys Arg Arg Lys Leu Arg Gly Leu Ile Ala Glu Lys Asn Cys
20 25 30

Ala Pro Ile Met Val Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp 35 40 45

Cys Gln Ser Arg Thr Gly Gly Pro Phe Gly Thr Met Arg Phe Asp Ala 50 55 60

Glu Gln Ala His Gly Ala Asn Ser Gly Ile His Ile Ala Leu Arg Leu 65 70 75 80

Leu Asp Pro Ile Arg Glu Gln Phe Pro Thr Ile Ser Phe Ala Asp Phe 85 90 95

His Gln Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp 100 105 110 110 Ile Pro Phe His Pro Gly Arg Glu Asp Lys Pro Gln Pro Pro Glu

```
125
                            120
        115
Gly Arg Leu Pro Asp Ala Val Cys
            135
    130
(2) INFORMATION FOR SEQ ID NO:507:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 101 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..101
          (D) OTHER INFORMATION: / Ceres Seq. ID 1586348
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:
Met Val Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp Cys Gln Ser
                                    10
Arg Thr Gly Gly Pro Phe Gly Thr Met Arg Phe Asp Ala Glu Gln Ala
                                25
His Gly Ala Asn Ser Gly Ile His Ile Ala Leu Arg Leu Leu Asp Pro
                            40
Ile Arg Glu Gln Phe Pro Thr Ile Ser Phe Ala Asp Phe His Gln Leu
                        55
Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp Ile Pro Phe
                                        75
                    70
His Pro Gly Arg Glu Asp Lys Pro Gln Pro Pro Glu Gly Arg Leu
                                     90
                85
Pro Asp Ala Val Cys
            100
(2) INFORMATION FOR SEQ ID NO:508:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1014 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..1014
           (D) OTHER INFORMATION: / Ceres Seq. ID 1586393
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:
 atgatgtett tgeteccaaa tecegaeeeg attactgtae eeetggteet caagetttge
 teettteete egecaeggag getettetet eteaggetea ggegetteae eegaaagtea
                                                                       120
 tcatctcttc ttccgttggt cgctgtttcg tctctctccg ctactgncgc aaaacctacc
 agatggagag agaagccgga attggcggaa agcgactcaa tttccctcct caacgagagg
                                                                       240
                                                                       300
 atteggegtg accteggeaa gagagagaet getagaeegg ceatggaete tgaggaggee
 gagaagtaca ttcacatggt caaggaacaa caagagaggg gtctgcagaa gctcaaagga
                                                                        360
                                                                        420
 attaggcaag gtacaaaggc tgctggtgac ggtgctttta gttacaaggt tgacccttac
 agtctccttt ccggtgatta tgtggtgcac aagaaagtag gcattgggcg ttttgttggg
                                                                        480
 atcaagtttg atgtccccaa ggactcctct gagcccctcg aatatgtctt tatagagtat
                                                                        540
 gctgatggta tggccaagct tcccctcaaa caggcctcgc gtttgctcta ccgatacaat
                                                                        600
 cttccaaatg agactaaacg gcctcggact ttgagtcggc tgagtgacac tagtgtttgg
                                                                        660
 gaaagaagaa agaccaaagg aaaagtagca attcagaaaa tggtcgttga cttgatggag
                                                                        720
 ctatatcttc ataggcttag acagaagaga tatccatatc cgaagaaccc catcatggct
 gattttgcgg ctcaatttcc ttataacgcc actcctgacc agaagcaggc tttcctggat
 gttgaaaagg atttgactga gagagaaaca cctatggacc gattgatctg tggagatgtt
                                                                        900
 ggctttggta aaacagaggt tgctctacga gccatctttt gtgtggtctc aactggaaaa
                                                                        960
 caagctatgg ttttagcacc gacaattgta ttggcgaana acattacgat gtaa
 (2) INFORMATION FOR SEQ ID NO:509:
```

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..337
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586394
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:
- Met Met Ser Leu Leu Pro Asn Pro Asp Pro Ile Thr Val Pro Leu Val 1 5 10
- Leu Lys Leu Cys Ser Phe Pro Pro Pro Arg Arg Leu Phe Ser Leu Arg 20 25 30
- Leu Arg Arg Phe Thr Arg Lys Ser Ser Ser Leu Leu Pro Leu Val Ala
- Val Ser Ser Leu Ser Ala Thr Xaa Ala Lys Pro Thr Arg Trp Arg Glu 50 55 60
- Lys Pro Glu Leu Ala Glu Ser Asp Ser Ile Ser Leu Leu Asn Glu Arg
 65 70 75 80
- Ile Arg Arg Asp Leu Gly Lys Arg Glu Thr Ala Arg Pro Ala Met Asp 85 90 95
- Ser Glu Glu Ala Glu Lys Tyr Ile His Met Val Lys Glu Gln Glu
 100 105 110
- Arg Gly Leu Gln Lys Leu Lys Gly Ile Arg Gln Gly Thr Lys Ala Ala 115 120 125
- Gly Asp Gly Ala Phe Ser Tyr Lys Val Asp Pro Tyr Ser Leu Leu Ser 130 135 140
- Gly Asp Tyr Val Val His Lys Lys Val Gly Ile Gly Arg Phe Val Gly 145 150 155 160
- Ile Lys Phe Asp Val Pro Lys Asp Ser Ser Glu Pro Leu Glu Tyr Val 165 170 175
- Phe Ile Glu Tyr Ala Asp Gly Met Ala Lys Leu Pro Leu Lys Gln Ala 180 185 190
- Ser Arg Leu Leu Tyr Arg Tyr Asn Leu Pro Asn Glu Thr Lys Arg Pro
 195 200 205
- Arg Thr Leu Ser Arg Leu Ser Asp Thr Ser Val Trp Glu Arg Arg Lys 210 215 220
- Thr Lys Gly Lys Val Ala Ile Gln Lys Met Val Val Asp Leu Met Glu 225 230 230 235 240
- Leu Tyr Leu His Arg Leu Arg Gln Lys Arg Tyr Pro Tyr Pro Lys Asn 245 250 250
- Pro Ile Met Ala Asp Phe Ala Ala Gln Phe Pro Tyr Asn Ala Thr Pro 260 265 270
- Asp Gln Lys Gln Ala Phe Leu Asp Val Glu Lys Asp Leu Thr Glu Arg 275 280 285
- Glu Thr Pro Met Asp Arg Leu Ile Cys Gly Asp Val Gly Phe Gly Lys 290 295 300
- Thr Glu Val Ala Leu Arg Ala Ile Phe Cys Val Val Ser Thr Gly Lys 305 310 315 320
- Gln Ala Met Val Leu Ala Pro Thr Ile Val Leu Ala Xaa Asn Ile Thr 325 330 335

Met

- (2) INFORMATION FOR SEQ ID NO:510:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510: Met Ser Leu Leu Pro Asn Pro Asp Pro Ile Thr Val Pro Leu Val Leu 1.0 Lys Leu Cys Ser Phe Pro Pro Pro Arg Arg Leu Phe Ser Leu Arg Leu 25 20 Arg Arg Phe Thr Arg Lys Ser Ser Ser Leu Leu Pro Leu Val Ala Val 4.0 Ser Ser Leu Ser Ala Thr Xaa Ala Lys Pro Thr Arg Trp Arg Glu Lys 60 55 Pro Glu Leu Ala Glu Ser Asp Ser Ile Ser Leu Leu Asn Glu Arg Ile 75 70 Arg Arg Asp Leu Gly Lys Arg Glu Thr Ala Arg Pro Ala Met Asp Ser 90 Glu Glu Ala Glu Lys Tyr Ile His Met Val Lys Glu Gln Gln Glu Arg 100 105 Gly Leu Gln Lys Leu Lys Gly Ile Arg Gln Gly Thr Lys Ala Ala Gly 125 120 Asp Gly Ala Phe Ser Tyr Lys Val Asp Pro Tyr Ser Leu Leu Ser Gly 140 135 Asp Tyr Val Val His Lys Lys Val Gly Ile Gly Arg Phe Val Gly Ile 150 155 Lys Phe Asp Val Pro Lys Asp Ser Ser Glu Pro Leu Glu Tyr Val Phe 165 170 Ile Glu Tyr Ala Asp Gly Met Ala Lys Leu Pro Leu Lys Gln Ala Ser 180 185 190 Arg Leu Leu Tyr Arg Tyr Asn Leu Pro Asn Glu Thr Lys Arg Pro Arg 195 200 205 Thr Leu Ser Arg Leu Ser Asp Thr Ser Val Trp Glu Arg Arg Lys Thr 220 210 215 Lys Gly Lys Val Ala Ile Gln Lys Met Val Val Asp Leu Met Glu Leu 235 240 225 230 Tyr Leu His Arg Leu Arg Gln Lys Arg Tyr Pro Tyr Pro Lys Asn Pro 250 255 245 Ile Met Ala Asp Phe Ala Ala Gln Phe Pro Tyr Asn Ala Thr Pro Asp 260 265 270 Gln Lys Gln Ala Phe Leu Asp Val Glu Lys Asp Leu Thr Glu Arg Glu 285 275 280 Thr Pro Met Asp Arg Leu Ile Cys Gly Asp Val Gly Phe Gly Lys Thr 290 295 300 Glu Val Ala Leu Arg Ala Ile Phe Cys Val Val Ser Thr Gly Lys Gln 305 310 315 320 Ala Met Val Leu Ala Pro Thr Ile Val Leu Ala Xaa Asn Ile Thr Met

- (2) INFORMATION FOR SEQ ID NO:511:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..409
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586438

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511: gagaaatagg atcgaaatgc ttaaggcaga tggttggtcgc tgggttacag acgcgaagga

gttggaattg atgacggtga attactataa aaggttgtac tccttggagg atgtgaatcc 120 agttttaact cctttaccgc ctgagggtt cactattcta tcacaaagtg ctctcacgga 180 gctgaatcga cctttcacgc ctgctgagat tgaagaatca gtacgaagta tggggaaatt taaggeccca ggccccgacg gctatcaacc cgttttctac cagcagaatt gggagaactgt ggggtcgtca gtgataaggt tcgctttaga cttctttgag acgggaatcc taccggagag 360 tatgaatgat gctttggtag tccttatcgc caaggtagcg aaccggaga

- (2) INFORMATION FOR SEQ ID NO:512:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586439
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Arg Asn Arg Ile Glu Met Leu Lys Ala Asp Gly Gly Arg Trp Val Thr 1 5 10 15

Asp Ala Lys Glu Leu Glu Leu Met Thr Val Asn Tyr Tyr Lys Arg Leu 20 25 30

Tyr Ser Leu Glu Asp Val Asn Pro Val Leu Thr Pro Leu Pro Pro Glu

Gly Phe Thr Ile Leu Ser Gln Ser Ala Leu Thr Glu Leu Asn Arg Pro 50 55 60

Phe Thr Pro Ala Glu Ile Glu Glu Ser Val Arg Ser Met Gly Lys Phe 65 70 75 80

Lys Ala Pro Gly Pro Asp Gly Tyr Gln Pro Val Phe Tyr Gln Gln Asn 85 90 95

Trp Glu Thr Val Gly Ser Ser Val Ile Arg Phe Ala Leu Asp Phe Phe 100 105 110

Glu Thr Gly Ile Leu Pro Glu Ser Met Asn Asp Ala Leu Val Val Leu 115 120 125

Ile Ala Lys Val Ala Asn Arg Arg 130 135

- (2) INFORMATION FOR SEQ ID NO:513:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

Met Leu Lys Ala Asp Gly Gly Arg Trp Val Thr Asp Ala Lys Glu Leu 1 5 5 10 10 15 Glu Leu Met Thr Val Asn Tyr Tyr Lys Arg Leu Tyr Ser Leu Glu Asp

Glu Leu Met Thr Val Asn Tyr Tyr Lys Arg Leu Tyr Ser Leu Glu Asp
20 25 30

Val Asn Pro Val Leu Thr Pro Leu Pro Pro Glu Gly Phe Thr Ile Leu 35 40 45

Ser Gln Ser Ala Leu Thr Glu Leu Asn Arg Pro Phe Thr Pro Ala Glu

Ile Glu Glu Ser Val Arg Ser Met Gly Lys Phe Lys Ala Pro Gly Pro
70 75 80

Asp Gly Tyr Gln Pro Val Phe Tyr Gln Gln Asn Trp Glu Thr Val Gly
85 90 95

Ser Ser Val Ile Arg Phe Ala Leu Asp Phe Phe Glu Thr Gly Ile Leu

105 110 100 Pro Glu Ser Met Asn Asp Ala Leu Val Val Leu Ile Ala Lys Val Ala 120 115 Asn Arg Arg 130 (2) INFORMATION FOR SEQ ID NO:514: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..113 (D) OTHER INFORMATION: / Ceres Seq. ID 1586441 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514: Met Thr Val Asn Tyr Tyr Lys Arg Leu Tyr Ser Leu Glu Asp Val Asn 10 Pro Val Leu Thr Pro Leu Pro Pro Glu Gly Phe Thr Ile Leu Ser Gln 25 Ser Ala Leu Thr Glu Leu Asn Arg Pro Phe Thr Pro Ala Glu Ile Glu 40 Glu Ser Val Arg Ser Met Gly Lys Phe Lys Ala Pro Gly Pro Asp Gly 55 Tyr Gln Pro Val Phe Tyr Gln Gln Asn Trp Glu Thr Val Gly Ser Ser 70 75 Val Ile Arg Phe Ala Leu Asp Phe Phe Glu Thr Gly Ile Leu Pro Glu 90 85 Ser Met Asn Asp Ala Leu Val Val Leu Ile Ala Lys Val Ala Asn Arg 105 Arg (2) INFORMATION FOR SEQ ID NO:515: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 519 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..519 (D) OTHER INFORMATION: / Ceres Seq. ID 1586467 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515: gctaaggtgg atgaactatc tgaatccgac tctgaagcgt ggaccgatga gtcaagaaga agagagaatc atctttcagc tccatgctct atggggtggt cgaagattgc gagaagatta cccggtagga ctgataacga gataaagaac tattggagaa ctcattatag aaagaaacag gaagctcaaa actatggaaa gctctttgag tggagaggaa atacaggaga agaattgttg 240 cacaagtata aggaaacaga gatcactagg acaaagacga cgtctcaaga acatggtttt 300 gttgaagttg tgagcatgga aagtggtaaa gaagccaacg gtggtgttgg tggaagagaa 360 agcttcggtg ttatgaaatc accgtatgaa aatcggattt cggattggat atcagagatt 420 tctactgacc agagtgaagc aaatctttca gaagatcaca gcagcaatag ctgcaagact 480 agggactttg aggagttttc atgttctcta tggtcataa (2) INFORMATION FOR SEQ ID NO:516: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..172
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Ala Lys Val Asp Glu Leu Ser Glu Ser Asp Ser Glu Ala Trp Thr Asp

1 10 15

2 10 Pro Cys Ser Met Gly

Glu Ser Arg Arg Glu Asn His Leu Ser Ala Pro Cys Ser Met Gly 20 25 30

Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile 35 40 45

Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala Gln Asn 50 55 60

Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu Leu Leu 65 70 75 80

His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr Ser Gln 85 90 95

Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys Glu Ala 100 105 110

Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys Ser Pro 115 120 125

Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr Asp Gln
130 135 140

Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys Lys Thr 145 150 155 160

Arg Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser 165 170

- (2) INFORMATION FOR SEQ ID NO:517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Gly Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn

1 10 15

15 10 15

Glu Ile Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala 20 25 30

Gln Asn Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu 35 40 45

Leu Leu His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr 50 55 60

Ser Gln Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys 65 70 75 80 Glu Ala Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys

Ser Pro Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr
100 105 110

Asp Gln Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys

115 120 125 Lys Thr Arg Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser

- 130 135 (2) INFORMATION FOR SEQ ID NO:518:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..558
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586470
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

(21) 51201101 210 0111						
gctaaggtgg atgaactatc	tgaatccgac	tctgaagcgt	ggaccgatga	gtcaagaaga	60	
agagagaatc atctttcagc	tagatagtat	atagaataat	cgaagattgc	gagaagatta	120	
agagagaate attitioned	tecatgetee	acggggcggc	ogaagassg	9	100	
cccggtagga ctgataacga	gataaagaac	tattggagaa	ctcattatag	aaagaaacag	180	
	+-++-	+~~~~~~~	atacaccaca	agaattgttg	240	
gaagctcaaa actatggaaa	getetttgag	Lygagaggaa	acacayyaya	agaaccgccg		
cacaagtata aggaaacaga	gatcactagg	acaaagacga	catctcaaga	acatggtttt	300	
cacaagcaca aggaaacaga	gaccaccagg	G. G. G. G. G. S.			360	
gttgaagttg tgagcatgga	aagtggtaaa	gaagccaacg	gtggtgttgg	tggaagagaa	300	
9-19-11-15-15-15-15-15-15-15-15-15-15-15-15-	a a a a t a t a a a	22+0002+++	cadattadat	atcadadatt	420	
agcttcggtg ttatgaaatc	accytatgaa	aattggattt	cggaccggac	accagagaco		
tctactgacc agagtgaagc	aaatctttca	gaagatcaca	gcagcaatag	ctgcagtgag	480	
cccaccade agagegaage		, -		~~~~	540	
aacaatatta acattggtac	ttggtggttt	caagagacta	gggactttga	ggagttttda	240	
tettatatat gatastaa						
tgttctctat ggtcataa						

- (2) INFORMATION FOR SEQ ID NO:519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..185
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586471
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

Ala Lys Val Asp Glu Leu Ser Glu Ser Asp Ser Glu Ala Trp Thr Asp 1 5 5 10 10 15 15 Glu Ser Arg Arg Glu Asn His Leu Ser Ala Pro Cys Ser Met Gly

20 25 30

Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile 35 40 45

Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala Gln Asn 50 55 60

Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu Leu Leu 65 70 70 75 80
His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr Ser Gln

85 95 Sor Cly Ive Cly Sor Cly Ive Cly Ala

Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys Glu Ala

100
105
110

Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys Ser Pro 115 120 125

Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr Asp Gln 130 135 140 Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys Ser Glu

Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln Glu Thr Arg Asp Phe 165 170 175

- Glu Glu Phe Ser Cys Ser Leu Trp Ser 180 185
- (2) INFORMATION FOR SEQ ID NO:520:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..155
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Glu Ile Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala
20 25 30

Gln Asn Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu 35 40 45

Leu Leu His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr 50 55 60

Ser Gln Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys 70 75 80

Glu Ala Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys 85 90 95

Ser Pro Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr 100 105 110

Asp Gln Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys 115 120 125

Ser Glu Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln Glu Thr Arg 130 135 140

Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser 145 150

- (2) INFORMATION FOR SEQ ID NO:521:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..363
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

aaaaaaacaa aaaaccaaat atcaaaccta aacttattaa aagataagag agttatgaag 60 gctttagggg ttttgttgaa tgtgaagttt ggtggatcta gtggtgaaga tactgagatg 120 aaggaggaggctg atgagaggaa agagcctgaa ccggagatgg aacctatgga gttgacggag 180 gaggagaggc agaagaagga gagaaaggag aaggctttga aggagaaagg ggaaggaaat 240 gttgcttata agaagaagga ttttgagaga gctgttgaac attatactaa ggccatggag 300 ctcgatgatg aggatatttc gtatttgacg aatcgtgctg ctgtttatct tgagatgggg 360 aag

- (2) INFORMATION FOR SEQ ID NO:522:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..121
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

Lys Lys Thr Lys Asn Gln Ile Ser Asn Leu Asn Leu Leu Lys Asp Lys

1 5 10 15

Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly 20 25 30 Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu

Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln 50

Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn 65

Val Ala Tyr Lys Lys Lys Asp Phe Glu Arg Ala Val Glu His Tyr Thr 85

Lys Ala Met Glu Leu Asp Asp Glu Asp 105

Ala Ala Val Tyr Leu Glu Met Gly Lys 105

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586548
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser 1 10 15

Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu 20 25 30

Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys 35 40 45

Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala 50 55 60

Tyr Lys Lys Lys Asp Phe Glu Arg Ala Val Glu His Tyr Thr Lys Ala 65 70 75 80

Met Glu Leu Asp Asp Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala 85 90 95

Val Tyr Leu Glu Met Gly Lys 100

(2) INFORMATION FOR SEQ ID NO:524:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro

1 5 10 15

Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys
20 25 30

Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp 35 40 45

Phe Glu Arg Ala Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp 50 55 60

Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met 65 70 75 80

Gly Lys

- (2) INFORMATION FOR SEQ ID NO:525:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2016 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2016
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586602
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525: qccaqctacg cttgaaggtc aagattctca accaatccaa ggtccgggtt tcagccggac 60 120 tgtgttctgt aatcagcctc atatgcacaa gaagaaacct ttgagatatc gttctaatta 180 tgtctctacg acgaggtaca atttgatcac tttctttcct aagtcgttgt acgagcagtt 240 ccaccgtgct gcgaatctct acttcttggt agctgcgatt ctctcggtgt ttcctctatc 300 accattcaac aagtggagca tgattgctcc tttggtcttt gttgttgggc ttagtatgtt 360 aaaagaggct ctagaagatt ggcgtaggtt tatgcaagac gtgaagatta atgcgcggaa aacttgtgtt cataaaagtg acggtgtgtt tcgtcagaga aagtggaaga aggttagcgt 420 tggggatatt gtgaaagtgg agaaggatga gtttttccct gctgatttgc ttcttttgtc 480 540 atcgagttac gaggatggga tttgctacgt tgagactatg aacttagatg gtgaaacaaa cttgaaagtg aaaagatctt tggaagtgtc actgccacta gatgatgatg aatctttcaa 600 660 gaatttcatg gcgacgataa gatgtgaaga tccaaacccg aatctctata cctttgttgg caatcttgag tttgagaggc aaacatttcc tctggatcca agtcagattc tcttaagaga 720 780 ctcaaagctt aggaatacaa cctatgttta tggagttgtg gtatttactg gttttgatac 840 caaagttatg cagaattcaa caaagtcgcc ttccaagaga agcagaatag aaaggacaat 900 ggactacatc atctacactc ttcttgtcct acttatttta atctcttgca tcagctcatc 960 aggatttgct tgggagacag agtttcacat gccaaaaatg tggtacttac gacctggcga 1020 gcctatagac ttcacaaatc cgatcaatcc aatctatgct ggggttgttc atctgatcac tgctctattg ctttatggat atttgattcc aatctctctt tatgtttcga tcgaggttgt 1080 caaagtctgg caagcaagtt tcatcaatca agacttacac atgtatgatg atgagagtgg 1140 1200 agtecetgea aatgegegea categaatet aaacgaagag ettggteagg tteataetat cctctctgac aaaacaggaa ctttgacatg taatcagatg gatttcttga aatgctccat 1260 tgctggtact tcttatggtg tgcgttccag cgaagtagaa gttgctgctg caaagcagat 1320 ggctgtggat cttgaagagc acggtgagat atcgagtact cctcagtctc agactaaagt 1380 gtatggtaca tgggacagta gccgtncgca agaaatcgag gtggaagggg ataataacta 1440 taatactcct agagctccta taaagggatt tggttttgag gataacagac ttatgaatgg 1500 1560 taattggttg agggaatcac aaccaaatga cattttgcag ttcttccgca tattagctat ttgtcacaca gctattcccg agctgaacga ggagactggc aagtacactt atgaagcaga 1620 1680 gtcacctgat gaggettett ttettgetge tgctagagag tttggttttg agttetteaa gagaacccag tcaagcgttt ttatccgcga gaggttctct ggttcagggc aaataatcga 1740 aagggagtac aaagttctga atttgttgga atttacgagc aaaagaaagc gaatgacagt 1800 aattgtacgc gatgaggaag ggcagattct tctactatgc aaaggagctg acagcatcat 1860 ctttgagcgg ttggcgaaga atggaaagac atacttggga cctaccacta ggcatttaac 1920 tgaatatgga gaagccggac tccgtacact cgcacttgct tacagaaagc ttgatgagga 1980 tgaatatgca gcttggaact ctgagtttct taagga
- (2) INFORMATION FOR SEQ ID NO:526:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..671
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586603
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

Pro Ala Thr Leu Glu Gly Gln Asp Ser Gln Pro Ile Gln Gly Pro Gly
1 5 10 15

Phe Ser Arg Thr Val Phe Cys Asn Gln Pro His Met His Lys Lys

2.5 Pro Leu Arg Tyr Arg Ser Asn Tyr Val Ser Thr Thr Arg Tyr Asn Leu 4.0 Ile Thr Phe Phe Pro Lys Ser Leu Tyr Glu Gln Phe His Arg Ala Ala Asn Leu Tyr Phe Leu Val Ala Ala Ile Leu Ser Val Phe Pro Leu Ser Pro Phe Asn Lys Trp Ser Met Ile Ala Pro Leu Val Phe Val Val Gly Leu Ser Met Leu Lys Glu Ala Leu Glu Asp Trp Arg Arg Phe Met Gln Asp Val Lys Ile Asn Ala Arg Lys Thr Cys Val His Lys Ser Asp Gly Val Phe Arg Gln Arg Lys Trp Lys Lys Val Ser Val Gly Asp Ile Val Lys Val Glu Lys Asp Glu Phe Phe Pro Ala Asp Leu Leu Leu Ser Ser Ser Tyr Glu Asp Gly Ile Cys Tyr Val Glu Thr Met Asn Leu Asp Gly Glu Thr Asn Leu Lys Val Lys Arg Ser Leu Glu Val Ser Leu Pro Leu Asp Asp Glu Ser Phe Lys Asn Phe Met Ala Thr Ile Arg Cys Glu Asp Pro Asn Pro Asn Leu Tyr Thr Phe Val Gly Asn Leu Glu Phe Glu Arg Gln Thr Phe Pro Leu Asp Pro Ser Gln Ile Leu Leu Arg Asp Ser Lys Leu Arg Asn Thr Thr Tyr Val Tyr Gly Val Val Val Phe Thr Gly Phe Asp Thr Lys Val Met Gln Asn Ser Thr Lys Ser Pro Ser Lys Arg Ser Arg Ile Glu Arg Thr Met Asp Tyr Ile Ile Tyr Thr Leu Leu Val Leu Leu Ile Leu Ile Ser Cys Ile Ser Ser Ser Gly Phe Ala Trp Glu Thr Glu Phe His Met Pro Lys Met Trp Tyr Leu Arg Pro Gly Glu Pro Ile Asp Phe Thr Asn Pro Ile Asn Pro Ile Tyr Ala Gly Val Val His Leu Ile Thr Ala Leu Leu Leu Tyr Gly Tyr Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu Val Val Lys Val Trp Gln Ala Ser Phe Ile Asn Gln Asp Leu His Met Tyr Asp Asp Glu Ser Gly Val Pro Ala Asn Ala Arg Thr Ser Asn Leu Asn Glu Glu Leu Gly Gln Val His Thr Ile Leu Ser Asp Lys Thr Gly Thr Leu Thr Cys Asn Gln Met Asp Phe Leu Lys Cys Ser Ile Ala Gly Thr Ser Tyr Gly Val Arg Ser Ser Glu Val Glu Val Ala Ala Ala Lys Gln Met Ala Val Asp Leu Glu Glu His Gly Glu Ile Ser Ser Thr Pro Gln Ser Gln Thr Lys Val Tyr Gly Thr Trp Asp Ser Ser Arg Xaa Gln Glu Ile Glu Val Glu Gly Asp Asn Asn Tyr Asn Thr Pro Arg Ala Pro Ile Lys Gly Phe Gly Phe Glu Asp Asn Arg Leu Met Asn Gly Asn Trp Leu Arg Glu Ser Gln Pro Asn Asp Ile Leu

Gln Phe Phe Arg Ile Leu Ala Ile Cys His Thr Ala Ile Pro Glu Leu 520 Asn Glu Glu Thr Gly Lys Tyr Thr Tyr Glu Ala Glu Ser Pro Asp Glu 535 540 Ala Ser Phe Leu Ala Ala Ala Arg Glu Phe Gly Phe Glu Phe Phe Lys 550 555 Arg Thr Gln Ser Ser Val Phe Ile Arg Glu Arg Phe Ser Gly Ser Gly 565 570 Gln Ile Ile Glu Arg Glu Tyr Lys Val Leu Asn Leu Leu Glu Phe Thr 580 585 590 Ser Lys Arg Lys Arg Met Thr Val Ile Val Arg Asp Glu Glu Gly Gln 600 605 Ile Leu Leu Cys Lys Gly Ala Asp Ser Ile Ile Phe Glu Arg Leu 615 620 Ala Lys Asn Gly Lys Thr Tyr Leu Gly Pro Thr Thr Arg His Leu Thr 635 630 Glu Tyr Gly Glu Ala Gly Leu Arg Thr Leu Ala Leu Ala Tyr Arg Lys 645 650 Leu Asp Glu Asp Glu Tyr Ala Ala Trp Asn Ser Glu Phe Leu Lys 660 665

- (2) INFORMATION FOR SEQ ID NO:527:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 644 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..644
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586604
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527: Met His Lys Lys Pro Leu Arg Tyr Arg Ser Asn Tyr Val Ser Thr

1 5 10 15 Thr Arg Tyr Asn Leu Ile Thr Phe Phe Pro Lys Ser Leu Tyr Glu Gln 20 25 30

Phe His Arg Ala Ala Asn Leu Tyr Phe Leu Val Ala Ala Ile Leu Ser 35 40 45

Val Phe Pro Leu Ser Pro Phe Asn Lys Trp Ser Met Ile Ala Pro Leu 50 55 60

Val Phe Val Val Gly Leu Ser Met Leu Lys Glu Ala Leu Glu Asp Trp 65 70 75 80

Arg Arg Phe Met Gln Asp Val Lys Ile Asn Ala Arg Lys Thr Cys Val 85 90 95

Val Gly Asp Ile Val Lys Val Glu Lys Asp Glu Phe Phe Pro Ala Asp 115 120 125

Leu Leu Leu Ser Ser Ser Tyr Glu Asp Gly Ile Cys Tyr Val Glu 130 135 140

Thr Met Asn Leu Asp Gly Glu Thr Asn Leu Lys Val Lys Arg Ser Leu 145 150 155 160

145 150 160
Glu Val Ser Leu Pro Leu Asp Asp Glu Ser Phe Lys Asn Phe Met
165 170 175

Ala Thr Ile Arg Cys Glu Asp Pro Asn Pro Asn Leu Tyr Thr Phe Val

Gly Asn Leu Glu Phe Glu Arg Gln Thr Phe Pro Leu Asp Pro Ser Gln
195 200 205

Ile Leu Leu Arg Asp Ser Lys Leu Arg Asn Thr Thr Tyr Val Tyr Gly
210 215 220

Val Val Val Phe Thr Gly Phe Asp Thr Lys Val Met Gln Asn Ser Thr

235 230 225 Lys Ser Pro Ser Lys Arg Ser Arg Ile Glu Arg Thr Met Asp Tyr Ile 245 250 255 Ile Tyr Thr Leu Leu Val Leu Leu Ile Leu Ile Ser Cys Ile Ser Ser 265 260 Ser Gly Phe Ala Trp Glu Thr Glu Phe His Met Pro Lys Met Trp Tyr 280 285 Leu Arg Pro Gly Glu Pro Ile Asp Phe Thr Asn Pro Ile Asn Pro Ile 295 300 Tyr Ala Gly Val Val His Leu Ile Thr Ala Leu Leu Leu Tyr Gly Tyr 305 310 315 320 Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu Val Val Lys Val Trp 325 330 Gln Ala Ser Phe Ile Asn Gln Asp Leu His Met Tyr Asp Asp Glu Ser 340 345 Gly Val Pro Ala Asn Ala Arg Thr Ser Asn Leu Asn Glu Glu Leu Gly 355 360 365 Gln Val His Thr Ile Leu Ser Asp Lys Thr Gly Thr Leu Thr Cys Asn 375 380 Gln Met Asp Phe Leu Lys Cys Ser Ile Ala Gly Thr Ser Tyr Gly Val 385 390 395 Arg Ser Ser Glu Val Glu Val Ala Ala Ala Lys Gln Met Ala Val Asp 410 405 Leu Glu Glu His Gly Glu Ile Ser Ser Thr Pro Gln Ser Gln Thr Lys 420 425 430 Val Tyr Gly Thr Trp Asp Ser Ser Arg Xaa Gln Glu Ile Glu Val Glu 435 440 445 Gly Asp Asn Asn Tyr Asn Thr Pro Arg Ala Pro Ile Lys Gly Phe Gly 450 455 460 Phe Glu Asp Asn Arg Leu Met Asn Gly Asn Trp Leu Arg Glu Ser Gln 465 470 475 Pro Asn Asp Ile Leu Gln Phe Phe Arg Ile Leu Ala Ile Cys His Thr 485 490 Ala Ile Pro Glu Leu Asn Glu Glu Thr Gly Lys Tyr Thr Tyr Glu Ala 500 505 510 Glu Ser Pro Asp Glu Ala Ser Phe Leu Ala Ala Ala Arg Glu Phe Gly 515 520 Phe Glu Phe Phe Lys Arg Thr Gln Ser Ser Val Phe Ile Arg Glu Arg 540 530 535 Phe Ser Gly Ser Gly Gln Ile Ile Glu Arg Glu Tyr Lys Val Leu Asn 555 545 550 Leu Leu Glu Phe Thr Ser Lys Arg Lys Arg Met Thr Val Ile Val Arg 565 570 Asp Glu Glu Gly Gln Ile Leu Leu Leu Cys Lys Gly Ala Asp Ser Ile 580 585 590 Ile Phe Glu Arg Leu Ala Lys Asn Gly Lys Thr Tyr Leu Gly Pro Thr 595 600 605 Thr Arg His Leu Thr Glu Tyr Gly Glu Ala Gly Leu Arg Thr Leu Ala 610 615 620 Leu Ala Tyr Arg Lys Leu Asp Glu Asp Glu Tyr Ala Ala Trp Asn Ser 630 635 Glu Phe Leu Lys

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..585

(D) OTHER INFORMATION: / Ceres Seq. ID 1586605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528: Met Ile Ala Pro Leu Val Phe Val Val Gly Leu Ser Met Leu Lys Glu 10 Ala Leu Glu Asp Trp Arg Arg Phe Met Gln Asp Val Lys Ile Asn Ala 25 Arg Lys Thr Cys Val His Lys Ser Asp Gly Val Phe Arg Gln Arg Lys 40 Trp Lys Lys Val Ser Val Gly Asp Ile Val Lys Val Glu Lys Asp Glu 55 Phe Phe Pro Ala Asp Leu Leu Leu Ser Ser Ser Tyr Glu Asp Gly 75 70 Ile Cys Tyr Val Glu Thr Met Asn Leu Asp Gly Glu Thr Asn Leu Lys 90 Val Lys Arg Ser Leu Glu Val Ser Leu Pro Leu Asp Asp Asp Glu Ser 105 110 100 Phe Lys Asn Phe Met Ala Thr Ile Arg Cys Glu Asp Pro Asn Pro Asn 120 125 Leu Tyr Thr Phe Val Gly Asn Leu Glu Phe Glu Arg Gln Thr Phe Pro 135 140 Leu Asp Pro Ser Gln Ile Leu Leu Arg Asp Ser Lys Leu Arg Asn Thr 150 155 Thr Tyr Val Tyr Gly Val Val Val Phe Thr Gly Phe Asp Thr Lys Val 170 165 Met Gln Asn Ser Thr Lys Ser Pro Ser Lys Arg Ser Arg Ile Glu Arg 185 190 180 Thr Met Asp Tyr Ile Ile Tyr Thr Leu Leu Val Leu Leu Ile Leu Ile 200 Ser Cys Ile Ser Ser Ser Gly Phe Ala Trp Glu Thr Glu Phe His Met 220 210 215 Pro Lys Met Trp Tyr Leu Arg Pro Gly Glu Pro Ile Asp Phe Thr Asn 235 230 Pro Ile Asn Pro Ile Tyr Ala Gly Val Val His Leu Ile Thr Ala Leu 250 245 Leu Leu Tyr Gly Tyr Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu 260 265 Val Val Lys Val Trp Gln Ala Ser Phe Ile Asn Gln Asp Leu His Met 280 Tyr Asp Asp Glu Ser Gly Val Pro Ala Asn Ala Arg Thr Ser Asn Leu 300 295 Asn Glu Glu Leu Gly Gln Val His Thr Ile Leu Ser Asp Lys Thr Gly 315 310 Thr Leu Thr Cys Asn Gln Met Asp Phe Leu Lys Cys Ser Ile Ala Gly 330 Thr Ser Tyr Gly Val Arg Ser Ser Glu Val Glu Val Ala Ala Ala Lys 345 Gln Met Ala Val Asp Leu Glu Glu His Gly Glu Ile Ser Ser Thr Pro 365 360 Gln Ser Gln Thr Lys Val Tyr Gly Thr Trp Asp Ser Ser Arg Xaa Gln 375 380 Glu Ile Glu Val Glu Gly Asp Asn Asn Tyr Asn Thr Pro Arg Ala Pro 390 395 Ile Lys Gly Phe Gly Phe Glu Asp Asn Arg Leu Met Asn Gly Asn Trp 410 Leu Arg Glu Ser Gln Pro Asn Asp Ile Leu Gln Phe Phe Arg Ile Leu 425 Ala Ile Cys His Thr Ala Ile Pro Glu Leu Asn Glu Glu Thr Gly Lys 440 445 Tyr Thr Tyr Glu Ala Glu Ser Pro Asp Glu Ala Ser Phe Leu Ala Ala

```
455
   450
Ala Arg Glu Phe Gly Phe Glu Phe Phe Lys Arg Thr Gln Ser Ser Val
                                      475
                   470
Phe Ile Arg Glu Arg Phe Ser Gly Ser Gly Gln Ile Ile Glu Arg Glu
                                   490
               485
Tyr Lys Val Leu Asn Leu Leu Glu Phe Thr Ser Lys Arg Lys Arg Met
                              505
           500
Thr Val Ile Val Arg Asp Glu Glu Gly Gln Ile Leu Leu Cys Lys
                        520
Gly Ala Asp Ser Ile Ile Phe Glu Arg Leu Ala Lys Asn Gly Lys Thr
                                          540
   530
                       535
Tyr Leu Gly Pro Thr Thr Arg His Leu Thr Glu Tyr Gly Glu Ala Gly
                                       555
                550
Leu Arg Thr Leu Ala Leu Ala Tyr Arg Lys Leu Asp Glu Asp Glu Tyr
                                   570
              565
Ala Ala Trp Asn Ser Glu Phe Leu Lys
           580
(2) INFORMATION FOR SEQ ID NO:529:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586689
- - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..39
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586690
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Lys Lys Arg Ile Asp Leu Gly Leu Arg Arg Arg Arg Arg Arg Arg Arg 20 25 30

Arg Arg Arg Ser Lys Lys Ile 35

- (2) INFORMATION FOR SEQ ID NO:531:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..38
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586691
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

- (2) INFORMATION FOR SEQ ID NO:532:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..705
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532: atgcgatggc atgctgagca ccaatcgaag gagggagaaa tgaatcatcc ttcaaatgcg 60 120 gcagagtgga gatatttcca agagttacat ccccggtttg ctgaagaacc ccgtaacgtt 180 tatctcgggt tgtgtactga tgggttcaat ccatttggca tgtctcgtaa tcattcgttg 240 tggcctgtga tcctaactcc atataatatt gatgttatgc atatagagaa gaattttctt gacaacatca tgaacactct cttgggtgtt aagggtaaat caaaagacaa tatcatgtca 300 agattggata ttgagaaata ttgttctcgg ccaggcttac atattcatag tacggatggt 360 420 tattcttcag atttggctag ttgtgtagat ttggagaatg gtaagttttc aggcatgaag 480 ggtcatgatt gtcatgtttt tatggagcga ctacttccat ttatctttgc tgaacttctt 540 gaccgaaatg tccaccttgc attatcagga attggagcat ttttccggga cctatgttcg 600 agaactttac agacaagtcg cgttcaaatt ctcaaacaga acatagtttt aatcatctgt 660 aacttggaaa agatctttcc accatcattt ttcgatgtta tggaacattt acctatccat ctcccatacg aagctgaatt gggtggccct gtccaatata ggtga
- (2) INFORMATION FOR SEQ ID NO:533:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..234
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1586697
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:
- Met Arg Trp His Ala Glu His Gln Ser Lys Glu Gly Glu Met Asn His 1 5 10 15
 Pro Ser Asn Ala Ala Glu Trp Arg Tyr Phe Gln Glu Leu His Pro Arg
- 20 25 30
 Phe Ala Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys Thr Asp Gly
 35 40 45
- Phe Asn Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp Pro Val Ile
- Leu Thr Pro Tyr Asn Ile Asp Val Met His Ile Glu Lys Asn Phe Leu 65 70 75 80
- Asp Asn Ile Met Asn Thr Leu Leu Gly Val Lys Gly Lys Ser Lys Asp 85 90 95
- Asn Ile Met Ser Arg Leu Asp Ile Glu Lys Tyr Cys Ser Arg Pro Gly
 100 105 110
- Leu His Ile His Ser Thr Asp Gly Tyr Ser Ser Asp Leu Ala Ser Cys
 115 120 125
- Val Asp Leu Glu Asn Gly Lys Phe Ser Gly Met Lys Gly His Asp Cys 130 - 135 - 140 His Val Phe Met Glu Arg Leu Leu Pro Phe Ile Phe Ala Glu Leu Leu

150 155 145 Asp Arg Asn Val His Leu Ala Leu Ser Gly Ile Gly Ala Phe Phe Arg 165 170 175 Asp Leu Cys Ser Arg Thr Leu Gln Thr Ser Arg Val Gln Ile Leu Lys 180 185 190 Gln Asn Ile Val Leu Ile Ile Cys Asn Leu Glu Lys Ile Phe Pro Pro 195 200 205 Ser Phe Phe Asp Val Met Glu His Leu Pro Ile His Leu Pro Tyr Glu 210 215 Ala Glu Leu Gly Gly Pro Val Gln Tyr Arg 230 (2) INFORMATION FOR SEQ ID NO:534: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 221 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..221 (D) OTHER INFORMATION: / Ceres Seq. ID 1586699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534: Met Asn His Pro Ser Asn Ala Ala Glu Trp Arg Tyr Phe Gln Glu Leu 10 5 His Pro Arg Phe Ala Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys 25 20 Thr Asp Gly Phe Asn Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp 40 Pro Val Ile Leu Thr Pro Tyr Asn Ile Asp Val Met His Ile Glu Lys 55 Asn Phe Leu Asp Asn Ile Met Asn Thr Leu Leu Gly Val Lys Gly Lys 75 70 Ser Lys Asp Asn Ile Met Ser Arg Leu Asp Ile Glu Lys Tyr Cys Ser 85 90 Arg Pro Gly Leu His Ile His Ser Thr Asp Gly Tyr Ser Ser Asp Leu 100 105 Ala Ser Cys Val Asp Leu Glu Asn Gly Lys Phe Ser Gly Met Lys Gly 115 120 His Asp Cys His Val Phe Met Glu Arg Leu Leu Pro Phe Ile Phe Ala 135 140 Glu Leu Leu Asp Arg Asn Val His Leu Ala Leu Ser Gly Ile Gly Ala 145 150 155 Phe Phe Arg Asp Leu Cys Ser Arg Thr Leu Gln Thr Ser Arg Val Gln 165 170 175 Ile Leu Lys Gln Asn Ile Val Leu Ile Ile Cys Asn Leu Glu Lys Ile 180 185 190 Phe Pro Pro Ser Phe Phe Asp Val Met Glu His Leu Pro Ile His Leu 195 200 205 Pro Tyr Glu Ala Glu Leu Gly Gly Pro Val Gln Tyr Arg 215 210 (2) INFORMATION FOR SEQ ID NO:535: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 996 base pairs (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..996

(D) OTHER INFORMATION: / Ceres Seq. ID 1587283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:						
atggacagaa	gaatccctgc	ttacctgaaa	ggaaaaagaa	aggagagtga	ttattcacct	60
cctcctagaa	agagggttag	agctcgagat	ctggataatt	ctgaacttat	aaaggagaat	120
acticticactic	ttatgggaag	acttaccaac	cctatgcatc	agagactctg	gtctctattc	180
ccttttatct	ctaatcgatg	gaacctgaaa	gggaaagctg	taggctcaga	tcttggaaga	240
ccctccatcc	astttagatt	tgattatgaa	gaagatttgc	agaaggtgct	agagaataaa	300
gggtgcttt	ttantanata	catacttata	ctccagcgtt	gggaacttgt	aatctctqct	360
ccctaccact	Ligalization	gatggccate	gaagtacaag	gtctcccaaa	gcactactgg	420
teettteegt	caacgatacc	Citciggata	gaagtacaag	aaatottooa	ccatgagatt	480
ctgccaaaga	tgctattcac	aateggtgag	gacctaagag	tagaagatat	taccaaddad	540
acccctacca	caattcagat	gaaagttctt	atcaatggtt	cggaacctcc	taccaaggag	600
acaatggtgg	actttcctga	tggcagtgaa	gtattgattg	acccacgaga	aaaaaayayt	660
gtccaggtct	acaaacagca	gtacctgtca	aaactgccaa	atcggtatca	caaccctctc	
ctcttaaaga	accacacact	tcaagggatg	gacccaattc	tactcaaaag	agttccaagt	720
caagaggagt	accttaccaa	caatcgcgcc	cgtcactcta	tctccactct	caaggcagat	780
ctcactctaa	cagaagaggt	catgaggagg	gtagccagca	aaactactcc	aactcagatt	840
acaddactd	tagacagaga	gaacggagtc	ttagagctgc	gtccacaaaa	tcccaagagc	900
acaggeacee	agacctaat	agagatttct	ctattcagca	acagtcaaga	cacacatcaa	960
accacagaag	agageeeaae	atagacccaa	gagtga	, ,		
atatgcagtg	gagagagaaa	gtaccccaaa	gagega			

- (2) INFORMATION FOR SEQ ID NO:536:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:536: Met Asp Arg Arg Ile Pro Ala Tyr Leu Lys Gly Lys Arg Lys Glu Ser 10 Asp Tyr Ser Pro Pro Pro Arg Lys Arg Val Arg Ala Arg Asp Leu Asp 25 20 Asn Ser Glu Leu Ile Lys Glu Asn Ala Leu Thr Leu Met Gly Arg Leu 45 40 Thr Asn Pro Met His Gln Arg Leu Trp Ser Leu Phe Pro Phe Ile Ser 60 55 Asn Arg Trp Asn Leu Lys Gly Lys Ala Val Gly Ser Asp Leu Gly Arg 75 70 Gly Cys Phe Gln Phe Arg Phe Asp Tyr Glu Glu Asp Leu Gln Lys Val 90 85 Leu Glu Asn Lys Pro Tyr His Phe Asp His Trp Met Val Ile Leu Gln 100 105 110 Arg Trp Glu Leu Val Ile Ser Ala Ser Phe Pro Ser Thr Ile Pro Phe 120 125 Trp Ile Glu Val Gln Gly Leu Pro Lys His Tyr Trp Leu Pro Lys Met 135 140 Leu Phe Thr Ile Gly Glu Asp Leu Arg Glu Ile Leu Asp His Glu Ile 155 150 Thr Pro Thr Thr Ile Gln Met Lys Val Leu Ile Asn Gly Leu Glu Pro 170 175 165 Leu Thr Lys Glu Thr Met Val Asp Phe Pro Asp Gly Ser Glu Val Leu

235

180 185

230

190

Gln Glu Glu Tyr Leu Thr Asn Asn Arg Ala Arg His Ser Ile Ser Thr
245
250
255

Leu Lys Ala Asp Leu Thr Leu Thr Glu Glu Val Met Arg Arg Val Ala 260 265 270

Ser Lys Thr Thr Pro Thr Gln Ile Thr Gly Thr Leu Asp Arg Glu Asn 275 280 285

Gly Val Leu Glu Leu Arg Pro Gln Asn Pro Lys Ser Thr Ile Glu Glu 290 295 300

Ser Leu Ile Glu Ile Ser Leu Phe Ser Asn Ser Gln Asp Thr His Gln 305 310 315 320

Ile Cys Ser Gly Glu Arg Lys Tyr Pro Lys Glu 325 330

- (2) INFORMATION FOR SEQ ID NO:537:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..287
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587286
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:
 Met Gly Arg Leu Thr Asn Pro Met His Gln Arg Leu Trp Ser Leu Phe

1 5 10 15 Pro Phe Ile Ser Asn Arg Trp Asn Leu Lys Gly Lys Ala Val Gly Ser 20 25 30

Asp Leu Gly Arg Gly Cys Phe Gln Phe Arg Phe Asp Tyr Glu Glu Asp

Leu Gln Lys Val Leu Glu Asn Lys Pro Tyr His Phe Asp His Trp Met
50 55 60

Val Ile Leu Gln Arg Trp Glu Leu Val Ile Ser Ala Ser Phe Pro Ser 65 70 75 80

Thr Ile Pro Phe Trp Ile Glu Val Gln Gly Leu Pro Lys His Tyr Trp 85 90 95

Leu Pro Lys Met Leu Phe Thr Ile Gly Glu Asp Leu Arg Glu Ile Leu 100 105 110

Asp His Glu Ile Thr Pro Thr Thr Ile Gln Met Lys Val Leu Ile Asn 115 120 125

Gly Leu Glu Pro Leu Thr Lys Glu Thr Met Val Asp Phe Pro Asp Gly 130 135 140
Ser Glu Val Leu Ile Asp Pro Arg Glu Lys Lys Ser Val Gln Val Tyr

145 150 155 160
Lys Gln Gln Tyr Leu Ser Lys Leu Pro Asn Arg Tyr His Asn Pro Leu

165 170 175 Leu Leu Lys Asn His Thr Leu Gln Gly Met Asp Pro Ile Leu Leu Lys

180 185 190
Arg Val Pro Ser Gln Glu Glu Tyr Leu Thr Asn Asn Arg Ala Arg His

195 200 205 Ser Ile Ser Thr Leu Lys Ala Asp Leu Thr Leu Thr Glu Glu Val Met

210 215 220

The Box No. 210 Sor Lya Thr Thr Pro Thr Glu Tle Thr Gly Thr Leu

Arg Arg Val Ala Ser Lys Thr Thr Pro Thr Gln Ile Thr Gly Thr Leu 225 230 240

Asp Arg Glu Asn Gly Val Leu Glu Leu Arg Pro Gln Asn Pro Lys Ser 245 250 255

Thr Ile Glu Glu Ser Leu Ile Glu Ile Ser Leu Phe Ser Asn Ser Gln 265 270

Asp Thr His Gln Ile Cys Ser Gly Glu Arg Lys Tyr Pro Lys Glu 275 280 285

(2) INFORMATION FOR SEQ ID NO:538:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 688 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..688
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538: atccacacaa catttacaca atacccttat tctccacgta gaatcaagag tacttctttt 60 120 ccttaaatct ctacaaaaaa aaaatcgatc tatttactaa gagatcataa atatagattc 180 atagacctat ttaagaaacg acttaagaag ctgttggatc atataccata taaaatagca atggatatga taacgaagat ggtgatggag agaccggtgg tgatttacag caagagctct 240 tgctgtatgt ctcacacgat caagactttg ctctgcgatt tcggagcaaa tccagcggtt 300 tacgagctgg atgagatatc tagagggagg gagatcgagc aggcgttgtt gcggctcggg 360 420 tgtagccccg cagttccggg cgttttcatt ggtggagagt tggtcggtgg agccaacgag gtcatgagtc tacatcttaa cggatccttg attcccatgc ttaagcgggc tggtgcattg 480 540 tgggtttgac ttatcatgtt tttaactagt ttacttaaca ctaagttaag tacgcagaat aattttaaca catctatgat cttggcatgg tgatatgatg agtccacgtc ggatcaataa 600 tcagtgtgtt gtctttttt ttttggttgt cttactttaa gatatgtatc gactgatacg 660 aacttctatg aaataaaaat atattgac
- (2) INFORMATION FOR SEQ ID NO:539:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539: Met Asp Met Ile Thr Lys Met Val Met Glu Arg Pro Val Val Ile Tyr

10 5 Ser Lys Ser Ser Cys Cys Met Ser His Thr Ile Lys Thr Leu Leu Cys 25 2.0

Asp Phe Gly Ala Asn Pro Ala Val Tyr Glu Leu Asp Glu Ile Ser Arg 40

Gly Arg Glu Ile Glu Gln Ala Leu Leu Arg Leu Gly Cys Ser Pro Ala 55

Val Pro Gly Val Phe Ile Gly Gly Glu Leu Val Gly Gly Ala Asn Glu 75 70

Val Met Ser Leu His Leu Asn Gly Ser Leu Ile Pro Met Leu Lys Arg 85

Ala Gly Ala Leu Trp Val

100

- (2) INFORMATION FOR SEQ ID NO:540:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..100
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587310
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met Ile Thr Lys Met Val Met Glu Arg Pro Val Val Ile Tyr Ser Lys 1 5 10 10 15 15 15 Ser Ser Cys Cys Met Ser His Thr Ile Lys Thr Leu Leu Cys Asp Phe 20 25 5 5 30 30 Gly Ala Asn Pro Ala Val Tyr Glu Leu Asp Glu Ile Ser Arg Gly Arg 35 40 40 45 Gly Gly Gly Ala Asn Gly Pro 50 55 60 Gly Val Phe Ile Gly Gly Gly Glu Leu Val Gly Gly Ala Asn Glu Val Met 65 70 75 80 Ser Leu His Leu Asn Gly Ser Leu Ile Pro Met Leu Lys Arg Ala Gly

90

Ala Leu Trp Val

100

- (2) INFORMATION FOR SEQ ID NO:541:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587311
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Met Ser His Thr Ile Lys Thr Leu Leu Cys Asp Phe Gly Ala Asn Pro
20 25 30

Ala Val Tyr Glu Leu Asp Glu Ile Ser Arg Gly Arg Glu Ile Glu Gln
35 40 45

Ala Leu Leu Arg Leu Gly Cys Ser Pro Ala Val Pro Gly Val Phe Ile 50 55 60 Gly Gly Glu Leu Val Gly Gly Ala Asn Glu Val Met Ser Leu His Leu

65 70 75 80
Asn Gly Ser Leu Ile Pro Met Leu Lys Arg Ala Gly Ala Leu Trp Val
85 90 95

- (2) INFORMATION FOR SEQ ID NO:542:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..150
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587406
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

atgtteteta teagtggagg tgeaaaateg teagetttea gattettete eggeteaaaa 60 egtgaageaa tttgggetea agaactttat teataceaaa gggaaaataa atgtgageat 120 eaagaaaage agetaaatta tgtaaattga

- (2) INFORMATION FOR SEQ ID NO:543:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..49 (D) OTHER INFORMATION: / Ceres Seq. ID 1587407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543: Met Phe Ser Ile Ser Gly Gly Ala Lys Ser Ser Ala Phe Arg Phe Phe 10 Ser Gly Ser Lys Arg Glu Ala Ile Trp Ala Gln Glu Leu Tyr Ser Tyr 25 20 Gln Arg Glu Asn Lys Cys Glu His Gln Glu Lys Gln Leu Asn Tyr Val 4.0 Asn (2) INFORMATION FOR SEQ ID NO:544: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..44 (D) OTHER INFORMATION: / Ceres Seq. ID 1587409 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544: Cys Ser Leu Ser Val Glu Val Gln Asn Arg Gln Leu Ser Asp Ser Ser 10 Pro Ala Gln Asn Val Lys Gln Phe Gly Leu Lys Asn Phe Ile His Thr 25 20 Lys Gly Lys Ile Asn Val Ser Ile Lys Lys Ser Ser 35 (2) INFORMATION FOR SEQ ID NO:545: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..465 (D) OTHER INFORMATION: / Ceres Seq. ID 1587537 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545: aggeegaate ttegeeagea taaggaeget caagtegaga aettegtgtg gaaacatate ctatgtcgtc acgggatacc ttatgagatt gtcacggata acggctcgca gtttatatca accegettee aaggettetg tgataagtgg ggaattegae ttageaagte aacaceaega tatececaag gaaaeggeea ageegaagee getaacaaaa caateetega eggattgaag 240 aaacggctcg atgctaaaaa gggctcgtgg tccgacgaac tcgaaggtgt acttttgtcg categgacaa eteetegeeg agecacagga gaaaceettt tegeeetagt etaeggaaeg 360 aaatgcgtaa ttccagccga aatgatagta ccgagttacg ccggagtcta tctcccgaga 420 acgatectga taacactcaa aggeteeteg acgaactega tetga (2) INFORMATION FOR SEQ ID NO:546: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

120

180

240

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1587538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Arg Pro Asn Leu Arg Gln His Lys Asp Ala Gln Val Glu Asn Phe Val

1 5 10 15

Trp Lys His Tle Leu Cys Arg His Gly Tle Pro Tyr Glu Tle Val Thr

Trp Lys His Ile Leu Cys Arg His Gly Ile Pro Tyr Glu Ile Val Thr

Asp Asn Gly Ser Gln Phe Ile Ser Thr Arg Phe Gln Gly Phe Cys Asp 35 40 45

Lys Trp Gly Ile Arg Leu Ser Lys Ser Thr Pro Arg Tyr Pro Gln Gly 50 55 60

Asn Gly Gln Ala Glu Ala Ala Asn Lys Thr Ile Leu Asp Gly Leu Lys 65 70 75 80

Lys Arg Leu Asp Ala Lys Lys Gly Ser Trp Ser Asp Glu Leu Glu Gly 85 90 95

Val Leu Leu Ser His Arg Thr Thr Pro Arg Arg Ala Thr Gly Glu Thr 100 $$ 105 $$ 110

Leu Phe Ala Leu Val Tyr Gly Thr Lys Cys Val Ile Pro Ala Glu Met 115 120 125

Ile Val Pro Ser Tyr Ala Gly Val Tyr Leu Pro Arg Thr Ile Leu Ile 130 135 140

Thr Leu Lys Gly Ser Ser Thr Asn Ser Ile 145

- (2) INFORMATION FOR SEQ ID NO:547:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

Gly Arg Ile Phe Ala Ser Ile Arg Thr Leu Lys Ser Arg Thr Ser Cys 1 5 10 15 Gly Asn Ile Ser Tyr Val Val Thr Gly Tyr Leu Met Arg Leu Ser Arg

20 25 30

Ile Thr Ala Arg Ser Leu Tyr Gln Pro Ala Ser Lys Ala Ser Val Ile

35 40 45
Ser Gly Glu Phe Asp Leu Ala Ser Gln His His Asp Ile Pro Lys Glu
50 55 60

Thr Ala Lys Pro Lys Pro Leu Thr Lys Gln Ser Ser Thr Asp 65 70 75

- (2) INFORMATION FOR SEQ ID NO:548:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2058
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587540
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

atgagtecta gacagtetec gteaateceg agegettete ttgtegatte tagegaetea aateaeceag atgatettee eeegatetae aaaeggagag eagtttggae gtettetgaa gaggatgetg tatettette gggtgeeeee gageagaega eteeetteae ggetegggaa gataceaatg eegatatege teeggaaetg gatttgeeeg atgateeega geegeetett

attcgcaggt cttttgtccc gatggctgac gaagccggga catccaattg gcgaaatgtg 300 cccgagccct tcatgccgac ggttaagatt gaggattttc tttatttcgg cccaaacgag 360 420 acagaagata tootgogtot taatgagcag aaagotttog aaaaggotga gaagaagaag aggaagaaca aaaaggtgat aatgccagat cctcccggct caacattgtg caccgagcgg 480 540 tctctctcgg accttagggc tcgatttggt cttggcgctg taaccttgcg tgtgccgagc cctgacgagc gagccgacaa tccccctgcg ggtttctata ccttgtatga gggtttcttt 600 tatggttgct tcttatggct accaatcccg aggctggtct tggagtatgt gcaatcatat 660 cagattgccc tttcccagat cacgatgcga tctttgagac atttgctcgg gattttgatt 720 780 cggagttatg aatccgaaac tgaaattacg ctcgttcatc tgaggaattt tctcgagatc 840 cggcgggttc caaaatccaa agtggatcgg tattatatat ctcctgctaa ggtaagaaga ttattgacgg gttcccgagc aaggacgatt cgtataccga ccacttcttc tacgtggctc 900 960 toggagatgo tgttcacgat gatottcccg ggacaacgca ctctcaagtt totcgagccg attectgacg atttectete ggettateae gegttateag eteggaagtg tgattggteg 1020 aaacacttct ctcgggatcg agtcaaacga gcactccgtc ttcttcacgg tgtttcctgt 1080 1140 cctaccagtt cagaatcttc ggaccacaga actcaattct tcgtcgatat gcagtcaact aagctcactt tgagggaggt gtacgcgaag aaaaaagaag ataaagagag acgcttggcg 1200 1260 gaagagaaac gcctcgcgga tgcaggattg atttcaccgc gggtagcctc tccagatgcg actcaaaacc gggatgttgc teeegaagtt geggeeeegg ttgaeeegae geettetaaa 1320 gctcaagagg tcgatcctac tgctgctgcg cctttgcccg aggcggttgt tgcgctgcct 1380 gcgagcgaca agacggcgga taagcgtgtt cggacggatg attcatcgct taagaagaaa 1440 agcaagaaga agaaggcctc gagtgccgag gcgggaaaag agctccccat ctttgaggac 1500 cgggttgttg cctcgatgaa ccgaatggtg cactcgtacg attcggccgt tagaacaaca 1560 1620 tggaggcggc caacaggttg gctgaagcgg atgctcggat ccaatctgcc gagcgagaaa gagatgaggc gctttcccaa gctgccgcgg cgaaaaaata gcaaaggagg aagccgaaaa 1680 ggaggctttc gtgaacaagg cgaatgcatt aagatggccg agctgaacct gagggcggac 1740 tccgaggttg ttcgcctcaa acgcatgctg gccgaggcga gggaactacg tgatagcgaa 1800 gtggctcggg cttctcaaac ggcaaaatgt gagacctccg aggttttcat cgccagactt 1860 aaggetgeeg aacagaaagt etegettete gaegggatea aegateagtt tetgtaetta 1920 tcccaggcgc gggctaatgc gcaactgatc aaggcacttg aggaaggtgg agtgttggcg 1980 accgagaaag accaggtcgn agaatggctg naagacttcg ccaatgccga ggtcgatttc 2040 gccaattttg tcgcctag

- (2) INFORMATION FOR SEQ ID NO:549:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..685
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587541
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

Met Ser Pro Arg Gln Ser Pro Ser Ile Pro Ser Ala Ser Leu Val Asp

1 5 10 15

Ser Ser Asp Ser Asn His Pro Asp Asp Leu Pro Pro Ile Tyr Lys Arg 20 25 30

Arg Ala Val Trp Thr Ser Ser Glu Glu Asp Ala Val Ser Ser Ser Gly 35 40 45

Ala Pro Glu Gln Thr Thr Pro Phe Thr Ala Arg Glu Asp Thr Asn Ala 50 55 60

Asp Ile Ala Pro Glu Leu Asp Leu Pro Asp Asp Pro Glu Pro Pro Leu 65 70 75 80

Ile Arg Arg Ser Phe Val Pro Met Ala Asp Glu Ala Gly Thr Ser Asn 85 90 95

Trp Arg Asn Val Pro Glu Pro Phe Met Pro Thr Val Lys Ile Glu Asp
100 105 110

Phe Leu Tyr Phe Gly Pro Asn Glu Thr Glu Asp Ile Leu Arg Leu Asn 115 120 125

Glu Gln Lys Ala Phe Glu Lys Ala Glu Lys Lys Lys Arg Lys Asn Lys 130 135 140 Lys Val Ile Met Pro Asp Pro Pro Gly Ser Thr Leu Cys Thr Glu Arg 155 150 Ser Leu Ser Asp Leu Arg Ala Arg Phe Gly Leu Gly Ala Val Thr Leu 170 165 Arg Val Pro Ser Pro Asp Glu Arg Ala Asp Asn Pro Pro Ala Gly Phe 185 Tyr Thr Leu Tyr Glu Gly Phe Phe Tyr Gly Cys Phe Leu Trp Leu Pro 205 200 Ile Pro Arg Leu Val Leu Glu Tyr Val Gln Ser Tyr Gln Ile Ala Leu 215 220 Ser Gln Ile Thr Met Arg Ser Leu Arg His Leu Leu Gly Ile Leu Ile 230 235 Arg Ser Tyr Glu Ser Glu Thr Glu Ile Thr Leu Val His Leu Arg Asn 250 245 Phe Leu Glu Ile Arg Arg Val Pro Lys Ser Lys Val Asp Arg Tyr Tyr 260 265 Ile Ser Pro Ala Lys Val Arg Arg Leu Leu Thr Gly Ser Arg Ala Arg 280 Thr Ile Arg Ile Pro Thr Thr Ser Ser Thr Trp Leu Ser Glu Met Leu 295 Phe Thr Met Ile Phe Pro Gly Gln Arg Thr Leu Lys Phe Leu Glu Pro 310 315 Ile Pro Asp Asp Phe Leu Ser Ala Tyr His Ala Leu Ser Ala Arg Lys 325 330 Cys Asp Trp Ser Lys His Phe Ser Arg Asp Arg Val Lys Arg Ala Leu 340 345 Arg Leu Leu His Gly Val Ser Cys Pro Thr Ser Ser Glu Ser Ser Asp 360 His Arg Thr Gln Phe Phe Val Asp Met Gln Ser Thr Lys Leu Thr Leu 375 380 Arg Glu Val Tyr Ala Lys Lys Lys Glu Asp Lys Glu Arg Arg Leu Ala 390 395 Glu Glu Lys Arg Leu Ala Asp Ala Gly Leu Ile Ser Pro Arg Val Ala 410 405 Ser Pro Asp Ala Thr Gln Asn Arg Asp Val Ala Pro Glu Val Ala Ala 425 420 Pro Val Asp Pro Thr Pro Ser Lys Ala Gln Glu Val Asp Pro Thr Ala 445 440 Ala Ala Pro Leu Pro Glu Ala Val Val Ala Leu Pro Ala Ser Asp Lys 460 455 Thr Ala Asp Lys Arg Val Arg Thr Asp Asp Ser Ser Leu Lys Lys 475 470 Ser Lys Lys Lys Ala Ser Ser Ala Glu Ala Gly Lys Glu Leu Pro 490 Ile Phe Glu Asp Arg Val Val Ala Ser Met Asn Arg Met Val His Ser 510 505 Tyr Asp Ser Ala Val Arg Thr Thr Trp Arg Arg Pro Thr Gly Trp Leu 525 520 Lys Arg Met Leu Gly Ser Asn Leu Pro Ser Glu Lys Glu Met Arg Arg 540 535 Phe Pro Lys Leu Pro Arg Arg Lys Asn Ser Lys Gly Gly Ser Arg Lys 550 555 Gly Gly Phe Arg Glu Gln Gly Glu Cys Ile Lys Met Ala Glu Leu Asn 570 Leu Arg Ala Asp Ser Glu Val Val Arg Leu Lys Arg Met Leu Ala Glu 585 Ala Arg Glu Leu Arg Asp Ser Glu Val Ala Arg Ala Ser Gln Thr Ala 600 605 Lys Cys Glu Thr Ser Glu Val Phe Ile Ala Arg Leu Lys Ala Ala Glu 620 615 Gln Lys Val Ser Leu Leu Asp Gly Ile Asn Asp Gln Phe Leu Tyr Leu

Phe Ala Asn Ala Glu Val Asp Phe Ala Asn Phe Val Ala 675 680 685

- (2) INFORMATION FOR SEQ ID NO:550:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587543 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550: Met Ala Asp Glu Ala Gly Thr Ser Asn Trp Arg Asn Val Pro Glu Pro 10 Phe Met Pro Thr Val Lys Ile Glu Asp Phe Leu Tyr Phe Gly Pro Asn 20 25 Glu Thr Glu Asp Ile Leu Arg Leu Asn Glu Gln Lys Ala Phe Glu Lys 40 Ala Glu Lys Lys Lys Arg Lys Asn Lys Lys Val Ile Met Pro Asp Pro Pro Gly Ser Thr Leu Cys Thr Glu Arg Ser Leu Ser Asp Leu Arg Ala 75 Arg Phe Gly Leu Gly Ala Val Thr Leu Arg Val Pro Ser Pro Asp Glu 90 85 Arg Ala Asp Asn Pro Pro Ala Gly Phe Tyr Thr Leu Tyr Glu Gly Phe 100 105 Phe Tyr Gly Cys Phe Leu Trp Leu Pro Ile Pro Arg Leu Val Leu Glu 115 120 Tyr Val Gln Ser Tyr Gln Ile Ala Leu Ser Gln Ile Thr Met Arg Ser 130 135 140 Leu Arg His Leu Leu Gly Ile Leu Ile Arg Ser Tyr Glu Ser Glu Thr 145 150 155 Glu Ile Thr Leu Val His Leu Arg Asn Phe Leu Glu Ile Arg Arg Val 165 170 Pro Lys Ser Lys Val Asp Arg Tyr Tyr Ile Ser Pro Ala Lys Val Arg 185 180 Arg Leu Leu Thr Gly Ser Arg Ala Arg Thr Ile Arg Ile Pro Thr Thr 200 205 Ser Ser Thr Trp Leu Ser Glu Met Leu Phe Thr Met Ile Phe Pro Gly 220 210 215 Gln Arg Thr Leu Lys Phe Leu Glu Pro Ile Pro Asp Asp Phe Leu Ser 235 230 Ala Tyr His Ala Leu Ser Ala Arg Lys Cys Asp Trp Ser Lys His Phe 245 250 Ser Arg Asp Arg Val Lys Arg Ala Leu Arg Leu Leu His Gly Val Ser 265 270 Cys Pro Thr Ser Ser Glu Ser Ser Asp His Arg Thr Gln Phe Phe Val 275 280 Asp Met Gln Ser Thr Lys Leu Thr Leu Arg Glu Val Tyr Ala Lys Lys 300 290 295 Lys Glu Asp Lys Glu Arg Arg Leu Ala Glu Glu Lys Arg Leu Ala Asp 315 310 Ala Gly Leu Ile Ser Pro Arg Val Ala Ser Pro Asp Ala Thr Gln Asn 330 325

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Arg Asp Val Ala Pro Glu Val Ala Ala Pro Val Asp Pro Thr Pro Ser
                             345
           340
Lys Ala Gln Glu Val Asp Pro Thr Ala Ala Ala Pro Leu Pro Glu Ala
                                   365
                        360
       355
Val Val Ala Leu Pro Ala Ser Asp Lys Thr Ala Asp Lys Arg Val Arg
                                        380
                     375
Thr Asp Asp Ser Ser Leu Lys Lys Lys Ser Lys Lys Lys Ala Ser
                 390
                                    395
Ser Ala Glu Ala Gly Lys Glu Leu Pro Ile Phe Glu Asp Arg Val Val
                                410
              405
Ala Ser Met Asn Arg Met Val His Ser Tyr Asp Ser Ala Val Arg Thr
                             425
          420
Thr Trp Arg Arg Pro Thr Gly Trp Leu Lys Arg Met Leu Gly Ser Asn
                         440
                                           445
Leu Pro Ser Glu Lys Glu Met Arg Arg Phe Pro Lys Leu Pro Arg Arg
                                        460
                     455
Lys Asn Ser Lys Gly Gly Ser Arg Lys Gly Gly Phe Arg Glu Gln Gly
                                    475
                  470
Glu Cys Ile Lys Met Ala Glu Leu Asn Leu Arg Ala Asp Ser Glu Val
                                490
              485
Val Arg Leu Lys Arg Met Leu Ala Glu Ala Arg Glu Leu Arg Asp Ser
                            505
Glu Val Ala Arg Ala Ser Gln Thr Ala Lys Cys Glu Thr Ser Glu Val
                                            525
                         520
Phe Ile Ala Arg Leu Lys Ala Ala Glu Gln Lys Val Ser Leu Leu Asp
                                        540
                     535
Gly Ile Asn Asp Gln Phe Leu Tyr Leu Ser Gln Ala Arg Ala Asn Ala
                                 555
                  550
Gln Leu Ile Lys Ala Leu Glu Glu Gly Gly Val Leu Ala Thr Glu Lys
                                570
              565
Asp Gln Val Xaa Glu Trp Leu Xaa Asp Phe Ala Asn Ala Glu Val Asp
                          585
          580
Phe Ala Asn Phe Val Ala
```

- (2) INFORMATION FOR SEQ ID NO:551:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

595

- (A) NAME/KEY: -
- (B) LOCATION: 1..450
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

ataatcatgt catatctagt taagctcgat gtcgttgccc ttaatgtatc tggcaaaaac 60 tatatgtcat gggcatcaga tattaagatg catcttagat caaatgggct tcttagcacc 120 ataaatgcat ctgaaacgac atcagatgag agcaaagcta aagccatgcc agacatgaat 180 ggcttaatct ccaccaggat gatattatgt ggtgaaaaag tgagggatta tgatatgatt 240 ggtcatggtc gtgggagagg tcgtggtcat ggccgaggaa aggaaaaagt tccatccca 360 ataatttcaa cacggaaaaa accaacaaaa ataatgttgg ccgtattaag aaaaggcatg 420 ttgaaagcac ttgccacaga tgcggcatga

- (2) INFORMATION FOR SEQ ID NO:552:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..149
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:
- Ile Ile Met Ser Tyr Leu Val Lys Leu Asp Val Val Ala Leu Asn Val $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$
- Ser Gly Lys Asn Tyr Met Ser Trp Ala Ser Asp Ile Lys Met His Leu 20 25 30
- Arg Ser Asn Gly Leu Leu Ser Thr Ile Asn Ala Ser Glu Thr Thr Ser 35 40 45
- Asp Glu Ser Lys Ala Lys Ala Met Pro Asp Met Asn Gly Leu Ile Ser 50 55 60
- Thr Arg Met Ile Leu Cys Gly Glu Lys Val Ser Asp Tyr Asp Met Ile 65 70 75 80
- Glu Lys Thr Leu Ser Thr Phe His Pro Gly Asn Arg Gly Pro Gly Pro 85 90 95
- Cys Arg Gly Cys Gly His Gly Arg Gly Arg Gly Arg Gly His Gly Arg
 100 105 110
- Gly Lys Glu Lys Val Ser Ile Pro Ile Ile Ser Thr Arg Lys Lys Pro 115 120 125
- Thr Lys Ile Met Leu Ala Val Leu Arg Lys Gly Met Leu Lys Ala Leu 130 135 140

Ala Thr Asp Ala Ala

145

- (2) INFORMATION FOR SEQ ID NO:553:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..147
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:
- Met Ser Tyr Leu Val Lys Leu Asp Val Val Ala Leu Asn Val Ser Gly
 1 5 10 15
- Lys Asn Tyr Met Ser Trp Ala Ser Asp Ile Lys Met His Leu Arg Ser 20 25 30
- Asn Gly Leu Leu Ser Thr Ile Asn Ala Ser Glu Thr Thr Ser Asp Glu 35 40 45
- Ser Lys Ala Lys Ala Met Pro Asp Met Asn Gly Leu Ile Ser Thr Arg 50 55 60
- Met Ile Leu Cys Gly Glu Lys Val Ser Asp Tyr Asp Met Ile Glu Lys 65 70 75 80

 Thr Leu Ser Thr Phe His Pro Gly Asn Arg Gly Pro Gly Pro Cys Arg
- 85 90 95
 Gly Cys Gly His Gly Arg Gly Arg Gly Arg Gly His Gly Arg Gly Lys
 100 105 110
- Glu Lys Val Ser Ile Pro Ile Ile Ser Thr Arg Lys Lys Pro Thr Lys
 115 120 125
- Ile Met Leu Ala Val Leu Arg Lys Gly Met Leu Lys Ala Leu Ala Thr 130 135 140

Asp Ala Ala

145

- (2) INFORMATION FOR SEQ ID NO:554:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met Ser Trp Ala Ser Asp Ile Lys Met His Leu Arg Ser Asn Gly Leu 1 5 10 15

Leu Ser Thr Ile Asn Ala Ser Glu Thr Thr Ser Asp Glu Ser Lys Ala 20 25 30

Lys Ala Met Pro Asp Met Asn Gly Leu Ile Ser Thr Arg Met Ile Leu 35 40 45

Cys Gly Glu Lys Val Ser Asp Tyr Asp Met Ile Glu Lys Thr Leu Ser 50 55 60

Thr Phe His Pro Gly Asn Arg Gly Pro Gly Pro Cys Arg Gly Cys Gly 70 75 80

His Gly Arg Gly Arg Gly Arg Gly His Gly Arg Gly Lys Glu Lys Val

Ser Ile Pro Ile Ile Ser Thr Arg Lys Lys Pro Thr Lys Ile Met Leu
100 105 110

Ala Val Leu Arg Lys Gly Met Leu Lys Ala Leu Ala Thr Asp Ala Ala 115 120 125

- (2) INFORMATION FOR SEQ ID NO:555:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..329
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587579
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

ccaacaccga tagccttctc tatgacgaag agtttaccaa gtacctaaaa gaccatccag 60 acaactttag gttcgacaag gcattgagca gagaggagaa gaacaagaaa ggtggaaaga 120 tgtacgtgca ggacaagatt gaagaatata gtgatgagat cttcaagctt ttggacaatg 180 gagctcatat ttacttctgt gggcttaaag gaatgatgcc tgggattcaa gatacactta agagaggtgc agaagagag ggtgagagct gggacttgaa gctttctcag ctcaggaaga 300 acaagcagtg gcacgttgaa gtctattga

- (2) INFORMATION FOR SEQ ID NO:556:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587580
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Asn Thr Asp Ser Leu Leu Tyr Asp Glu Glu Phe Thr Lys Tyr Leu Lys 1 10 15

Asp His Pro Asp Asn Phe Arg Phe Asp Lys Ala Leu Ser Arg Glu Glu 20 25 30

Lys Asn Lys Lys Gly Gly Lys Met Tyr Val Gln Asp Lys Ile Glu Glu

1020

1080

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45
                            40
        35
Tyr Ser Asp Glu Ile Phe Lys Leu Leu Asp Asn Gly Ala His Ile Tyr
                        55
Phe Cys Gly Leu Lys Gly Met Met Pro Gly Ile Gln Asp Thr Leu Lys
                                        75
                    70
Arg Val Ala Glu Glu Arg Gly Glu Ser Trp Asp Leu Lys Leu Ser Gln
                                    90
                85
Leu Arg Lys Asn Lys Gln Trp His Val Glu Val Tyr
            100
                                105
(2) INFORMATION FOR SEQ ID NO:557:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..69
          (D) OTHER INFORMATION: / Ceres Seq. ID 1587581
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:
Met Tyr Val Gln Asp Lys Ile Glu Glu Tyr Ser Asp Glu Ile Phe Lys
                                    10
Leu Leu Asp Asn Gly Ala His Ile Tyr Phe Cys Gly Leu Lys Gly Met
                                 25
            20
Met Pro Gly Ile Gln Asp Thr Leu Lys Arg Val Ala Glu Glu Arg Gly
                            40
Glu Ser Trp Asp Leu Lys Leu Ser Gln Leu Arg Lys Asn Lys Gln Trp
His Val Glu Val Tyr
(2) INFORMATION FOR SEQ ID NO:558:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1872 base pairs
          (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..1872
           (D) OTHER INFORMATION: / Ceres Seq. ID 1587594
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:
atgtctcgct cccagaacga ggagtttcaa caatggtgga acaagcaacg agataggaac
                                                                         60
aatcacgacg ttctttacgc cggcgacgat gaagcattcc tcaccgttga aatccgtact
                                                                        120
ceggecaceg ttgaccetga taaggategg atceggacte gtacegtteg teagetetet
                                                                        180
cgtctctacc tcctcaagtt caagcaactc gcatcttcct tcctctggat cggtaactct
                                                                        240
ttcctttacc ttgttcgcac cgccaatcgc cgcattgcca acgataatcc tccatccgtg
                                                                        300
                                                                        360
tetteeteeg etagattgta eegtttaate aagggattte tegttggtgt tgtgettett
                                                                        420
 ctctgtttcg agcttgccgc ttatttcaag ggatggcact tcacacctcc ctctgttgcc
 tccgccgagg tcgctgtgga ggtggtttac gcttggtggt tggagatcag ggcatcttac
                                                                        480
                                                                        540
 cttgcgccac cgcttcagag cttgaccaat attccaatgt gcaatgaaaa ggaggtttac
 caacaatcta ttggagctgt gtgtatgctt gactggccaa gggaaagaat gctagttcag
                                                                        600
 gttcttgatg actccagtga attggatgtt cagcagctta taaaagcgga agtacaaaaa
                                                                        660
 tggcaacaaa ggggtgtccg gatagtgtat agacatcgtc tcatacgtac tggttacaag
                                                                        720
 gctggaaacc ttaaagctgc aatgaactgt gaatatgtca aagactacga gtttgtcgcc
                                                                        780
 atatttgatg cagatttcca gccacctgcg gatttcttga agaaaactgt gcctcatttt
                                                                        840
                                                                        900
 aagggtaatg aagaattagc cttggtccaa acacggtggg cttttgtgaa caaagacgaa
 aacttgctta caagactcca gaacataaat ttgtctttcc actttgaagt tgaacagcag
                                                                        960
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gtcaatggtg tttttattaa cttctttggc tttaatggaa ctgctggtgt ttggagaatc

aaagccctcg aggattgcgg gggatggttg gagcgaacaa ctgttgagga catggatatt

gccgttcgtg cgcatctttg tggatggaag ttcatttatc tgaatgatgt taagtgtctc 1140 tgtgaacttc cggagtccta tgaggcatac aaaaaacagc aataccgctg gcattcgggt 1200 ccaatgcaat tgttccgttt gtgcttcttt gacattcttc ggtcaaaggt gagtgctgcc 1260 aagaaagcaa atatgatatt totottotto ttgotacgga agottatott gocattotac 1320 tcattcacgc tcttctgcgt cattcttcca ttaacgatgt tcttcccaga agctaactta 1380 ccatcttggg ttgtttgcta tatccctggg atcatgtcca tcttaaacat catcccagcc 1440 ccaagateet teeettteat agtteegtat eteetttteg aaaacaccat gteagttace 1500 aaatttggag ccatgatctc tggtttgttc aagtttgata gttcttacga gtgggtagtc accaaaaagc tagggagatc ctctgaggcg gatctggttg catacgcaga gtccggctct 1620 ttggttgagt ccacaaccat ccaacgatca tcctctgatt caggtctgac cgagcttagc aaactaggag cagcaaagaa agctggcaaa accaaaagaa accgtctgta cagaacggaa atcgcactcg cgtttatcct cttggcagcc tcggtgagaa gcttgttgtc tgcgcaaggg 1800 1860 atccatttct atttcctctt gttccaagga atcacgttcg ttattgtcgg tctagatttg atcggggaac ag

- (2) INFORMATION FOR SEQ ID NO:559:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 624 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..624
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587595
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559: Met Ser Arg Ser Gln Asn Glu Glu Phe Gln Gln Trp Trp Asn Lys Gln 10 5 Arg Asp Arg Asn Asn His Asp Val Leu Tyr Ala Gly Asp Asp Glu Ala 25 2.0 Phe Leu Thr Val Glu Ile Arg Thr Pro Ala Thr Val Asp Pro Asp Lys 40 Asp Arg Ile Arg Thr Arg Thr Val Arg Gln Leu Ser Arg Leu Tyr Leu 55 Leu Lys Phe Lys Gln Leu Ala Ser Ser Phe Leu Trp Ile Gly Asn Ser 7.5 70 Phe Leu Tyr Leu Val Arg Thr Ala Asn Arg Arg Ile Ala Asn Asp Asn 90 8.5 Pro Pro Ser Val Ser Ser Ser Ala Arg Leu Tyr Arg Leu Ile Lys Gly 105 100 Phe Leu Val Gly Val Val Leu Leu Cys Phe Glu Leu Ala Ala Tyr 125 120 Phe Lys Gly Trp His Phe Thr Pro Pro Ser Val Ala Ser Ala Glu Val 140 135 Ala Val Glu Val Val Tyr Ala Trp Trp Leu Glu Ile Arg Ala Ser Tyr 150 155 Leu Ala Pro Pro Leu Gln Ser Leu Thr Asn Ile Pro Met Cys Asn Glu 170 165 Lys Glu Val Tyr Gln Gln Ser Ile Gly Ala Val Cys Met Leu Asp Trp 190 185 180 Pro Arg Glu Arg Met Leu Val Gln Val Leu Asp Asp Ser Ser Glu Leu 200 205 Asp Val Gln Gln Leu Ile Lys Ala Glu Val Gln Lys Trp Gln Gln Arg 220 215 Gly Val Arg Ile Val Tyr Arg His Arg Leu Ile Arg Thr Gly Tyr Lys 235 230 Ala Gly Asn Leu Lys Ala Ala Met Asn Cys Glu Tyr Val Lys Asp Tyr 255 250 245 Glu Phe Val Ala Ile Phe Asp Ala Asp Phe Gln Pro Pro Ala Asp Phe 265 Leu Lys Lys Thr Val Pro His Phe Lys Gly Asn Glu Glu Leu Ala Leu

280 285 275 Val Gln Thr Arg Trp Ala Phe Val Asn Lys Asp Glu Asn Leu Leu Thr 295 300 Arg Leu Gln Asn Ile Asn Leu Ser Phe His Phe Glu Val Glu Gln Gln 315 320 310 Val Asn Gly Val Phe Ile Asn Phe Phe Gly Phe Asn Gly Thr Ala Gly 325 330 Val Trp Arg Ile Lys Ala Leu Glu Asp Cys Gly Gly Trp Leu Glu Arg 340 345 Thr Thr Val Glu Asp Met Asp Ile Ala Val Arg Ala His Leu Cys Gly 360 355 Trp Lys Phe Ile Tyr Leu Asn Asp Val Lys Cys Leu Cys Glu Leu Pro 375 Glu Ser Tyr Glu Ala Tyr Lys Lys Gln Gln Tyr Arg Trp His Ser Gly 395 390 Pro Met Gln Leu Phe Arg Leu Cys Phe Phe Asp Ile Leu Arg Ser Lys 405 410 Val Ser Ala Ala Lys Lys Ala Asn Met Ile Phe Leu Phe Phe Leu Leu 425 Arg Lys Leu Ile Leu Pro Phe Tyr Ser Phe Thr Leu Phe Cys Val Ile 440 445 Leu Pro Leu Thr Met Phe Phe Pro Glu Ala Asn Leu Pro Ser Trp Val 455 460 Val Cys Tyr Ile Pro Gly Ile Met Ser Ile Leu Asn Ile Ile Pro Ala 470 475 480 Pro Arg Ser Phe Pro Phe Ile Val Pro Tyr Leu Leu Phe Glu Asn Thr 485 490 Met Ser Val Thr Lys Phe Gly Ala Met Ile Ser Gly Leu Phe Lys Phe 505 500 Asp Ser Ser Tyr Glu Trp Val Val Thr Lys Lys Leu Gly Arg Ser Ser 525 520 Glu Ala Asp Leu Val Ala Tyr Ala Glu Ser Gly Ser Leu Val Glu Ser 535 540 Thr Thr Ile Gln Arg Ser Ser Ser Asp Ser Gly Leu Thr Glu Leu Ser 555 560 550 Lys Leu Gly Ala Ala Lys Lys Ala Gly Lys Thr Lys Arg Asn Arg Leu 570 575 565 Tyr Arg Thr Glu Ile Ala Leu Ala Phe Ile Leu Leu Ala Ala Ser Val 580 585 590 Arg Ser Leu Leu Ser Ala Gln Gly Ile His Phe Tyr Phe Leu Leu Phe 595 600 605 Gln Gly Ile Thr Phe Val Ile Val Gly Leu Asp Leu Ile Gly Glu Gln 620 615 610

- (2) INFORMATION FOR SEQ ID NO:560:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..452
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587597
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met Cys Asn Glu Lys Glu Val Tyr Gln Gln Ser Ile Gly Ala Val Cys

1 10 15

Met Leu Asp Trp Pro Arg Glu Arg Met Leu Val Gln Val Leu Asp Asp 20 25 30

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Ser Ser Glu Leu Asp Val Gln Gln Leu Ile Lys Ala Glu Val Gln Lys
Trp Gln Gln Arg Gly Val Arg Ile Val Tyr Arg His Arg Leu Ile Arg
Thr Gly Tyr Lys Ala Gly Asn Leu Lys Ala Ala Met Asn Cys Glu Tyr
                  70
Val Lys Asp Tyr Glu Phe Val Ala Ile Phe Asp Ala Asp Phe Gln Pro
                                90
              8.5
Pro Ala Asp Phe Leu Lys Lys Thr Val Pro His Phe Lys Gly Asn Glu
                          105
Glu Leu Ala Leu Val Gln Thr Arg Trp Ala Phe Val Asn Lys Asp Glu
                     120
Asn Leu Leu Thr Arg Leu Gln Asn Ile Asn Leu Ser Phe His Phe Glu
                                      140
                    135
Val Glu Gln Gln Val Asn Gly Val Phe Ile Asn Phe Phe Gly Phe Asn
                                 155
                 150
Gly Thr Ala Gly Val Trp Arg Ile Lys Ala Leu Glu Asp Cys Gly Gly
                               170
              165
Trp Leu Glu Arg Thr Thr Val Glu Asp Met Asp Ile Ala Val Arg Ala
                            185
His Leu Cys Gly Trp Lys Phe Ile Tyr Leu Asn Asp Val Lys Cys Leu
                                          205
                        200
Cys Glu Leu Pro Glu Ser Tyr Glu Ala Tyr Lys Lys Gln Gln Tyr Arg
                                      220
                    215
Trp His Ser Gly Pro Met Gln Leu Phe Arg Leu Cys Phe Phe Asp Ile
                                   235
     230
Leu Arg Ser Lys Val Ser Ala Ala Lys Lys Ala Asn Met Ile Phe Leu
             245
                  250
Phe Phe Leu Leu Arg Lys Leu Ile Leu Pro Phe Tyr Ser Phe Thr Leu
                                              270
 260
                            265
Phe Cys Val Ile Leu Pro Leu Thr Met Phe Phe Pro Glu Ala Asn Leu
                        280
                                285
Pro Ser Trp Val Val Cys Tyr Ile Pro Gly Ile Met Ser Ile Leu Asn
                                       300
 290 295
Ile Ile Pro Ala Pro Arg Ser Phe Pro Phe Ile Val Pro Tyr Leu Leu
305 310
                                   315
Phe Glu Asn Thr Met Ser Val Thr Lys Phe Gly Ala Met Ile Ser Gly
                                330
              325
Leu Phe Lys Phe Asp Ser Ser Tyr Glu Trp Val Val Thr Lys Lys Leu
        340 345
Gly Arg Ser Ser Glu Ala Asp Leu Val Ala Tyr Ala Glu Ser Gly Ser
       355 360
Leu Val Glu Ser Thr Thr Ile Gln Arg Ser Ser Ser Asp Ser Gly Leu
                     375
Thr Glu Leu Ser Lys Leu Gly Ala Ala Lys Lys Ala Gly Lys Thr Lys
                  390
                                    395
Arg Asn Arg Leu Tyr Arg Thr Glu Ile Ala Leu Ala Phe Ile Leu Leu
                   410
              405
Ala Ala Ser Val Arg Ser Leu Leu Ser Ala Gln Gly Ile His Phe Tyr
           420 425
 Phe Leu Leu Phe Gln Gly Ile Thr Phe Val Ile Val Gly Leu Asp Leu
                      440
 Ile Gly Glu Gln
    450
```

- (2) INFORMATION FOR SEQ ID NO:561:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2049
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561: atgtctcgct cccagaacga ggagtttcaa caatggtgga acaagcaacg agataggaac 60 aatcacgacg ttctttacgc cggcgacgat gaagcattcc tcaccgttga aatccgtact 120 ccggccaccg ttgaccctga taaggatcgg atccggactc gtaccgttcg tcagctctct 180 cgtctctacc tcctcaagtt caagcaactc gcatcttcct tcctctggat cggtaactct 240 300 ttcctttacc ttgttcgcac cgccaatcgc cgcattgcca acgataatcc tccatccgtg 360 tcttcctccg ctagattgta ccgtttaatc aagggatttc tcgttggtgt tgtgcttctt 420 ctctgtttcg agcttgccgc ttatttcaag ggatggcact tcacacctcc ctctgttgcc 480 tccgccgagg tcgctgtgga ggtggtttac gcttggtggt tggagatcag ggcatcttac 540 cttgcgccac cgcttcagag cttgaccaat gtatgtatag ttctcttctt gattcaatcg 600 gttgaccgtc tggtgcttgt gcttggatgc ttctggatca agctccgccg tattaagcct 660 gttgcatcta tggagtaccc gactaaattg gttggagagg gagttagatt ggaagattat 720 ccaatggtga ttgttcagat tccaatgtgc aatgaaaagg aggtttacca acaatctatt 780 ggagctgtgt gtatgcttga ctggccaagg gaaagaatgc tagttcaggt tcttgatgac tccagtgaat tggatgttca gcagcttata aaagcggaag tacaaaaatg gcaacaaagg 840 ggtgtccgga tagtgtatag acatcgtctc atacgtactg gttacaaggc tggaaacctt 900 aaagctgcaa tgaactgtga atatgtcaaa gactacgagt ttgtcgccat atttgatgca 960 1020 gatttccagc cacctgcgga tttcttgaag aaaactgtgc ctcattttaa gggtaatgaa 1080 gaattageet tggteeaaac aeggtggget tttgtgaaca aagaegaaaa ettgettaca agactccaga acataaattt gtctttccac tttgaagttg aacagcaggt caatggtgtt 1140 tttattaact tctttggctt taatggaact gctggtgttt ggagaatcaa agccctcgag 1200 gattgcgggg gatggttgga gcgaacaact gttgaggaca tggatattgc cgttcgtgcg 1260 catctttgtg gatggaagtt catttatctg aatgatgtta agtgtctctg tgaacttccg 1320 gagtcctatg aggcatacaa aaaacagcaa taccgctggc attcgggtcc aatgcaattg 1380 1440 ttccgtttgt gcttctttga cattcttcgg tcaaaggtga gtgctgccaa gaaagcaaat 1500 atgatatttc tcttcttctt gctacggaag cttatcttgc cattctactc attcacgctc 1560 ttctgcgtca ttcttccatt aacgatgttc ttcccagaag ctaacttacc atcttgggtt gtttgctata tccctgggat catgtccatc ttaaacatca tcccagcccc aagatccttc 1620 cctttcatag ttccgtatct ccttttcgaa aacaccatgt cagttaccaa atttggagcc 1680 atgatetetg gtttgtteaa gtttgatagt tettaegagt gggtagteae caaaaageta 1740 gggagatect etgaggegga tetggttgea tacgeagagt eeggetettt ggttgagtee 1800 acaaccatcc aacgatcatc ctctgattca ggtctgaccg agcttagcaa actaggagca 1860 gcaaagaaag ctggcaaaac caaaagaaac cgtctgtaca gaacggaaat cgcactcgcg 1920 tttatcctct tggcagcctc ggtgagaagc ttgttgtctg cgcaagggat ccatttctat 1980 ttcctcttgt tccaaggaat cacgttcgtt attgtcggtc tagatttgat cggggaacag 2040

- (2) INFORMATION FOR SEQ ID NO:562:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

gtcagttag

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..682
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

Met Ser Arg Ser Gln Asn Glu Glu Phe Gln Gln Trp Trp Asn Lys Gln 5 10 Arg Asp Arg Asn Asn His Asp Val Leu Tyr Ala Gly Asp Asp Glu Ala

25

Phe Leu Thr Val Glu Ile Arg Thr Pro Ala Thr Val Asp Pro Asp Lys 45 40

Asp Arg Ile Arg Thr Arg Thr Val Arg Gln Leu Ser Arg Leu Tyr Leu 55 Leu Lys Phe Lys Gln Leu Ala Ser Ser Phe Leu Trp Ile Gly Asn Ser

75 Phe Leu Tyr Leu Val Arg Thr Ala Asn Arg Arg Ile Ala Asn Asp Asn 90 85 Pro Pro Ser Val Ser Ser Ser Ala Arg Leu Tyr Arg Leu Ile Lys Gly 105 100 Phe Leu Val Gly Val Val Leu Leu Cys Phe Glu Leu Ala Ala Tyr 120 Phe Lys Gly Trp His Phe Thr Pro Pro Ser Val Ala Ser Ala Glu Val 135 Ala Val Glu Val Val Tyr Ala Trp Trp Leu Glu Ile Arg Ala Ser Tyr 155 160 150 Leu Ala Pro Pro Leu Gln Ser Leu Thr Asn Val Cys Ile Val Leu Phe 165 170 Leu Ile Gln Ser Val Asp Arg Leu Val Leu Val Leu Gly Cys Phe Trp 185 Ile Lys Leu Arg Arg Ile Lys Pro Val Ala Ser Met Glu Tyr Pro Thr 200 Lys Leu Val Gly Glu Gly Val Arg Leu Glu Asp Tyr Pro Met Val Ile 220 215 Val Gln Ile Pro Met Cys Asn Glu Lys Glu Val Tyr Gln Gln Ser Ile 235 230 Gly Ala Val Cys Met Leu Asp Trp Pro Arg Glu Arg Met Leu Val Gln 245 250 Val Leu Asp Asp Ser Ser Glu Leu Asp Val Gln Gln Leu Ile Lys Ala 265 Glu Val Gln Lys Trp Gln Gln Arg Gly Val Arg Ile Val Tyr Arg His 280 Arg Leu Ile Arg Thr Gly Tyr Lys Ala Gly Asn Leu Lys Ala Ala Met 300 295 Asn Cys Glu Tyr Val Lys Asp Tyr Glu Phe Val Ala Ile Phe Asp Ala 310 315 Asp Phe Gln Pro Pro Ala Asp Phe Leu Lys Lys Thr Val Pro His Phe 325 330 Lys Gly Asn Glu Glu Leu Ala Leu Val Gln Thr Arg Trp Ala Phe Val 340 345 350 Asn Lys Asp Glu Asn Leu Leu Thr Arg Leu Gln Asn Ile Asn Leu Ser 355 360 Phe His Phe Glu Val Glu Gln Gln Val Asn Gly Val Phe Ile Asn Phe 375 380 Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Lys Ala Leu Glu 390 395 Asp Cys Gly Gly Trp Leu Glu Arg Thr Thr Val Glu Asp Met Asp Ile 410 405 Ala Val Arg Ala His Leu Cys Gly Trp Lys Phe Ile Tyr Leu Asn Asp 425 420 Val Lys Cys Leu Cys Glu Leu Pro Glu Ser Tyr Glu Ala Tyr Lys Lys 435 440 Gln Gln Tyr Arg Trp His Ser Gly Pro Met Gln Leu Phe Arg Leu Cys 455 460 Phe Phe Asp Ile Leu Arg Ser Lys Val Ser Ala Ala Lys Lys Ala Asn 470 475 Met Ile Phe Leu Phe Phe Leu Leu Arg Lys Leu Ile Leu Pro Phe Tyr 490 485 Ser Phe Thr Leu Phe Cys Val Ile Leu Pro Leu Thr Met Phe Phe Pro 500 505 Glu Ala Asn Leu Pro Ser Trp Val Val Cys Tyr Ile Pro Gly Ile Met 520 Ser Ile Leu Asn Ile Ile Pro Ala Pro Arg Ser Phe Pro Phe Ile Val 530 535 540 Pro Tyr Leu Leu Phe Glu Asn Thr Met Ser Val Thr Lys Phe Gly Ala 555 550

Met Ile Ser Gly Leu Phe Lys Phe Asp Ser Ser Tyr Glu Trp Val Val 570 565 Thr Lys Lys Leu Gly Arg Ser Ser Glu Ala Asp Leu Val Ala Tyr Ala 585 580 Glu Ser Gly Ser Leu Val Glu Ser Thr Thr Ile Gln Arg Ser Ser Ser 600 595 Asp Ser Gly Leu Thr Glu Leu Ser Lys Leu Gly Ala Ala Lys Lys Ala 620 615 Gly Lys Thr Lys Arg Asn Arg Leu Tyr Arg Thr Glu Ile Ala Leu Ala 635 630 Phe Ile Leu Leu Ala Ala Ser Val Arg Ser Leu Leu Ser Ala Gln Gly 645 650

Ile His Phe Tyr Phe Leu Leu Phe Gln Gly Ile Thr Phe Val Ile Val 660 665 670

Gly Leu Asp Leu Ile Gly Glu Gln Val Ser 675 680

- (2) INFORMATION FOR SEQ ID NO:563:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..479
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587601
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563: Met Glu Tyr Pro Thr Lys Leu Val Gly Glu Gly Val Arg Leu Glu Asp 10 Tyr Pro Met Val Ile Val Gln Ile Pro Met Cys Asn Glu Lys Glu Val 20 25 Tyr Gln Gln Ser Ile Gly Ala Val Cys Met Leu Asp Trp Pro Arg Glu 4.0 Arg Met Leu Val Gln Val Leu Asp Asp Ser Ser Glu Leu Asp Val Gln 60 Gln Leu Ile Lys Ala Glu Val Gln Lys Trp Gln Gln Arg Gly Val Arg 70 75 Ile Val Tyr Arg His Arg Leu Ile Arg Thr Gly Tyr Lys Ala Gly Asn 8.5 Leu Lys Ala Ala Met Asn Cys Glu Tyr Val Lys Asp Tyr Glu Phe Val 105 100 Ala Ile Phe Asp Ala Asp Phe Gln Pro Pro Ala Asp Phe Leu Lys Lys 120 Thr Val Pro His Phe Lys Gly Asn Glu Glu Leu Ala Leu Val Gln Thr 130 135 140 Arg Trp Ala Phe Val Asn Lys Asp Glu Asn Leu Leu Thr Arg Leu Gln 150 155 Asn Ile Asn Leu Ser Phe His Phe Glu Val Glu Gln Gln Val Asn Gly 170 165 Val Phe Ile Asn Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg 185 180 Ile Lys Ala Leu Glu Asp Cys Gly Gly Trp Leu Glu Arg Thr Thr Val 200 205 Glu Asp Met Asp Ile Ala Val Arg Ala His Leu Cys Gly Trp Lys Phe 215 Ile Tyr Leu Asn Asp Val Lys Cys Leu Cys Glu Leu Pro Glu Ser Tyr 235 230 Glu Ala Tyr Lys Lys Gln Gln Tyr Arg Trp His Ser Gly Pro Met Gln 250 245 Leu Phe Arg Leu Cys Phe Phe Asp Ile Leu Arg Ser Lys Val Ser Ala

```
270
                                265
            260
Ala Lys Lys Ala Asn Met Ile Phe Leu Phe Phe Leu Leu Arg Lys Leu
                            280
        275
Ile Leu Pro Phe Tyr Ser Phe Thr Leu Phe Cys Val Ile Leu Pro Leu
                                            300
                        295
Thr Met Phe Phe Pro Glu Ala Asn Leu Pro Ser Trp Val Val Cys Tyr
                                        315
                    310
Ile Pro Gly Ile Met Ser Ile Leu Asn Ile Ile Pro Ala Pro Arg Ser
                                    330
                325
Phe Pro Phe Ile Val Pro Tyr Leu Leu Phe Glu Asn Thr Met Ser Val
                                                     350
                                345
Thr Lys Phe Gly Ala Met Ile Ser Gly Leu Phe Lys Phe Asp Ser Ser
                                                 365
                            360
        355
Tyr Glu Trp Val Val Thr Lys Lys Leu Gly Arg Ser Ser Glu Ala Asp
                                            380
                        375
Leu Val Ala Tyr Ala Glu Ser Gly Ser Leu Val Glu Ser Thr Thr Ile
                    390
                                         395
Gln Arg Ser Ser Ser Asp Ser Gly Leu Thr Glu Leu Ser Lys Leu Gly
                                    410
                405
Ala Ala Lys Lys Ala Gly Lys Thr Lys Arg Asn Arg Leu Tyr Arg Thr
                                425
                                                    430
            420
Glu Ile Ala Leu Ala Phe Ile Leu Leu Ala Ala Ser Val Arg Ser Leu
        435
                            440
                                                 445
Leu Ser Ala Gln Gly Ile His Phe Tyr Phe Leu Leu Phe Gln Gly Ile
                                            460
                        455
Thr Phe Val Ile Val Gly Leu Asp Leu Ile Gly Glu Gln Val Ser
                    470
                                         475
```

- (2) INFORMATION FOR SEQ ID NO:564:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1728 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1728
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587617
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

atggcggaaa ctgagagacc ccaccggtct tcaagtatta acagtagtag caacaacaac 60 120 agtggttcat caaccgatct attcatttgt ttcacatctc gtttctcttc ttcttcctct 180 atgcgtctct cttctaaatc catccatagc ccagctcgtt ccgcttgtct caccacttct cttagccgtc gtctccgtac tagcggacgg aagagatctg gatctggcta cgagaatagt 240 aacaacaaca acaataataa catagagccg tcgtctccga agaagcatgt gaagaagaag 300 atgagagcta gatctagaag gaaaggaggt gagaatagtt tcaggagatc cgttgatcaa 360 aacgacggtg gtggtggatg tcgttttaaa gcgagtgaga atcgtttggt gcatcttccg 420 gtgactatct gcgagtcgtt gagatcgttt gggtctgagc tcaactgctt cttcccgtgt 480 cgatcttcct gtacggagaa tagtcatgga gatgggagga gagctgagag taacaacgac 540 ggttgcggcg gcggcggagg aggaagtaat tcgtgtggtg cggtgtttac gaggtggttt 600 gtggcggtgg aggagacttc gggagggaag agaagagaga ttgagcttgt tgttggtgga 660 720 gaagacgaat tgaggaggat aggcggagga gtcgtcggag catgttgcgg cgttagtaac cgggttcgtg aaagacagtt gtcgttaaac gacggcgtat acacagagga ggaagaagat 780 gagagaagaa gaaggtttga gctggaaatt gaagataaga aacggatcga cttgtgtgag 840 aaatggatct ctggtgagac tactgtggaa acagaagaag tttcagtagc agttgcagaa 900 gcagaagcag aagcagaagc agaagctcct ttgccttcaa atccagctac agaggaagaa 960 gaaagagtca aagttgtgga agattcgatt gttgaagaag aacaagaagc ttcgaaaatt 1020 1080 ctggattcgt ttgaggaaga aatagaagct acgatcatga aaaaaattga agacgaaatc agaaacgcta tagaagaaga ggagaaactt gctgagatgg aagaattagc ggttgtggcg gtggctgaga cggaggaggt agaagaaagc aaagaggttg ttcctgattg tatacctcaa 1200 aatgaggaaa gatccgaaca aggaaaccgg gaacccgacc cgagtccgga agtggtgatg 1260 agaagaagto tacaagagga aacaacggag aaagagaaga cgacggcgac gcagataaga 1320 tttcgtcaga tgtttaccag gaagacctc ggcgaagaag ataccaccag aagccgtcgg 1380
agaaatcatc atcatca acccaagaag cgaatcgtca cagccgttga ttccaacgca 1440
tcctctcgcc ggcggtcaat cgatagacca ccacttcacc tacagccgcc acggtcatcg 1500
tgttcatacc cagcagctcc accgataata acggcagctg cggcggttgg ggaacagagg 1560
gtagccggag ctaataaggt acagccacca gtgctgcac gttgcaaatc ggaaccgagg 1620
aagtcagcgt cgaagctagc gccggaagct tgttctgga aaaataggaa gcttgtagcc 1680
acaccctccg gcaaccgtcg gtgcgcgc cgcggagtag ggttctag

- (2) INFORMATION FOR SEQ ID NO:565:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 575 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..575
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:565: Met Ala Glu Thr Glu Arg Pro His Arg Ser Ser Ser Ile Asn Ser Ser

1 5 10 15 Ser Asn Asn Ser Gly Ser Ser Thr Asp Leu Phe Ile Cys Phe Thr 20 25 30

Ser Arg Phe Ser Ser Ser Ser Met Arg Leu Ser Ser Lys Ser Ile 35 40 45

His Ser Pro Ala Arg Ser Ala Cys Leu Thr Thr Ser Leu Ser Arg Arg 50 55 60

Leu Arg Thr Ser Gly Arg Lys Arg Ser Gly Ser Gly Tyr Glu Asn Ser 65 70 75 80

Asn Asn Asn Asn Asn Asn Ile Glu Pro Ser Ser Pro Lys Lys His 85 90 95

Val Lys Lys Met Arg Ala Arg Ser Arg Arg Lys Gly Glu Asn 100 105 110

Ser Phe Arg Arg Ser Val Asp Gln Asn Asp Gly Gly Gly Cys Arg 115 120 125

Phe Lys Ala Ser Glu Asn Arg Leu Val His Leu Pro Val Thr Ile Cys 130 135 140

Glu Ser Leu Arg Ser Phe Gly Ser Glu Leu Asn Cys Phe Phe Pro Cys 145 150 155 160

Arg Ser Ser Cys Thr Glu Asn Ser His Gly Asp Gly Arg Arg Ala Glu
165 170 175

Ser Asn Asn Asp Gly Cys Gly Gly Gly Gly Gly Gly Ser Asn Ser Cys 180 185

Gly Ala Val Phe Thr Arg Trp Phe Val Ala Val Glu Glu Thr Ser Gly
195 200 205

Gly Lys Arg Arg Glu Ile Glu Leu Val Val Gly Gly Glu Asp Glu Leu 210 215 220

Arg Arg Ile Gly Gly Val Val Gly Ala Cys Cys Gly Val Ser Asn 225 230 235 240

Arg Val Arg Glu Arg Gln Leu Ser Leu Asn Asp Gly Val Tyr Thr Glu 245 250 255

Glu Glu Glu Asp Glu Arg Arg Arg Phe Glu Leu Glu Ile Glu Asp 260 265 270

Lys Lys Arg Ile Asp Leu Cys Glu Lys Trp Ile Ser Gly Glu Thr Thr

Val Glu Thr Glu Glu Val Ser Val Ala Val Ala Glu Ala Glu Ala Glu 290 295 300

Ala Glu Ala Glu Ala Pro Leu Pro Ser Asn Pro Ala Thr Glu Glu Glu 305 310 315 320

Glu Arg Val Lys Val Val Glu Asp Ser Ile Val Glu Glu Glu Glu Glu 325 330 335

Ala Ser Lys Ile Leu Asp Ser Phe Glu Glu Glu Ile Glu Ala Thr Ile 345 Met Lys Lys Ile Glu Asp Glu Ile Arg Asn Ala Ile Glu Glu Glu 355 360 Lys Leu Ala Glu Met Glu Glu Leu Ala Val Val Ala Val Ala Glu Thr 380 375 Glu Glu Val Glu Glu Ser Lys Glu Val Val Pro Asp Cys Ile Pro Gln 395 390 Asn Glu Glu Arg Ser Glu Gln Gly Asn Arg Glu Pro Asp Pro Ser Pro 405 410 Glu Val Val Met Arg Arg Ser Leu Gln Glu Glu Thr Thr Glu Lys Glu 420 425 430 Lys Thr Thr Ala Thr Gln Ile Arg Phe Arg Gln Met Phe Thr Arg Lys 435 440 445 Thr Ser Gly Glu Glu Asp Thr Thr Arg Ser Arg Arg Arg Asn His His 450 455 460 His His Gln Pro Lys Lys Arg Ile Val Thr Ala Val Asp Ser Asn Ala 470 475 Ser Ser Arg Arg Arg Ser Ile Asp Arg Pro Pro Leu His Leu Gln Pro 485 490 495 Pro Arg Ser Ser Cys Ser Tyr Pro Ala Ala Pro Pro Ile Ile Thr Ala 500 505 510 Ala Ala Ala Val Gly Glu Gln Arg Val Ala Gly Ala Asn Lys Val Gln 515 520 525 Pro Pro Val Leu Pro Arg Cys Lys Ser Glu Pro Arg Lys Ser Ala Ser 530 535 540 Lys Leu Ala Pro Glu Ala Cys Phe Trp Lys Asn Arg Lys Leu Val Ala 545 550 555 560 Thr Pro Ser Gly Asn Arg Arg Cys Arg Arg Arg Gly Val Gly Phe 570 565

- (2) INFORMATION FOR SEQ ID NO:566:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..535
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587620
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:
- Met Arg Leu Ser Ser Lys Ser Ile His Ser Pro Ala Arg Ser Ala Cys

 1 10 15
- Leu Thr Thr Ser Leu Ser Arg Arg Leu Arg Thr Ser Gly Arg Lys Arg 20 25 30
- Ser Gly Ser Gly Tyr Glu Asn Ser Asn Asn Asn Asn Asn Asn Ile
 35 40 45
- Glu Pro Ser Ser Pro Lys Lys His Val Lys Lys Lys Met Arg Ala Arg
 50 55 60
- Ser Arg Arg Lys Gly Gly Glu Asn Ser Phe Arg Arg Ser Val Asp Gln 65 70 75 80
- Asn Asp Gly Gly Gly Cys Arg Phe Lys Ala Ser Glu Asn Arg Leu
 85 90 95
- Val His Leu Pro Val Thr Ile Cys Glu Ser Leu Arg Ser Phe Gly Ser
- Glu Leu Asn Cys Phe Phe Pro Cys Arg Ser Ser Cys Thr Glu Asn Ser 115 120 125
- His Gly Asp Gly Arg Arg Ala Glu Ser Asn Asn Asp Gly Cys Gly Gly 130 135 140
- Gly Gly Gly Ser Asn Ser Cys Gly Ala Val Phe Thr Arg Trp Phe

155 150 145 Val Ala Val Glu Glu Thr Ser Gly Gly Lys Arg Arg Glu Ile Glu Leu 170 175 165 Val Val Gly Gly Glu Asp Glu Leu Arg Arg Ile Gly Gly Val Val 185 Gly Ala Cys Cys Gly Val Ser Asn Arg Val Arg Glu Arg Gln Leu Ser 195 200 Leu Asn Asp Gly Val Tyr Thr Glu Glu Glu Glu Asp Glu Arg Arg 215 220 Arg Phe Glu Leu Glu Ile Glu Asp Lys Lys Arg Ile Asp Leu Cys Glu 235 240 230 Lys Trp Ile Ser Gly Glu Thr Thr Val Glu Thr Glu Glu Val Ser Val 245 250 Ala Val Ala Glu Ala Glu Ala Glu Ala Glu Ala Glu Ala Pro Leu Pro 260 265 Ser Asn Pro Ala Thr Glu Glu Glu Glu Arg Val Lys Val Val Glu Asp 275 285 280 Ser Ile Val Glu Glu Glu Glu Ala Ser Lys Ile Leu Asp Ser Phe 300 295 Glu Glu Glu Ile Glu Ala Thr Ile Met Lys Lys Ile Glu Asp Glu Ile 305 310 315 Arg Asn Ala Ile Glu Glu Glu Lys Leu Ala Glu Met Glu Glu Leu 325 330 335 Ala Val Val Ala Val Ala Glu Thr Glu Glu Val Glu Glu Ser Lys Glu 340 345 Val Val Pro Asp Cys Ile Pro Gln Asn Glu Glu Arg Ser Glu Gln Gly 355 360 365 Asn Arg Glu Pro Asp Pro Ser Pro Glu Val Val Met Arg Arg Ser Leu 370 375 380 Gln Glu Glu Thr Thr Glu Lys Glu Lys Thr Thr Ala Thr Gln Ile Arg 390 395 400 Phe Arg Gln Met Phe Thr Arg Lys Thr Ser Gly Glu Glu Asp Thr Thr 410 405 Arg Ser Arg Arg Arg Asn His His His Gln Pro Lys Lys Arg Ile 420 425 Val Thr Ala Val Asp Ser Asn Ala Ser Ser Arg Arg Arg Ser Ile Asp 435 440 445 Arg Pro Pro Leu His Leu Gln Pro Pro Arg Ser Ser Cys Ser Tyr Pro 450 455 460 Ala Ala Pro Pro Ile Ile Thr Ala Ala Ala Ala Val Gly Glu Gln Arg 475 470 Val Ala Gly Ala Asn Lys Val Gln Pro Pro Val Leu Pro Arg Cys Lys 490 485 Ser Glu Pro Arg Lys Ser Ala Ser Lys Leu Ala Pro Glu Ala Cys Phe 500 505 510 Trp Lys Asn Arg Lys Leu Val Ala Thr Pro Ser Gly Asn Arg Arg Cys 515 520 Arg Arg Arg Gly Val Gly Phe

- 535
- (2) INFORMATION FOR SEQ ID NO:567:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1032 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1032
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587654
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

atgtcttctg ctactgcgac ttataactac gatgtttttc tgagtttcag aggacccgac 60 120 actogoogca agttoatoag otttototao aaagaacttg ttggaaggga cattogaaco ttcaaagacg acaaagagct agagaatggc cagatgattt ctccggagct caaacgcgcc 180 atcgaggagt ccaaattcgc cgtcgttgtt gtctcagaga actacgctgc gtcttcttgg 240 tgtctcaatg agctcgtgga gatcatgaaa gtccagaaga acaagggttc catcaccgtg 300 atgcctatct tctacggcgt ggatccgtgt gatttgagga ggcagatcgg agatgtcgct 360 gaacagttta agaagcacga ggctagagaa gaagatcttg agaaagtagc ttcgtggaga 420 cgagcattga ccagtttggc tagtatctcc ggagattgtt catccaaatg tgaagatgac 480 tcggagctgg tggatgtaat tgctgacaag atatcaaaag agctgatgct tgttacaaca 540 600 ataagcaatg ggaggaacct agttgggatt gataaacaca tgaaggaact gaacctattg 660 atggatttga attccaacaa aggtaagaga atggttggga tttgggtaag aggaggaagt 720 tgtagatcgg ctctagctaa atatgtttat cagacatcct gtcaacactt tgatagccat tgttttcttg gaaacgtgaa aaggatttgt cacggtaact actttgaaag ccatctacac 780 840 aaagagette tggcaaatat taaaggagaa aactetagea aacaaagtet caagaageaa 900 aaggttctgc ttgtggcaga cgacgtcgat aagcttgaac agttagatgc tcttgcaggg 960 gatttcaacg gttttggtcc ggggagtgtt gttatcatca ctacaaaaga taagcagttg ttgatatctt atggtataca gcttgtctac gaagctgagt ttttgacatt ccagaaattt 1020 tgtcgtagct tc

- (2) INFORMATION FOR SEQ ID NO:568:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

230

- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587655
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:568: Met Ser Ser Ala Thr Ala Thr Tyr Asn Tyr Asp Val Phe Leu Ser Phe 10 Arg Gly Pro Asp Thr Arg Arg Lys Phe Ile Ser Phe Leu Tyr Lys Glu 30 25 2.0 Leu Val Gly Arg Asp Ile Arg Thr Phe Lys Asp Asp Lys Glu Leu Glu 40 Asn Gly Gln Met Ile Ser Pro Glu Leu Lys Arg Ala Ile Glu Glu Ser 60 55 Lys Phe Ala Val Val Val Ser Glu Asn Tyr Ala Ala Ser Ser Trp 75 70 Cys Leu Asn Glu Leu Val Glu Ile Met Lys Val Gln Lys Asn Lys Gly 90 85 Ser Ile Thr Val Met Pro Ile Phe Tyr Gly Val Asp Pro Cys Asp Leu 105 100 Arg Arg Gln Ile Gly Asp Val Ala Glu Gln Phe Lys Lys His Glu Ala 120 Arg Glu Glu Asp Leu Glu Lys Val Ala Ser Trp Arg Arg Ala Leu Thr 140 135 Ser Leu Ala Ser Ile Ser Gly Asp Cys Ser Ser Lys Cys Glu Asp Asp 155 150 Ser Glu Leu Val Asp Val Ile Ala Asp Lys Ile Ser Lys Glu Leu Met 170 165 Leu Val Thr Thr Ile Ser Asn Gly Arg Asn Leu Val Gly Ile Asp Lys 185 180 His Met Lys Glu Leu Asn Leu Leu Met Asp Leu Asn Ser Asn Lys Gly 205 200 Lys Arg Met Val Gly Ile Trp Val Arg Gly Gly Ser Cys Arg Ser Ala 220 215 Leu Ala Lys Tyr Val Tyr Gln Thr Ser Cys Gln His Phe Asp Ser His

Cys Phe Leu Gly Asn Val Lys Arg Ile Cys His Gly Asn Tyr Phe Glu

235

Ser His Leu His Lys Glu Leu Leu Ala Asn Ile Lys Gly Gly Asn Ser Lys Gln Ser Leu Leu Lys Lys Gln Lys Val Leu Leu Val Ala Asp Asp Asp 275

Val Asp Lys Leu Glu Gln Leu Asp Ala Leu Ala Gly Asp Phe Asn Gly 290

Phe Gly Pro Gly Ser Val Val Ile Ile Thr Thr Lys Asp Lys Gln Leu 310

Leu Ile Ser Tyr Gly Ile Gln Leu Val Tyr Glu Ala Glu Phe Leu Thr 325

Phe Gln Lys Phe Cys Arg Ser Phe

- 340
- (2) INFORMATION FOR SEQ ID NO:569: (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..293
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569: Met Ile Ser Pro Glu Leu Lys Arg Ala Ile Glu Glu Ser Lys Phe Ala 10 Val Val Val Ser Glu Asn Tyr Ala Ala Ser Ser Trp Cys Leu Asn 25 Glu Leu Val Glu Ile Met Lys Val Gln Lys Asn Lys Gly Ser Ile Thr 40 Val Met Pro Ile Phe Tyr Gly Val Asp Pro Cys Asp Leu Arg Arg Gln Ile Gly Asp Val Ala Glu Gln Phe Lys Lys His Glu Ala Arg Glu Glu 70 75 Asp Leu Glu Lys Val Ala Ser Trp Arg Arg Ala Leu Thr Ser Leu Ala 85 Ser Ile Ser Gly Asp Cys Ser Ser Lys Cys Glu Asp Asp Ser Glu Leu 100 105 Val Asp Val Ile Ala Asp Lys Ile Ser Lys Glu Leu Met Leu Val Thr 115 120 125 Thr Ile Ser Asn Gly Arg Asn Leu Val Gly Ile Asp Lys His Met Lys 135 140 Glu Leu Asn Leu Leu Met Asp Leu Asn Ser Asn Lys Gly Lys Arg Met 155 150 Val Gly Ile Trp Val Arg Gly Gly Ser Cys Arg Ser Ala Leu Ala Lys 170 165 Tyr Val Tyr Gln Thr Ser Cys Gln His Phe Asp Ser His Cys Phe Leu 185 180 Gly Asn Val Lys Arg Ile Cys His Gly Asn Tyr Phe Glu Ser His Leu 195 200 His Lys Glu Leu Leu Ala Asn Ile Lys Gly Glu Asn Ser Ser Lys Gln 210 215 Ser Leu Lys Lys Gln Lys Val Leu Leu Val Ala Asp Asp Val Asp Lys 235 225 230 Leu Glu Gln Leu Asp Ala Leu Ala Gly Asp Phe Asn Gly Phe Gly Pro 250 255 245 Gly Ser Val Val Ile Ile Thr Thr Lys Asp Lys Gln Leu Leu Ile Ser 260 265 270 Tyr Gly Ile Gln Leu Val Tyr Glu Ala Glu Phe Leu Thr Phe Gln Lys 280 275

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Phe Cys Arg Ser Phe
290
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- (2) INFORMATION FOR SEQ ID NO:570:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..609
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587778
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570: ctcgtgatct ctacatgaga agcatcacag gttgtgcagc tcgaactcac tactcttcag 60 ccgtcgacgc cgcatccgtt ccatttccga gaagccggag tacttcctcc gccttctctt 120 cctctgcctc ttctcggaga agatcttcgg atttcacttt cgacgatgat tatagcgagc 180 tgcttagagc tgcttccgtt agagtttagg tcataagaat gagattgaca tgatcataca 240 300 acaacagcaa cagcagcagc agcaacggca ggagaatcgc gttgcgatgg gagcggttac ggttaaaggc ggtttgccta agagctcgag tgttgggatg acaatggcta ggattgatga 360 420 agaagatgaa gaagaaggat ctgtaaagaa tcaaaagaag ggatctgatt tcttatatcc 480 tcgtagcaga tcacatgctg ttactattag aggatccaag ttttaatata tactagaaat taattgtcag ttttattttt cttttgattt aattttaaag aatgttccta attatacatg 540 gttatggaat tattttgatg taaagttact gtcatggatt tatacaaaaa aaagttactg 600 tcaaaatta
- (2) INFORMATION FOR SEQ ID NO:571:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..68
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587779
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

Arg Asp Leu Tyr Met Arg Ser Ile Thr Gly Cys Ala Ala Arg Thr His 1 5 10 15 Tyr Ser Ser Ala Val Asp Ala Ala Ser Val Pro Phe Pro Arg Ser Arg

20 25 30

Ser Thr Ser Ser Ala Phe Ser Ser Ser Ala Ser Ser Arg Arg Ser

Ser Thr Ser Ser Ala Phe Ser Ser Ser Ala Ser Sel Alg Alg Alg Sel 40 45

Ser Asp Phe Thr Phe Asp Asp Asp Tyr Ser Glu Leu Leu Arg Ala Ala 50 55 60

Ser Val Arg Val

65

- (2) INFORMATION FOR SEQ ID NO:572:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

(xi) SEQUENCE DESCRIPTION: SEQ 1D NO.372.

Met Arg Ser Ile Thr Gly Cys Ala Ala Arg Thr His Tyr Ser Ser Ala

10 15

 Val
 Asp
 Ala
 Ala
 Ser
 Val
 Pro
 Phe
 Pro
 Arg
 Ser
 Arg
 Ser
 Thr
 Ser
 Ser
 Ser
 Arg
 Arg
 Arg
 Arg
 Ser
 Ser
 Asp
 Phe
 Thr
 Arg
 Arg
 Arg
 Arg
 Ser
 Ser
 Asp
 Phe
 Thr
 Thr
 Arg
 A

- (2) INFORMATION FOR SEQ ID NO:573:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

Met Ile Ile Gln Gln Gln Gln Gln Gln Gln Gln Arg Gln Glu Asn

Arg Val Ala Met Gly Ala Val Thr Val Lys Gly Gly Leu Pro Lys Ser 20 25 30

Ser Ser Val Gly Met Thr Met Ala Arg Ile Asp Glu Glu Asp Glu Glu 35 40 45

Glu Gly Ser Val Lys Asn Gln Lys Lys Gly Ser Asp Phe Leu Tyr Pro 50 55 60

Arg Ser Arg Ser His Ala Val Thr Ile Arg Gly Ser Lys Phe 65 70 75

- (2) INFORMATION FOR SEQ ID NO:574:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..495
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587821
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

tetttgtgca tgcaaacteg atecaaaggt tetgcacace aattaccatt cagagacaga 60 120 attgacagaa taactcgtga gttacaagaa accaaagcaa aggcagcctg tgatcagcca 180 agaccaattt ctatggatca acagaacaaa ccagttgatg ttcaaggccc acctaatgtt gatcaaccaa gaaacattgg tgctggtgat gccccaagga atcatcacca aagacaaggg 240 atagtgccac aaccagttca aaacaacaac tttgagatca agagtggtct catctccatg 300 atccaaggaa acaagtttta tggtctacct atggaagatc ccctggacca tcttgacagc 360 tttaataggc tctgtggccg tacaaagatc aatggtgtca ctaaagatat gtttaagctc 420 agattatttc ccttctcttt gggagacaag gcacaacact gggagaagac tctgcccca 480 gactccatca actaa

- (2) INFORMATION FOR SEQ ID NO:575:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1587822 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:575: Ser Leu Cys Met Gln Thr Arg Ser Lys Gly Ser Ala His Gln Leu Pro 1.0 Phe Arg Asp Arg Ile Asp Arg Ile Thr Arg Glu Leu Gln Glu Thr Lys 25 Ala Lys Ala Ala Cys Asp Gln Pro Arg Pro Ile Ser Met Asp Gln Gln 40 Asn Lys Pro Val Asp Val Gln Gly Pro Pro Asn Val Asp Gln Pro Arg 55 Asn Ile Gly Ala Gly Asp Ala Pro Arg Asn His His Gln Arg Gln Gly 75 7.0 Ile Val Pro Gln Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly 90 85 Leu Ile Ser Met Ile Gln Gly Asn Lys Phe Tyr Gly Leu Pro Met Glu 105 100 Asp Pro Leu Asp His Leu Asp Ser Phe Asn Arg Leu Cys Gly Arg Thr 120 Lys Ile Asn Gly Val Thr Lys Asp Met Phe Lys Leu Arg Leu Phe Pro 135 140 Phe Ser Leu Gly Asp Lys Ala Gln His Trp Glu Lys Thr Leu Pro Pro 155 150 Asp Ser Ile Asn

- (2) INFORMATION FOR SEQ ID NO:576:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587823
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Gln Thr Arg Ser Lys Gly Ser Ala His Gln Leu Pro Phe Arg Asp

1 10 15

15 10 Leu Pro Phe Arg Ala Lys Ala

Arg Ile Asp Arg Ile Thr Arg Glu Leu Gln Glu Thr Lys Ala Lys Ala 20 25 30

Ala Cys Asp Gln Pro Arg Pro Ile Ser Met Asp Gln Gln Asn Lys Pro 35 40 45

Val Asp Val Gln Gly Pro Pro Asn Val Asp Gln Pro Arg Asn Ile Gly 50 55 60

Ala Gly Asp Ala Pro Arg Asn His His Gln Arg Gln Gly Ile Val Pro
65 70 75 80

Gln Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ser
85 90 95

Met Ile Gln Gly Asn Lys Phe Tyr Gly Leu Pro Met Glu Asp Pro Leu

100
105
110

The Har Law Asp Ser Pho Asp Arg Leu Cys Gly Arg Thr Lys Ile Asp

Asp His Leu Asp Ser Phe Asn Arg Leu Cys Gly Arg Thr Lys Ile Asn 115 120 125

Gly Val Thr Lys Asp Met Phe Lys Leu Arg Leu Phe Pro Phe Ser Leu 130 135 140

Gly Asp Lys Ala Gln His Trp Glu Lys Thr Leu Pro Pro Asp Ser Ile 145 150 155 160

- (2) INFORMATION FOR SEQ ID NO:577:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587824
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Met Asp Gln Gln Asn Lys Pro Val Asp Val Gln Gly Pro Pro Asn Val 1 5 10 15

Asp Gln Pro Arg Asn Ile Gly Ala Gly Asp Ala Pro Arg Asn His His 20 25 30

Gln Arg Gln Gly Ile Val Pro Gln Pro Val Gln Asn Asn Asn Phe Glu 35 40 45

Ile Lys Ser Gly Leu Ile Ser Met Ile Gln Gly Asn Lys Phe Tyr Gly 50 60

Leu Pro Met Glu Asp Pro Leu Asp His Leu Asp Ser Phe Asn Arg Leu 65 70 75 80

Cys Gly Arg Thr Lys Ile Asn Gly Val Thr Lys Asp Met Phe Lys Leu 85 90 95

Arg Leu Phe Pro Phe Ser Leu Gly Asp Lys Ala Gln His Trp Glu Lys 100 105 110

Thr Leu Pro Pro Asp Ser Ile Asn 115 120

- (2) INFORMATION FOR SEQ ID NO:578:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..376
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

atgetteteg acaetgeete caatgaaaac tteetgaaaa aggatgtage agaaggatgg 60 gagttggtea aaaatetage acaatetgat gggtgetaca atgaagaeta tgategetea 120 gtgagaggag etggaggeea tgaggataaa cagageaagg atateaagge tetgaatgaa aggtgttget ggeteageag aageagatae actaeateae tgatgaagag 240 caetteecaa tgeaagaaag ggggaatgat caaaetgaag agetgtgeta cateeagaac 300 aageactaatg tageta

- (2) INFORMATION FOR SEQ ID NO:579:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587826
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met Leu Leu Asp Thr Ala Ser Asn Glu Asn Phe Leu Lys Lys Asp Val 1 5 10

Ala Glu Gly Trp Glu Leu Val Lys Asn Leu Ala Gln Ser Asp Gly Cys
20 25 30

Tyr Asn Glu Asp Tyr Asp Arg Ser Val Arg Gly Ala Gly Gly His Glu

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                            40
                                                 45
        35
Asp Lys Gln Ser Lys Asp Ile Lys Ala Leu Asn Glu Lys Leu Asp Lys
                                             60
                        55
Leu Leu Leu Ala Gln Gln Lys Gln Ile His Tyr Ile Thr Asp Glu Glu
                    70
                                        75
His Phe Pro Met Gln Glu Arg Gly Asn Asp Gln Thr Glu Glu Leu Cys
                85
Tyr Ile Gln Asn Gln Gly Gly Phe Asn Lys Gly Tyr Asn Asn Tyr Lys
                                105
            100
Pro Asn Pro Asn Leu Ser Tyr Thr Ser Thr Asn Val Ala
                            120
        115
(2) INFORMATION FOR SEQ ID NO;580:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1072 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..1072
          (D) OTHER INFORMATION: / Ceres Seq. ID 1587913
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:
                                                                        60
gaggacgtgg tggtggagga ttcagaggtg gaagagatgg tggtggaaga ggttttggag
                                                                       120
gtggaagaag ctttggagga ggccgtagtg gtgacagagg ccgtagtggg cctcgcggca
gaggacgtgg tgcgcctcgt ggtcgtggag gaccacctcg tggaggaatg aaaggaggaa
                                                                       180
gcaaagtgat tgttgagcct cacagacatg cgggagtgtt tattgctaaa ggtaaagaag
                                                                        240
atgctcttgt cactaagaat ttggttcctg gtgaagctgt ttacaatgag aagagaatct
                                                                        300
ctgttcagaa tgaagatgga actaaggttg aatacagagt ttggaatccg tttagatcta
                                                                        360
agttagctgc tgcaattctt ggtggtgtcg acaacatttg gatcaaacct ggtgccaaag
                                                                        420
ttctttactt gggtgctgct tctgggacca ctgtctctca tgtttctgac ctcgttggcc
                                                                        480
                                                                        540
ctgagggatg tgtttatgct gttgagtttt ctcatagaag tggtagagat ttggtgaaca
tggccaagaa gagaactaac gttattccaa tcattgaaga tgctagacat ccggctaagt
                                                                        600
acagaatgct cgtgggcatg gttgatgtca tattctctga tgttgctcag ccagatcagg
                                                                        660
caagaatett ggeeetgaat geeteatttt teeteaaaae tggtggaeae tttgttatet
                                                                        720
                                                                        780
caatcaaggc caactgtatc gactctacag ttgcagcaga agcagtcttc cagagcgagg
                                                                        840
tgaagaagtt gcaacaagag cagtttaaac cagcagaaca ggtgactctc gagccgtttg
                                                                        900
agegtgacca tgcctgtgtt gttggtggtt accgcatgcc caagaaacaa aaagccccag
                                                                        960
cctcatagag gaactgtgga cagtagtacc tgtgtattaa gacttattta ctgggttttg
tttttatctc ttcgcttgtt gtattaagct agagatggat aatgctttta tgtctcattt
                                                                       1020
ggaaatttta ttctcgttta agaactaata tatattgatg caacattttc gt
 (2) INFORMATION FOR SEQ ID NO:581:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 301 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..301
           (D) OTHER INFORMATION: / Ceres Seq. ID 1587914
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581: Gly Arg Gly Gly Gly Phe Arg Gly Gly Arg Asp Gly Gly Arg

10 Gly Phe Gly Gly Gly Arg Ser Phe Gly Gly Gly Arg Ser Gly Asp Arg 25 20

Gly Arg Ser Gly Pro Arg Gly Arg Gly Arg Gly Ala Pro Arg Gly Arg 40

Gly Gly Pro Pro Arg Gly Gly Met Lys Gly Gly Ser Lys Val Ile Val 50

```
Glu Pro His Arg His Ala Gly Val Phe Ile Ala Lys Gly Lys Glu Asp
                                 75
Ala Leu Val Thr Lys Asn Leu Val Pro Gly Glu Ala Val Tyr Asn Glu
                            90
          8.5
Lys Arg Ile Ser Val Gln Asn Glu Asp Gly Thr Lys Val Glu Tyr Arg
                       105
Val Trp Asn Pro Phe Arg Ser Lys Leu Ala Ala Ala Ile Leu Gly Gly
             120
Val Asp Asn Ile Trp Ile Lys Pro Gly Ala Lys Val Leu Tyr Leu Gly
  130 135
Ala Ala Ser Gly Thr Thr Val Ser His Val Ser Asp Leu Val Gly Pro
      150
                       155
Glu Gly Cys Val Tyr Ala Val Glu Phe Ser His Arg Ser Gly Arg Asp
                    170
           165
Leu Val Asn Met Ala Lys Lys Arg Thr Asn Val Ile Pro Ile Ile Glu
              185
         180
Asp Ala Arg His Pro Ala Lys Tyr Arg Met Leu Val Gly Met Val Asp
             200
Val Ile Phe Ser Asp Val Ala Gln Pro Asp Gln Ala Arg Ile Leu Ala
         215
                                   220
Leu Asn Ala Ser Phe Phe Leu Lys Thr Gly Gly His Phe Val Ile Ser
                                235
    230
Ile Lys Ala Asn Cys Ile Asp Ser Thr Val Ala Ala Glu Ala Val Phe
           245 250
Gln Ser Glu Val Lys Lys Leu Gln Gln Glu Gln Phe Lys Pro Ala Glu
              265
         260
Gln Val Thr Leu Glu Pro Phe Glu Arg Asp His Ala Cys Val Val Gly
    275 280
Gly Tyr Arg Met Pro Lys Lys Gln Lys Ala Pro Ala Ser
```

- (2) INFORMATION FOR SEQ ID NO:582:
 - (i) SEQUENCE CHARACTERISTICS:

295

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..246
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1587915
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:
- Met Lys Gly Gly Ser Lys Val Ile Val Glu Pro His Arg His Ala Gly
 1 5 10 15
- Val Phe Ile Ala Lys Gly Lys Glu Asp Ala Leu Val Thr Lys Asn Leu 20 25 30
- Val Pro Gly Glu Ala Val Tyr Asn Glu Lys Arg Ile Ser Val Gln Asn 35 40 45
- Glu Asp Gly Thr Lys Val Glu Tyr Arg Val Trp Asn Pro Phe Arg Ser
- Lys Leu Ala Ala Ala Ile Leu Gly Gly Val Asp Asn Ile Trp Ile Lys 65 70 75 80
- Pro Gly Ala Lys Val Leu Tyr Leu Gly Ala Ala Ser Gly Thr Thr Val
- Ser His Val Ser Asp Leu Val Gly Pro Glu Gly Cys Val Tyr Ala Val 100 105 110 Glu Phe Ser His Arg Ser Gly Arg Asp Leu Val Asn Met Ala Lys Lys
- 115 120 125

 Arg Thr Asn Val Ile Pro Ile Ile Glu Asp Ala Arg His Pro Ala Lys
- 130 135 140
 Tyr Arg Met Leu Val Gly Met Val Asp Val Ile Phe Ser Asp Val Ala

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                                        155
                    150
145
Gln Pro Asp Gln Ala Arg Ile Leu Ala Leu Asn Ala Ser Phe Phe Leu
                                170
                165
Lys Thr Gly Gly His Phe Val Ile Ser Ile Lys Ala Asn Cys Ile Asp
                                185
                                                    190
            180
Ser Thr Val Ala Ala Glu Ala Val Phe Gln Ser Glu Val Lys Lys Leu
                                                 205
                            200
Gln Gln Glu Gln Phe Lys Pro Ala Glu Gln Val Thr Leu Glu Pro Phe
                        215
                                            220
Glu Arg Asp His Ala Cys Val Val Gly Gly Tyr Arg Met Pro Lys Lys
                    230
                                        235
Gln Lys Ala Pro Ala Ser
                245
(2) INFORMATION FOR SEQ ID NO:583:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 176 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..176
          (D) OTHER INFORMATION: / Ceres Seq. ID 1588129
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:
                                                                        60
atqaqctttq aaataggtga caaagatgaa atcaaaaaga ggaagagaca caaagaagat
                                                                       120
ccgattattc acgtcttcaa tacgaaatca tcaattgatg aaaaggttgc tttagatgat
gggtataaat ggaggaaata cggaaagaag ccgataacgg gtagtccatt tccaag
(2) INFORMATION FOR SEQ ID NO:584:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 58 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..58
          (D) OTHER INFORMATION: / Ceres Seq. ID 1588130
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:
Met Ser Phe Glu Ile Gly Asp Lys Asp Glu Ile Lys Lys Arg Lys Arg
                5
                                     10
His Lys Glu Asp Pro Ile Ile His Val Phe Asn Thr Lys Ser Ser Ile
                                 25
Asp Glu Lys Val Ala Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly
                            40
                                                 45
Lys Lys Pro Ile Thr Gly Ser Pro Phe Pro
    50
 (2) INFORMATION FOR SEQ ID NO:585:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 613 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..613

(D) OTHER INFORMATION: / Ceres Seq. ID 1592521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585: aaaacccaaa aacattgacc caaagagaga gagacttcta tcgtgcgcac ctctctctct

taatcettta teetgegeac caccaccacc atettettet ceggegaaaa caaacccacc 120 gccatgggga aaggtcgtgc actttccgac ggagtgatca aaaagatcat cctttcatac 180 acctatgtcg caatctggat cttcctcagc ttcacagtca tcgtctacaa caaatacatc 240 ctcgacaaga agatagtaaa ggttgtagga ttggaaggtc acgtgatgga gcagttcaag 300 gtgtatgaga ttgacttcca atttattccc aagtctgaag aagattgcgt ctgcaaaatc 360 actatgatat gggagaagcg caacgatgat ttccccgaac caagcagcta catgcaactc 420 ctcaagagta tggttattga tatggaggac cacgtcctta aagcttaatc aatatcacaa 480 ccaccaccat catcacaacc accatcatca tcatcctata tgtttattaa attgttttca 540 600 tttatatata atagactaga taagaacctg tataatgtgc gggataaaat gattgaaata aattattatg cgt

- (2) INFORMATION FOR SEQ ID NO:586:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592522
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Asn Pro Lys Thr Leu Thr Gln Arg Glu Arg Asp Phe Tyr Arg Ala His 1 5 10 15

Leu Ser Leu Leu Ile Leu Tyr Pro Ala His His His His Leu Leu 20 25 30

Leu Arg Arg Lys Gln Thr His Arg His Gly Glu Arg Ser Cys Thr Phe 35 40 45

Arg Arg Ser Asp Gln Lys Asp His Pro Phe Ile His Leu Cys Arg Asn 50 55 60

Leu Asp Leu Pro Gln Leu His Ser His Arg Leu Gln Gln Ile His Pro 65 70 75 80

Arg Gln Glu Asp Ser Lys Gly Cys Arg Ile Gly Arg Ser Arg Asp Gly 85 90 95

Ala Val Gln Gly Val

100

- (2) INFORMATION FOR SEQ ID NO:587:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592523
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met Gly Lys Gly Arg Ala Leu Ser Asp Gly Val Ile Lys Lys Ile Ile
1 10 15

Leu Ser Tyr Thr Tyr Val Ala Ile Trp Ile Phe Leu Ser Phe Thr Val

Ile Val Tyr Asn Lys Tyr Ile Leu Asp Lys Lys Ile Val Lys Val Val 35 40 45

Gly Leu Glu Gly His Val Met Glu Gln Phe Lys Val Tyr Glu Ile Asp 50 55 60

Phe Gln Phe Ile Pro Lys Ser Glu Glu Asp Cys Val Cys Lys Ile Thr 65 70 75 80

Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro Glu Pro Ser Ser Tyr 85 90 95

Met Gln Leu Leu Lys Ser Met Val Ile Asp Met Glu Asp His Val Leu

110 100 105 Lys Ala (2) INFORMATION FOR SEQ ID NO:588: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..60 (D) OTHER INFORMATION: / Ceres Seq. ID 1592524 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588: Met Glu Gln Phe Lys Val Tyr Glu Ile Asp Phe Gln Phe Ile Pro Lys 10 Ser Glu Glu Asp Cys Val Cys Lys Ile Thr Met Ile Trp Glu Lys Arg 25 2.0 Asn Asp Asp Phe Pro Glu Pro Ser Ser Tyr Met Gln Leu Leu Lys Ser 40 35 Met Val Ile Asp Met Glu Asp His Val Leu Lys Ala 55 (2) INFORMATION FOR SEQ ID NO:589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 473 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..473 (D) OTHER INFORMATION: / Ceres Seq. ID 1592525 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589: atcaaccaaa acaaaacata aaaaacaagt ggaagcttta aaacgagagg gagagagcaa 60 aaatggcgac gtcgggaacg tacgtgacgg aagttccgct aaaaggatcg gccgagaaat 120 actacaagag gtggaagaac gagaaccatg tetteeetga tgetategge caccacatee 180 aaaatgttac cgttcacgaa ggcgaacatg actctcacgg gtctatcagg agttggaact 240 acacatggga tggaaaggag gaggtgttca aggagagaag agagatagac gatgagacca 300 aaacgttgac gttaagagga cttgagggtc acgtgatgga gcagctcaaa gtgtacgacg 360 tcgtctacca attcattccc aaatctgagg atacctgcat cggcaaaatc actttaatat 420 gggagaagcg caacgatgat tccccatatt gaacttgatt tgaaatccta ata (2) INFORMATION FOR SEQ ID NO:590: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..129 (D) OTHER INFORMATION: / Ceres Seq. ID 1592526 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590: Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser 10 5 Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro 30 25 Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu 45 40

His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly 55 Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys 70 75 Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys 85 90 Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys 105 Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro 120 Tyr

- (2) INFORMATION FOR SEQ ID NO:591:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..343
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592527
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591: agatctaggg tttatatagt ttgccgsttc atctscgttt sttctttccg attcgtgttt 60 tcccgtcggc cggagatata tcgcaaccct aatcsgaaat ggsgdnggag aagaanctat 120 180 cgaacccaat gagggacatt aaagtgcaga agctggttct caacatctcc gttggtgaga 240 gtggagatcg tctcacsaga gcctccaagg tgttggarca rttgagtggt cagactcctg 300 ttttctccaa ggctcgatac actgttcgtt cttttggtat aagacgtaat gagaagattg cttrctatgt gastgtcagg ggagwgaagg caatgcagct cct
- (2) INFORMATION FOR SEQ ID NO:592:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..43
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592528
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

Arg Ser Arg Val Tyr Ile Val Cys Xaa Phe Ile Xaa Val Xaa Ser Phe 10 5

Arg Phe Val Phe Ser Arg Arg Pro Glu Ile Tyr Arg Asn Pro Asn Xaa 25

Lys Trp Xaa Xaa Arg Arg Xaa Tyr Arg Thr Gln 35 40

- (2) INFORMATION FOR SEQ ID NO:593:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592529
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met Xaa Xaa Glu Lys Xaa Leu Ser Asn Pro Met Arg Asp Ile Lys Val

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide (B) LOCATION: 1..75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

(D) OTHER INFORMATION: / Ceres Seq. ID 1592532

(ix) FEATURE:

10 Gln Lys Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu 25 20 Xaa Arg Ala Ser Lys Val Leu Xaa Xaa Leu Ser Gly Gln Thr Pro Val 40 Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser Phe Gly Ile Arg Arg Asn 55 60 Glu Lys Ile Ala Xaa Tyr Val Xaa Val Arg Gly Xaa Lys Ala Met Gln 70 Leu (2) INFORMATION FOR SEQ ID NO:594: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1592530 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594: Met Arg Asp Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly 10 Glu Ser Gly Asp Arg Leu Xaa Arg Ala Ser Lys Val Leu Xaa Xaa Leu 25 20 Ser Gly Gln Thr Pro Val Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser 40 Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Xaa Tyr Val Xaa Val Arg 55 Gly Xaa Lys Ala Met Gln Leu 70 (2) INFORMATION FOR SEQ ID NO:595: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..225 (D) OTHER INFORMATION: / Ceres Seq. ID 1592531 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595: acacacttca ctaaacttca gatacttttt gttttttcct caagatcaac gataatggcg 60 gcgtcaacga actcattcct catcggaaac caaacccaaa tcccttcttt gaaacccaaa 120 tcaatttctc aatcetttat ccacttcaca agaacccaac accatcaacc tcaccaccag 180 aaccaaatcc gtttcaatcc gatgcgcttc cccttcaacc accgt (2) INFORMATION FOR SEQ ID NO:596: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear

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Thr His Phe Thr Lys Leu Gln Ile Leu Phe Val Phe Ser Ser Arg Ser
                                    10
Thr Ile Met Ala Ala Ser Thr Asn Ser Phe Leu Ile Gly Asn Gln Thr
                                25
            20
Gln Ile Pro Ser Leu Lys Pro Lys Ser Ile Ser Gln Ser Phe Ile His
                            40
Phe Thr Arg Thr Gln His His Gln Pro His His Gln Asn Gln Ile Arg
                        55
Phe Asn Pro Met Arg Phe Pro Phe Asn His Arg
                    70
(2) INFORMATION FOR SEQ ID NO:597:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 57 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..57
          (D) OTHER INFORMATION: / Ceres Seq. ID 1592533
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:
Met Ala Ala Ser Thr Asn Ser Phe Leu Ile Gly Asn Gln Thr Gln Ile
                                    10
                5
Pro Ser Leu Lys Pro Lys Ser Ile Ser Gln Ser Phe Ile His Phe Thr
                                                     30
                                25
            20
Arg Thr Gln His His Gln Pro His His Gln Asn Gln Ile Arg Phe Asn
                            40
Pro Met Arg Phe Pro Phe Asn His Arg
                        55
(2) INFORMATION FOR SEQ ID NO:598:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 293 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..293
           (D) OTHER INFORMATION: / Ceres Seq. ID 1592538
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:
tataacattg atgtctctcg ttctgatggc tcctgtgact ttctttacgg aaggcatcaa
gttcactcct tcatacattc aatcagctgg tgtgaatgtt caacaaatat atacaaagtc
tettateget geactetget tecaegeata ceageaggtg tegtacatga tattggegag
                                                                        180
                                                                        240
agtatcaccg gttacacatt ctgtcggaaa ctgtgtgaaa cgtgttgtgg ttattgtgag
ctctgtcatc ttcttcaaga cacccgtctc gcctgttaat gctttcggaa ctg
(2) INFORMATION FOR SEQ ID NO:599:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 92 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..92
           (D) OTHER INFORMATION: / Ceres Seq. ID 1592539
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:
 Tyr Asn Ile Asp Val Ser Arg Ser Asp Gly Ser Cys Asp Phe Leu Tyr
                                     10
```

Gly Arg His Gln Val His Ser Phe Ile His Ser Ile Ser Trp Cys Glu $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30 \hspace{1.5cm}$

Cys Ser Thr Asn Ile Tyr Lys Val Ser Tyr Arg Cys Thr Leu Leu Pro 35 40

Arg Ile Pro Ala Gly Val Val His Asp Ile Gly Glu Ser Ile Thr Gly 50 55 60

Tyr Thr Phe Cys Arg Lys Leu Cys Glu Thr Cys Cys Gly Tyr Cys Glu 65 70 75 80

Leu Cys His Leu Leu Gln Asp Thr Arg Leu Ala Cys 85 90

- (2) INFORMATION FOR SEQ ID NO:600:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592540
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Ile Thr Leu Met Ser Leu Val Leu Met Ala Pro Val Thr Phe Phe Thr 1 5 10 15

Glu Gly Ile Lys Phe Thr Pro Ser Tyr Ile Gln Ser Ala Gly Val Asn 20 25 30

Val Gln Gln Ile Tyr Thr Lys Ser Leu Ile Ala Ala Leu Cys Phe His
35 40 45

Ala Tyr Gln Gln Val Ser Tyr Met Ile Leu Ala Arg Val Ser Pro Val 50 55 60

Thr His Ser Val Gly Asn Cys Val Lys Arg Val Val Val Ile Val Ser

70

75

80

Ser Val Ile Phe Phe Lys Thr Pro Val Ser Pro Val Asn Ala Phe Gly 85 90 95

Thr

- (2) INFORMATION FOR SEQ ID NO:601:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592541
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Met Ser Leu Val Leu Met Ala Pro Val Thr Phe Phe Thr Glu Gly Ile

5 10 15

Lys Phe Thr Pro Ser Tyr Ile Gln Ser Ala Gly Val Asn Val Gln Gln 20 25 30

Ile Tyr Thr Lys Ser Leu Ile Ala Ala Leu Cys Phe His Ala Tyr Gln
35 40 45

Gln Val Ser Tyr Met Ile Leu Ala Arg Val Ser Pro Val Thr His Ser 50 60

Val Gly Asn Cys Val Lys Arg Val Val Val Ile Val Ser Ser Val Ile 65 70 75 80

Phe Phe Lys Thr Pro Val Ser Pro Val Asn Ala Phe Gly Thr 85 90

(2) INFORMATION FOR SEQ ID NO:602:

60

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..280 (D) OTHER INFORMATION: / Ceres Seq. ID 1592546 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602: agctagacat tttcgttttc atctccccac gaatcaaaga tggcttttgc cattgcttct gctctcactt ccacactcac attatccacg agcagagtcc aaaatcctac ccagagaaga 120 180 ccacatgtag cgtccacatc atccaccggt ggaagattaa tgagagagcg cttggtggtg 240 gttcgtgccg gcaaagaagt ttctagcgtc tgtgaaaatg agatattata tgtgcaactt ttttcttttt ttttttgtgt cctttsttca astttgaaat (2) INFORMATION FOR SEQ ID NO:603: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..42 (D) OTHER INFORMATION: / Ceres Seq. ID 1592547 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603: Ala Arg His Phe Arg Phe His Leu Pro Thr Asn Gln Arg Trp Leu Leu 10 5 Pro Leu Leu Leu Ser Leu Pro His Ser His Tyr Pro Arg Ala Glu 25 20 Ser Lys Ile Leu Pro Arg Glu Asp His Met 35 (2) INFORMATION FOR SEQ ID NO:604: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..67 (D) OTHER INFORMATION: / Ceres Seq. ID 1592548 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604: Leu Asp Ile Phe Val Phe Ile Ser Pro Arg Ile Lys Asp Gly Phe Cys 1.0 5 His Cys Phe Cys Ser His Phe His Thr His Ile Ile His Glu Gln Ser 25 20 Pro Lys Ser Tyr Pro Glu Lys Thr Thr Cys Ser Val His Ile Ile His 45 4.0 Arg Trp Lys Ile Asn Glu Arg Ala Leu Gly Gly Gly Ser Cys Arg Gln 55 Arg Ser Phe 65 (2) INFORMATION FOR SEQ ID NO:605:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..80 (D) OTHER INFORMATION: / Ceres Seq. ID 1592549 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605: Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu Thr Leu Ser 1.0 Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His Val Ala Ser 20 25 Thr Ser Ser Thr Gly Gly Arg Leu Met Arg Glu Arg Leu Val Val Val 40 Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Asn Glu Ile Leu Tyr 55 Val Gln Leu Phe Ser Phe Phe Phe Cys Val Leu Xaa Ser Xaa Leu Lys 75 70 (2) INFORMATION FOR SEQ ID NO:606: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..304 (D) OTHER INFORMATION: / Ceres Seq. ID 1592567 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606: aatcggagca acagtcatca aagagccaat ggcttcttca ggtttcagcg gcgatgaaac tgcgcctttc ttcggattcc tcggcgccgs sgctgcgctc gttttctcct gtatgggagc agcgtacggg acggcgaaga gtggagttgg agttgcgtcg atgggagtga tgagacctga acttgttatg aaatcgattg ttcctgttgt catggctggt gtcttagata tttatggttt 240 gatcatcgct gttatcatca gtactgggat taaccccaag gccaagtttt tttttttt (2) INFORMATION FOR SEQ ID NO:607: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..101 (D) OTHER INFORMATION: / Ceres Seq. ID 1592568 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607: Ile Gly Ala Thr Val Ile Lys Glu Pro Met Ala Ser Ser Gly Phe Ser 5 10 Gly Asp Glu Thr Ala Pro Phe Phe Gly Phe Leu Gly Ala Xaa Ala Ala 25 Leu Val Phe Ser Cys Met Gly Ala Ala Tyr Gly Thr Ala Lys Ser Gly 40 Val Gly Val Ala Ser Met Gly Val Met Arg Pro Glu Leu Val Met Lys 60 55 Ser Ile Val Pro Val Val Met Ala Gly Val Leu Asp Ile Tyr Gly Leu 75

70

85

Ile Ile Ala Val Ile Ile Ser Thr Gly Ile Asn Pro Lys Ala Lys Phe

90

Phe Phe Phe Phe

100

- (2) INFORMATION FOR SEQ ID NO:608:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592569
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met Ala Ser Ser Gly Phe Ser Gly Asp Glu Thr Ala Pro Phe Phe Gly
1 10 15

Phe Leu Gly Ala Xaa Ala Ala Leu Val Phe Ser Cys Met Gly Ala Ala 20 25 30

Tyr Gly Thr Ala Lys Ser Gly Val Gly Val Ala Ser Met Gly Val Met 35 40 45

Arg Pro Glu Leu Val Met Lys Ser Ile Val Pro Val Val Met Ala Gly 50 55 60

Val Leu Asp Ile Tyr Gly Leu Ile Ile Ala Val Ile Ile Ser Thr Gly 65 70 75 80

Ile Asn Pro Lys Ala Lys Phe Phe Phe Phe Phe Phe 85 90

- (2) INFORMATION FOR SEQ ID NO:609:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592570
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

Met Gly Ala Ala Tyr Gly Thr Ala Lys Ser Gly Val Gly Val Ala Ser 1 5 10 15

Met Gly Val Met Arg Pro Glu Leu Val Met Lys Ser Ile Val Pro Val 20 25 30

Val Met Ala Gly Val Leu Asp Ile Tyr Gly Leu Ile Ile Ala Val Ile 35 40 45

Ile Ser Thr Gly Ile Asn Pro Lys Ala Lys Phe Phe Phe Phe Phe Phe Phe 50 55 60

- (2) INFORMATION FOR SEQ ID NO:610:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..494
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592602
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

ggcatctcct aattcgtcaa tcggagaatg gatacatcaa gtcctgctgc ttttgtgaat 120 ggagctttgt tgagaaggta cattggtcag aaagtgagag cagtgattca agttatcaga 180 tcagatgttg gatcagtgat tggtaaatcg actgatgatc aacagattgt tgttaaaggt 240 tctcctcaac cgcctttaac tacttacctt gaggtaattg gaattgctga gactgacaac 300 actattcgtg ctgaagtttg gaccaacttt ggtgatagtt tcgatgtgca aaactacaat 360 gagctatgta agcttgcaaa tggtgagtt agacacttgt tcatctaaat cacagggtat 420 tggtgatgat cttt

- (2) INFORMATION FOR SEQ ID NO:611:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..67
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Ser Ser Ile Gln Arg Leu Gly Phe Ser Ser Arg Arg Asn Leu Thr Gly
1 10 15

Asn Ser Leu Arg His Leu Leu Ile Arg Gln Ser Glu Asn Gly Tyr Ile
20 25 30

Lys Ser Cys Cys Phe Cys Glu Trp Ser Phe Val Glu Lys Val His Trp 35 40 45

Ser Glu Ser Glu Ser Ser Asp Ser Ser Tyr Gln Ile Arg Cys Trp Ile 50 55 60

Ser Asp Trp

65

- (2) INFORMATION FOR SEQ ID NO:612:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592604
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Asp Thr Ser Ser Pro Ala Ala Phe Val Asn Gly Ala Leu Leu Arg
1 5 10 15

Arg Tyr Ile Gly Gln Lys Val Arg Ala Val Ile Gln Val Ile Arg Ser

Asp Val Gly Ser Val Ile Gly Lys Ser Thr Asp Asp Gln Gln Ile Val 35 40 45

Val Lys Gly Ser Pro Gln Pro Pro Leu Thr Thr Tyr Leu Glu Val Ile
50 55 60

Gly Ile Ala Glu Thr Asp Asn Thr Ile Arg Ala Glu Val Trp Thr Asn 65 70 75 80

Phe Gly Asp Ser Phe Asp Val Gln Asn Tyr Asn Glu Leu Cys Lys Leu 85 90 95

Ala Asn Gly Glu Phe Arg His Leu Phe Ile 100 105

- (2) INFORMATION FOR SEQ ID NO:613:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613: acttttcagc gtttctgacc aaattctctc cgtgtttcct tctgcttcag gtgatatttt 60 aacaaagttc ttagtacaat gggatctgtt gatgctgcta atggaagtgg gaagaaacct 120 acagttatat ttgttcttgg tggtccagga agtggaaaag gtacccagtg tgcttatatt 180 gttgaacatt atggttacac acatctgagt gctggagatc ttcttagagc tgagattaaa 240 300 tcaggttctg aaaatggaac tatgatccag aatatgatta aagaggggaa gattgtacct tctgaggtta ctatcaagct tctacagaaa gctattcagg aaaacgggaa tgacaagttc 360 ctcattgatg gtttccctcg taatgaggaa aaccgagcag catttgaaaa agttactgag 420 480 attgaaccaa agtttgtctt attcttcgat tgtcctgagg aagagatgga gaagcgcctg

- ttgggccgaa accaggggga gagaggatga c (2) INFORMATION FOR SEQ ID NO:614:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592628
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Met Gly Ser Val Asp Ala Ala Asn Gly Ser Gly Lys Lys Pro Thr Val 1 5 10 15

Ile Phe Val Leu Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys Ala 20 25 30

Tyr Ile Val Glu His Tyr Gly Tyr Thr His Leu Ser Ala Gly Asp Leu 35 40 45

Leu Arg Ala Glu Ile Lys Ser Gly Ser Glu Asn Gly Thr Met Ile Gln 50 55 60

Asn Met Ile Lys Glu Gly Lys Ile Val Pro Ser Glu Val Thr Ile Lys 65 70 75 80
Leu Leu Gln Lys Ala Ile Gln Glu Asn Gly Asn Asp Lys Phe Leu Ile

85 90 95
Asp Gly Phe Pro Arg Asn Glu Glu Asn Arg Ala Ala Phe Glu Lys Val

100 105 110
Thr Glu Ile Glu Pro Lys Phe Val Leu Phe Phe Asp Cys Pro Glu Glu

115 120 125
Glu Met Glu Lys Arg Leu Leu Gly Arg Asn Gln Gly Glu Arg Gly
130 135 140

- (2) INFORMATION FOR SEQ ID NO:615:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592629
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

Met Ile Gln Asn Met Ile Lys Glu Gly Lys Ile Val Pro Ser Glu Val

1 5 10 15

Thr Ile Lys Leu Leu Gln Lys Ala Ile Gln Glu Asn Gly Asn Asp Lys

- (2) INFORMATION FOR SEQ ID NO:616:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

Met Ile Lys Glu Gly Lys Ile Val Pro Ser Glu Val Thr Ile Lys Leu
1 10 15

Leu Gln Lys Ala Ile Gln Glu Asn Gly Asn Asp Lys Phe Leu Ile Asp 20 25 30

Gly Phe Pro Arg Asn Glu Glu Asn Arg Ala Ala Phe Glu Lys Val Thr 35 40 45

Glu Ile Glu Pro Lys Phe Val Leu Phe Phe Asp Cys Pro Glu Glu Glu 50 55 60

Met Glu Lys Arg Leu Leu Gly Arg Asn Gln Gly Glu Arg Gly 65 70 75

- (2) INFORMATION FOR SEQ ID NO:617:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..488
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592639
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

gtgaggtttg gggatcgcga aaatggaggt tccaggttca tcgaagaaga tgatcgcaac 60 gcaagaagag atgtctgcag ctaaaatagc acttggatct agagatatgt gcgctcatct 120 cttgattccg ctcaacaaat gtcgtcaggc tgagttttac cttccaagga aatgtgaaga 180 cgagcgtcac gtttatgaga agtgtgaata cgagcttgtt atggagagaa tgcttgcnat 240 gaagaagatc cgtgaagaag aagctttggc taaacagaat aaactacaag gaaacgctgc 300 tgttcctctt atccctaaaa ctgctaatgc ttaggattcg attccttctc caatttgccg 360 attccagatt ccgggattct ctggaactgt gaagatggtg ggggctctgc ttttcaakct 420 ktttcttctt gctagtgatg aaaaatggca gcaacatttg caacaccatc gacggtgata 480 ggcctcgq

- (2) INFORMATION FOR SEQ ID NO:618:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1592640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

Met Glu Val Pro Gly Ser Ser Lys Lys Met Ile Ala Thr Gln Glu Glu 1 5 10 15 ...

Met Ser Ala Ala Lys Ile Ala Leu Gly Ser Arg Asp Met Cys Ala His
20 25 30

Leu Leu Ile Pro Leu Asn Lys Cys Arg Gln Ala Glu Phe Tyr Leu Pro 35 40 45

Arg Lys Cys Glu Asp Glu Arg His Val Tyr Glu Lys Cys Glu Tyr Glu 50 60

Leu Val Met Glu Arg Met Leu Xaa Met Lys Lys Ile Arg Glu Glu Glu 65 70 75 80

Ala Leu Ala Lys Gln Asn Lys Leu Gln Gly Asn Ala Ala Val Pro Leu 85 90 95

Ile Pro Lys Thr Ala Asn Ala 100

- (2) INFORMATION FOR SEQ ID NO:619:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

Met Ile Ala Thr Gln Glu Glu Met Ser Ala Ala Lys Ile Ala Leu Gly 1 5 10

Ser Arg Asp Met Cys Ala His Leu Leu Ile Pro Leu Asn Lys Cys Arg 20 25 30

Gln Ala Glu Phe Tyr Leu Pro Arg Lys Cys Glu Asp Glu Arg His Val 35 40 45

Tyr Glu Lys Cys Glu Tyr Glu Leu Val Met Glu Arg Met Leu Xaa Met 50 55 60

Lys Lys Ile Arg Glu Glu Glu Ala Leu Ala Lys Gln Asn Lys Leu Gln 65 70 75 80

Gly Asn Ala Ala Val Pro Leu Ile Pro Lys Thr Ala Asn Ala 85 90

- (2) INFORMATION FOR SEQ ID NO:620:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Ser Ala Ala Lys Ile Ala Leu Gly Ser Arg Asp Met Cys Ala His 1 5 10 15

Leu Leu Ile Pro Leu Asn Lys Cys Arg Gln Ala Glu Phe Tyr Leu Pro 20 25 30

Arg Lys Cys Glu Asp Glu Arg His Val Tyr Glu Lys Cys Glu Tyr Glu 35 40 45

Leu Val Met Glu Arg Met Leu Xaa Met Lys Lys Ile Arg Glu Glu Glu 50 55 60

Ala Leu Ala Lys Gln Asn Lys Leu Gln Gly Asn Ala Ala Val Pro Leu 7.0

Ile Pro Lys Thr Ala Asn Ala 8.5

- (2) INFORMATION FOR SEQ ID NO:621:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..493
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592649
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:621: 60 attattgaac ggtgtttgtt attcggagaa gaagaagaag aagaactgaa gaagcatatt cgacggtcac caccaaacct cttccgtcgg attttcactc tccgtttatc gaacatctga 120 gatetetete caetteegte acegaagatg catteeagte atettettet egaggageeg 180 atcaggatgg cttcaatcct cgagccttcc aaatctagtt tcttcccggc attgactaag 240 300 atcqtcqqaa ctctaggtcc taaatcccga tccgtcgagg ctctctccgg ctgtctcaaa qccqqcatqt ctqtqqctcg atttqatttc tcgtggggag atgctgatta tcaccaggag 360 420 acacttgata atttgaaagt tgctgtgagg agcactaaga agctttgtgc tgttatgctt gatactgttg gacctgagct acaagttatt aacaaatctg agaaagctat tactttgaag 480 ctgatggcct tgt
- (2) INFORMATION FOR SEQ ID NO:622:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

Met His Ser Ser His Leu Leu Leu Glu Glu Pro Ile Arg Met Ala Ser 10 5 Ile Leu Glu Pro Ser Lys Ser Ser Phe Phe Pro Ala Leu Thr Lys Ile

25 20 Val Gly Thr Leu Gly Pro Lys Ser Arg Ser Val Glu Ala Leu Ser Gly

40 Cys Leu Lys Ala Gly Met Ser Val Ala Arg Phe Asp Phe Ser Trp Gly 60

Asp Ala Asp Tyr His Gln Glu Thr Leu Asp Asn Leu Lys Val Ala Val 75 70

Arg Ser Thr Lys Lys Leu Cys Ala Val Met Leu Asp Thr Val Gly Pro 90 85

Glu Leu Gln Val Ile Asn Lys Ser Glu Lys Ala Ile Thr Leu Lys Leu 105 110 100

Met Ala Leu

115

- (2) INFORMATION FOR SEQ ID NO:623:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids

55

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

Met Ala Ser Ile Leu Glu Pro Ser Lys Ser Ser Phe Phe Pro Ala Leu 1 5 10 15

Thr Lys Ile Val Gly Thr Leu Gly Pro Lys Ser Arg Ser Val Glu Ala 20 25 30

Leu Ser Gly Cys Leu Lys Ala Gly Met Ser Val Ala Arg Phe Asp Phe 35 40 45

Ser Trp Gly Asp Ala Asp Tyr His Gln Glu Thr Leu Asp Asn Leu Lys 50 55 60

Val Ala Val Arg Ser Thr Lys Lys Leu Cys Ala Val Met Leu Asp Thr 65 70 75 80

Val Gly Pro Glu Leu Gln Val Ile Asn Lys Ser Glu Lys Ala Ile Thr 85 90 95

Leu Lys Leu Met Ala Leu 100

- (2) INFORMATION FOR SEQ ID NO:624:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met Ser Val Ala Arg Phe Asp Phe Ser Trp Gly Asp Ala Asp Tyr His

1 10 15

Cly Chy Thr Ley Asp Asp Ley Lys Val Ala Val Arg Ser Thr Lys Lys

Gln Glu Thr Leu Asp Asn Leu Lys Val Ala Val Arg Ser Thr Lys Lys
20 25 30

Leu Cys Ala Val Met Leu Asp Thr Val Gly Pro Glu Leu Gln Val Ile
35 40 45

Asn Lys Ser Glu Lys Ala Ile Thr Leu Lys Leu Met Ala Leu 50 55 60

- (2) INFORMATION FOR SEQ ID NO:625:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..450
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625: tcaaaattaa tacacacatt cattaaagaa aaacaccagg acgagattac ttttggcgaa 60 aagtccaaat taggacgagg gggtatgact gcaaaagtta aagctgctgt taatgcagct 120 tatggtggcg ttcctgttat cataaccagt ggatatgcag ctgagaatat aagtaaagtc 180 cttagaggac tgcgtgttgg taccctgttc catcaagatg ctcatttatg ggctccggtc 240 gtagatacta cttctcgtga catggcagtt gctgcaaggg aaagctcaag aaagcttcag 300 geettatett cagaagatag gaaacaaatt etacaegaca tigeeaatge eetigaagta 360 420 aatgagsaaa caattaaaag ctgagaatga tttagaatgt tgctgcagca caagaagctg gatatgaaga gtctttggta gctcgcttag

- (2) INFORMATION FOR SEQ ID NO:626:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:
- Ser Lys Leu Ile His Thr Phe Ile Lys Glu Lys His Gln Asp Glu Ile 1 5 10 15
- Thr Phe Gly Glu Lys Ser Lys Leu Gly Arg Gly Gly Met Thr Ala Lys 20 25 30
- Val Lys Ala Ala Val As
n Ala Ala Tyr Gly Gly Val Pro Val Ile Ile 35 40 45
- Thr Ser Gly Tyr Ala Ala Glu Asn Ile Ser Lys Val Leu Arg Gly Leu 50 55 60
- Arg Val Gly Thr Leu Phe His Gln Asp Ala His Leu Trp Ala Pro Val 65 70 75 80
- Val Asp Thr Thr Ser Arg Asp Met Ala Val Ala Ala Arg Glu Ser Ser 85 90 95
- Arg Lys Leu Gln Ala Leu Ser Ser Glu Asp Arg Lys Gln Ile Leu His
 100 105 110
- Asp Ile Ala Asn Ala Leu Glu Val Asn Glu Xaa Thr Ile Lys Ser 115 120 125
- (2) INFORMATION FOR SEQ ID NO:627:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592661
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:
- Met Thr Ala Lys Val Lys Ala Ala Val Asn Ala Ala Tyr Gly Gly Val 1 5 10 15
- Pro Val Ile Ile Thr Ser Gly Tyr Ala Ala Glu Asn Ile Ser Lys Val 20 25 30
- Leu Arg Gly Leu Arg Val Gly Thr Leu Phe His Gln Asp Ala His Leu $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$
- Trp Ala Pro Val Val Asp Thr Thr Ser Arg Asp Met Ala Val Ala Ala 50 55 60
- Arg Glu Ser Ser Arg Lys Leu Gln Ala Leu Ser Ser Glu Asp Arg Lys 65 70 75 80
- Gln Ile Leu His Asp Ile Ala Asn Ala Leu Glu Val Asn Glu Xaa Thr 85 90 95
- Ile Lys Ser
- (2) INFORMATION FOR SEQ ID NO:628:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1592685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:							
agaattgett etettagtat ttgettteae caacceaete gaeggagtet ecaaegeett	60						
cctcctcatt ctccactctc acaccaccaa cttctgattc cagatctcaa cgatgcaaag	120						
ctccgccgta ttctccctct ctccgtcgct ncctctccta aaaccacgtc ggctctctct	180						
ccgccaccat cccataacca ccgcsgcttc ttcaanngat ctaaacgttt ctccaaatgt	240						
tgtctctatt ccttctttat ctcgtcgatc ttggcgtctc gcttcgtctg attcgcctct	300						
ccqtqcttqq tccqgtqttc cttctccqat ctctcactcc ttagacacqa atcqtttcag	360						
aaccgccgct actgcagttc ctgaaagtgc tgaggaaggt gataacagtg gtaaattgac	420						
gaaggttttg gaacttggct tgttgttcgc tatgtggtac cttttcaata tctacttcaa	480						
catctacaat aaac							
Calciacaac aaac							

- (2) INFORMATION FOR SEQ ID NO:629:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592686
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

 Arg Ile Ala Ser Leu Ser Ile Cys Phe His Gln Pro Thr Arg Arg Ser
 1 5 10 15

 Leu Gln Arg Leu Pro Pro His Ser Pro Leu Ser His His Gln Leu Leu
 20 25 30

Ile Pro Asp Leu Asn Asp Ala Lys Leu Arg Arg Ile Leu Pro Leu Ser

Val Ala Xaa Ser Pro Lys Thr Thr Ser Ala Leu Ser Pro Pro Pro Ser 50 55 60

His Asn His Arg Xaa Phe Phe Xaa Xaa Ser Lys Arg Phe Ser Lys Cys 65 70 75 80

Cys Leu Tyr Ser Phe Phe Ile Ser Ser Ile Leu Ala Ser Arg Phe Val

(2) INFORMATION FOR SEQ ID NO:630:

85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
- Met Gln Ser Ser Ala Val Phe Ser Leu Ser Pro Ser Xaa Pro Leu Leu 1 5 10 15
- Lys Pro Arg Arg Leu Ser Leu Arg His His Pro Ile Thr Thr Xaa Ala 20 25 30
- Ser Ser Xaa Asp Leu Asn Val Ser Pro Asn Val Val Ser Ile Pro Ser 35 40 45
- Leu Ser Arg Arg Ser Trp Arg Leu Ala Ser Ser Asp Ser Pro Leu Arg 50 55 60
- Ala Trp Ser Gly Val Pro Ser Pro Ile Ser His Ser Leu Asp Thr Asn 65 70 75 80

Arg Phe Arg Thr Ala Ala Thr Ala Val Pro Glu Ser Ala Glu Gly 85 90 95 Asp Asn Ser Gly Lys Leu Thr Lys Val Leu Glu Leu Gly Leu Leu Phe
100
105
110

Ala Met Trp Tyr Leu Phe Asn Ile Tyr Phe Asn Ile Tyr Asn Lys 115 120 125

- (2) INFORMATION FOR SEQ ID NO:631:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..494
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592718
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

60 atcaaccaaa acaaaacata aaaaacaagt ggaagcttta aaacgagagg gagagagcaa aaatggcgac gtcgggaacg tacgtgacgg aagttccgct aaaaggatcg gccgagaaat 120 180 actacaaqaq gtggaagaac gagaaccatg tcttccctga tgctatcggc caccacatcc 240 aaaatgttac cgttcacgaa ggcgaacatg actctcacgg gtctatcagg agttggaact acacatggga tggaaaggag gaggtgttca aggagagaag agagatagac gatgagacca 300 aaacgttgac gttaagagga cttgagggtc acgtgatgga gcagctcaaa gtgtacgacg 360 tcgtctacca attcattccc aaatctgagg atacctgcat cggcanaatc actttaatat 420 gggagawgaa tgatggaatg gagcactgtg tgtttgtgac tcaggggctg tttttgttgt 480 tgtttgtgac tggg

- (2) INFORMATION FOR SEQ ID NO:632:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592719
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632: Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser

1 5 10 15
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro
20 25 30

20 25 30
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu
35 40 45

His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly
50 55 60

Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys 65 70 75 80

Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys 85 90 95

Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys \$100\$ \$105\$ \$110\$

Ile Gly Xaa Ile Thr Leu Ile Trp Glu Xaa Asn Asp Gly Met Glu His 115 120 125

Cys Val Phe Val Thr Gln Gly Leu Phe Leu Leu Phe Val Thr Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..471
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592742
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

 caatatctac ttcaacatct acaataaaca ggttttgaaa gctctacatg ctccaatgac 60
 tgtgactttg gttcagtttg ctttggtagt gtgctcatta ctatcatgtg ggttcttaac 120
 ctgtacaaga gaccaaagat cagtggtgct cagctagctg ccatcttgcc gcttgctgtt 180
 gtgcacacac ttggtaatct gtttacgaac atgagtcttg ggaaagtttc tgttccttt 240
 actcacacca ttaaagccat ggagcctttc ttctctgttt tattgtctgc tatgtttetc 300
 ggggagaaac ctactccatg ggtactcggt gccattgtac caattgttgg tggagttgca 360
 cttgcttcaa ttcggaggt ctcattcaac tgggctggat ttcgggtga aatggcatca 420
 aacttgacta accaatcccg taatgtgctg agtaagaaag tcatggttaa g
- (2) INFORMATION FOR SEQ ID NO:634:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592743
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Met Trp Val Leu Asn Leu Tyr Lys Arg Pro Lys Ile Ser Gly Ala Gln 1 5 10 15 Leu Ala Ala Ile Leu Pro Leu Ala Val Val His Thr Leu Gly Asn Leu

20 25 30
Phe Thr Asn Met Ser Leu Gly Lys Val Ser Val Ser Phe Thr His Thr

35 40 45

Ile Lys Ala Met Glu Pro Phe Phe Ser Val Leu Leu Ser Ala Met Phe

50 55 60

Leu Gly Glu Lys Pro Thr Pro Trp Val Leu Gly Ala Ile Val Pro Ile
65 70 75 80

Val Gly Gly Val Ala Leu Ala Ser Ile Ser Glu Val Ser Phe Asn Trp

85 90 95

Ala Gly Phe Ser Ser Ala Met Ala Ser Asn Leu Thr Asn Gln Ser Arg

Asn Val Leu Ser Lys Lys Val Met Val Lys 115 120

- (2) INFORMATION FOR SEQ ID NO:635:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592744
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met Ser Leu Gly Lys Val Ser Val Ser Phe Thr His Thr Ile Lys Ala 1 10 15

Met Glu Pro Phe Phe Ser Val Leu Leu Ser Ala Met Phe Leu Gly Glu 20 25 30

Lys Pro Thr Pro Trp Val Leu Gly Ala Ile Val Pro Ile Val Gly Gly

(ix) FEATURE:

(A) NAME/KEY: peptide(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1592761

45 40 Val Ala Leu Ala Ser Ile Ser Glu Val Ser Phe Asn Trp Ala Gly Phe 55 60 Ser Ser Ala Met Ala Ser Asn Leu Thr Asn Gln Ser Arg Asn Val Leu 75 70 Ser Lys Lys Val Met Val Lys 85 (2) INFORMATION FOR SEQ ID NO:636: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1592745 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:636: Met Glu Pro Phe Phe Ser Val Leu Leu Ser Ala Met Phe Leu Gly Glu 10 Lys Pro Thr Pro Trp Val Leu Gly Ala Ile Val Pro Ile Val Gly Gly 25 20 Val Ala Leu Ala Ser Ile Ser Glu Val Ser Phe Asn Trp Ala Gly Phe 40 4.5 35 Ser Ser Ala Met Ala Ser Asn Leu Thr Asn Gln Ser Arg Asn Val Leu 5.5 Ser Lys Lys Val Met Val Lys 70 (2) INFORMATION FOR SEQ ID NO:637: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 524 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..524 (D) OTHER INFORMATION: / Ceres Seq. ID 1592760 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637: acttetteat egeegtetge acaaaaceet aateteacaa teteetaega gateeateag 60 120 tctccacgaa aatgaaggtt gttgccgcat acttctcgct gttttgagcg gaaaagcttc 180 accaaccagt gccgatatca agactatcct tggatcagtt ggtgctgaga cagaggattc tcaqattgag cttttgttga aggaagtgaa aggaaaagat ttggctgagt tgattgctgc 240 300 tggaagggag aagttagctt cagtgccgtc tggtggcgga ggtggtgttg cggttgcttc tgctacatct ggaggtggag gaggtggtgg tgctcctgct gctgagtcca agaaagaaga 360 gaagaaggaa gaaaaggaag aatccgatga tgacatgggt ttcagtctat tcgagtaagc 420 tggtagtagc atgaaaagtc cggttttgtt gtcctctttt aatattgtaa ccttttgaag 480 gtagtatcat actgtgcaag gcaggtgggt caacctggta tgat (2) INFORMATION FOR SEQ ID NO:638: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638: Leu Leu His Arg Arg Leu His Lys Thr Leu Ile Ser Gln Ser Pro Thr 10 Arg Ser Ile Ser Leu His Glu Asn Glu Gly Cys Cys Arg Ile Leu Leu Ala Val Leu Ser Gly Lys Ala Ser Pro Thr Ser Ala Asp Ile Lys Thr 40 Ile Leu Gly Ser Val Gly Ala Glu Thr Glu Asp Ser Gln Ile Glu Leu Leu Leu Lys Glu Val Lys Gly Lys Asp Leu Ala Glu Leu Ile Ala Ala 70 75 Gly Arg Glu Lys Leu Ala Ser Val Pro Ser Gly Gly Gly Gly Val 85 Ala Val Ala Ser Ala Thr Ser Gly Gly Gly Gly Gly Gly Ala Pro 105 100 Ala Ala Glu Ser Lys Lys Glu Glu Lys Lys Glu Glu Lys Glu Glu Ser 120 125 115 Asp Asp Asp Met Gly Phe Ser Leu Phe Glu 135 130

- (2) INFORMATION FOR SEQ ID NO:639:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..495
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:639: gtgccgcgtc gaaatatgag aaacgaatga tttgatcatc aatcaacgag aaacacacac 60 ggagaaagag aatctcaaat tagctccagc tcctgatcga ttccgatttt cacaattctt 120 180 teettggate tgetettace ttgtcacgat ttcactteee tgtgtttttt atttataett ggtcatccaa taacgaaact ttgatcaaac tggaactaca gtttattgga actccctgaa 240 300 gcatttagat ggcagaaaaa gcttgtataa agcgtcttca aaaagaatac agagcgcttt gcaaggaacc agtctcgcat gttgttgctc gtccttcccc aaatgacatt cttgaatggc 360 attatgtgtt ggaaggcagt gagggaacgc cttttgcagg tggattttac tatggaaaga 420 tcaagttccc tccagaatat ccttacaagc cacctggaat cacaatgacc acaccaaatg 480 gtcgatttgt gacgc
- (2) INFORMATION FOR SEQ ID NO:640:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592790
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:
- Met Ala Glu Lys Ala Cys Ile Lys Arg Leu Gln Lys Glu Tyr Arg Ala 10
- Leu Cys Lys Glu Pro Val Ser His Val Val Ala Arg Pro Ser Pro Asn 25
- Asp Ile Leu Glu Trp His Tyr Val Leu Glu Gly Ser Glu Gly Thr Pro 40 Phe Ala Gly Gly Phe Tyr Tyr Gly Lys Ile Lys Phe Pro Pro Glu Tyr
- 55 Pro Tyr Lys Pro Pro Gly Ile Thr Met Thr Thr Pro Asn Gly Arg Phe

80 70 75 65 Val Thr (2) INFORMATION FOR SEQ ID NO:641: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..49 (D) OTHER INFORMATION: / Ceres Seq. ID 1592791 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:641: Met Leu Leu Val Leu Pro Gln Met Thr Phe Leu Asn Gly Ile Met 10 Cys Trp Lys Ala Val Arg Glu Arg Leu Leu Gln Val Asp Phe Thr Met 20 25 Glu Arg Ser Ser Ser Leu Gln Asn Ile Leu Thr Ser His Leu Glu Ser 4 0 Gln (2) INFORMATION FOR SEQ ID NO:642: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..41 (D) OTHER INFORMATION: / Ceres Seq. ID 1592792 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:642: Met Thr Phe Leu Asn Gly Ile Met Cys Trp Lys Ala Val Arg Glu Arg 10 Leu Leu Gln Val Asp Phe Thr Met Glu Arg Ser Ser Ser Leu Gln Asn 25 20 Ile Leu Thr Ser His Leu Glu Ser Gln 35 (2) INFORMATION FOR SEQ ID NO:643: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 511 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..511 (D) OTHER INFORMATION: / Ceres Seq. ID 1592801 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643: aggcatcttt taggtcatat caatacaaaa tacacatata dvatattttt caacacctga 60 ggtgcgcgaa gacagacabt tksttcatcc tdctccgtaa ttctcaaaat tagggttttd 120 vttccggcag ytctctcagt tgtactgcaa gcattctttt stagatattt aagatgtcaa 180 ggacgaggac tgctgcttct gaggctcatg actccatgga atctgaggaa agggtagacc 240 ttgatggtga caatgateet gaggagatte tggaggagga agttgaatae gaagaagttg 300 aagaggagga ggagattgaa gagatagaag aggagataga ggaggaggtt gaagtggaag aagaggagga ggaggaggat gctgttgcaa cggaagagga agaagaaaag aaaaggcatg 420 ttgaacttct tgcacttcct ccacatggtt cagaggttta nttggaggga ttcctactga

Client Docket No. 80146.003 tgctactgaa ggggacttaa agggcttctg t (2) INFORMATION FOR SEQ ID NO:644: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..108 (D) OTHER INFORMATION: / Ceres Seq. ID 1592802 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644: Met Ser Arg Thr Arg Thr Ala Ala Ser Glu Ala His Asp Ser Met Glu 10 Ser Glu Glu Arg Val Asp Leu Asp Gly Asp Asn Asp Pro Glu Glu Ile 25 20 Leu Glu Glu Glu Val Glu Tyr Glu Glu Val Glu Glu Glu Glu Ile 40 Glu Glu Ile Glu Glu Glu Ile Glu Glu Glu Val Glu Val Glu Glu Glu 60 55 Glu Glu Glu Glu Asp Ala Val Ala Thr Glu Glu Glu Glu Lys Lys 70 75 Arg His Val Glu Leu Leu Ala Leu Pro Pro His Gly Ser Glu Val Xaa 90 85 Leu Glu Gly Phe Leu Leu Met Leu Leu Lys Gly Thr 100 105 (2) INFORMATION FOR SEQ ID NO:645: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..94 (D) OTHER INFORMATION: / Ceres Seq. ID 1592803 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645: Met Glu Ser Glu Glu Arg Val Asp Leu Asp Gly Asp Asn Asp Pro Glu 10 5 Glu Ile Leu Glu Glu Glu Val Glu Tyr Glu Glu Val Glu Glu Glu 25 Glu Ile Glu Glu Ile Glu Glu Glu Ile Glu Glu Val Glu Val Glu 45 40 Glu Glu Glu Glu Glu Asp Ala Val Ala Thr Glu Glu Glu Glu 55 60 Lys Lys Arg His Val Glu Leu Leu Ala Leu Pro Pro His Gly Ser Glu 75 70 Val Xaa Leu Glu Gly Phe Leu Leu Met Leu Leu Lys Gly Thr 90 85 (2) INFORMATION FOR SEQ ID NO:646: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 491 base pairs (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..491

120 180

240 300

360

420

480

(D) OTHER INFORMATION: / Ceres Seq. ID 1592822 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646: aaaacacaaa acttgatctc acgactccat cttctaaaat tcagaatctt tctttgaaac ttttttcgtg tgaagaaaat ggcaccaaag gcagagaaga agccggcaga gaagaaacca gtggaagaga aatcaaaagc cgagaaagct ccggcggaga agaaaccaaa agccggcaag aaactcccga agaagccggt gccggcgcga taagaagaag aagatgaaga agaagagtgt tgagacqtac aagatctaca ctcttcttct tcatcatctc atttctcacc tgcctccgcc gtcatggctt ccgagaaaga agctgctctc gccgccactc cttccgattc tcccaccata tttgacaaga tcatcagcaa agagattcca tccaccgtgg tttttgagga tgacaaggtc ttagctttta gggacataac gccccagggt cctgttcaca tcctccttat tccaaaagtg agggatggcc t (2) INFORMATION FOR SEQ ID NO:647: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..74 (D) OTHER INFORMATION: / Ceres Seq. ID 1592823 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647: Asn Thr Lys Leu Asp Leu Thr Thr Pro Ser Ser Lys Ile Gln Asn Leu 5 10 Ser Leu Lys Leu Phe Ser Cys Glu Glu Asn Gly Thr Lys Gly Arg Glu 25 2.0 Glu Ala Gly Arg Glu Glu Thr Ser Gly Arg Glu Ile Lys Ser Arg Glu 40 35 Ser Ser Gly Gly Glu Glu Thr Lys Ser Arg Gln Glu Thr Pro Glu Glu 55 Ala Gly Ala Gly Ala Ile Arg Arg Arg 70 (2) INFORMATION FOR SEQ ID NO:648: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..66 (D) OTHER INFORMATION: / Ceres Seq. ID 1592824 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:648: Met Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr Thr Leu Leu Leu 10 His His Leu Ile Ser His Leu Pro Pro Pro Ser Trp Leu Pro Arg Lys 25 30 Lys Leu Leu Ser Pro Pro Leu Leu Pro Ile Leu Pro Pro Tyr Leu Thr 40 4.5 Arg Ser Ser Ala Lys Arg Phe His Pro Pro Trp Phe Leu Arg Met Thr 50 Arg Ser

- (2) INFORMATION FOR SEQ ID NO:649:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

Met Ala Ser Glu Lys Glu Ala Ala Leu Ala Ala Thr Pro Ser Asp Ser 1 10 15

Pro Thr Ile Phe Asp Lys Ile Ile Ser Lys Glu Ile Pro Ser Thr Val 20 25 30

Val Phe Glu Asp Asp Lys Val Leu Ala Phe Arg Asp Ile Thr Pro Gln 35 40 45

Gly Pro Val His Ile Leu Leu Ile Pro Lys Val Arg Asp Gly 50 60

- (2) INFORMATION FOR SEQ ID NO:650:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592832
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650: aaaaccatca ctccttttgc attgtgtgaa accttcgagt tttctcttca tcttctcaaa 60 gtaacaaact ttctccaaac agattattat taaaacaatc tcatcaagaa ctacgatgaa 120 attcccggct gtaaaagttc ttattatctc tcttctcatc acatcttctt tgttcatact 180 ctcaaccgcg gattcgtcac catgcggagg aaaatgcaac gtgagatgtt caaaggcagg 240 aagacaagat aggtgtctca agtattgtaa tatatgttgc gagaagtgta actattgtgt 300 teetteagge acttatggaa acaaagatga atgeeettgt taeegegata tgaagaacte 360 caaaggcacg tccaaatgtc cttgatcatg ttcttaagat tatccttata gacacaatat 420 480 cttgaaatgt taagattgtg cttgatgcca gagtgaagga aggattggga actaggcgtg attgg
- (2) INFORMATION FOR SEQ ID NO:651:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592833
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

Met Lys Phe Pro Ala Val Lys Val Leu Ile Ile Ser Leu Leu Ile Thr

Ser Ser Leu Phe Ile Leu Ser Thr Ala Asp Ser Ser Pro Cys Gly Gly 20 25 30

Lys Cys Asn Val Arg Cys Ser Lys Ala Gly Arg Gln Asp Arg Cys Leu 35 40 45

Lys Tyr Cys Asn Ile Cys Cys Glu Lys Cys Asn Tyr Cys Val Pro Ser 50 60

Gly Thr Tyr Gly Asn Lys Asp Glu Cys Pro Cys Tyr Arg Asp Met Lys 65 70 75 80

Asn Ser Lys Gly Thr Ser Lys Cys Pro

- (2) INFORMATION FOR SEQ ID NO:652:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..450
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592838
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

 acttcgttaa cggccccgcc tccactctat cctaccgccg acgtccgtga tcgccgaaat 60

 gactgaagca gagtccaaga ctgttgttcc tgagtcagtg ttgaagaaga gaaagaggga 120

 ggaagagtggaat ctcatattta accgggctaa acagtactcc aaggagtacc aggagaaaga 240

 aagggaatta atccagctga agcgtgaggc aaaattgaaa ggaggctttt atgttgaccc aggagactaaa ctgctttca ttatccgtat ccgtggtatc aatgccattg acccaaagac 360

 aaagaagatt ttgcaacttt tgcgtttaag acagatttc aatgaaacag catgtcctgt 420
- gaactttgag tttatgaact acacgatcat
 (2) INFORMATION FOR SEQ ID NO:653:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592839 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:
- Met
 Thr
 Glu
 Ala
 Glu
 Ser
 Lys
 Thr
 Val
 Val
 Pro
 Glu
 Ser
 Val
 Lys
 Leu
 Lys
 Glu
 Ser
 Lys
 15
 Lys
 15
 Lys
 Lys
 15
 Lys
 Lys
 15
 Lys
 Lys
 Glu
 Lys
 Lys
 Glu
 Leu
 Lys
 Lys
 Lys
 Glu
 Leu
 Leu
 Ala
 Lys
 Lys
 Leu
 He
 Asn
 Asn
 Ala
 Glu
 Lys
 Glu
 Lys
 Glu
 Lys
 Glu
 Lys
 Lys
 Glu
 Arg
 Glu
 Lys
 Lys
 Glu
 Lys
 Lys
 Glu
 Lys
 Lys</t

Ile Gln Leu Lys Arg Glu Ala Lys Leu Lys Gly Gly Phe Tyr Val Asp
65 70 75 80

Pro Glu Ala Lys Leu Leu Phe Ile Ile Arg Ile Arg Gly Ile Asn Ala 85 90 95

Ile Asp Pro Lys Thr Lys Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln 100 105 110

Ile Phe Asn Glu Thr Ala Cys Pro Val Asn Phe Glu Phe Met Asn Tyr 115 120 125

Thr Ile

- (2) INFORMATION FOR SEQ ID NO:654:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..490
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592844
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654: agactttagt ttttttcaca gttgagaaat ctcgccgccg tttgaagaaa gaagaagaga

tgggagtttt ctcattcgtg tgcaaaagca aaggcggaga atggaccgca aagcaacacg 120 aaggagatct tgaagcttca gcttctcca cctacgatct ccagcgcaas ttgtttcaga 180 ctgctctctc cgccgattca tctggcggcg ttcagtcttc tttctctctt gtctctccta 240 cctccgcgt cttcgtggtg gtcattggtg gtggtggtgg tggaggattt gctgccggag 300 aggtgcagct gctggaggtg gtggtggtgg tgaggctgcc gcagccacaa aggaggaaga 360 gaagaagaaga gaagaatctg aagaggaaga gggagacttt ggatttgatc tctttggtta 420 aggaggctac

- (2) INFORMATION FOR SEQ ID NO:655:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..149
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592845
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:655: Thr Leu Val Phe Phe Thr Val Glu Lys Ser Arg Arg Leu Lys Lys

1 5 10 15 Glu Glu Glu Met Gly Val Phe Ser Phe Val Cys Lys Ser Lys Gly Gly 20 25 30

Glu Trp Thr Ala Lys Gln His Glu Gly Asp Leu Glu Ala Ser Ala Ser 35 40 45

Ser Thr Tyr Asp Leu Gln Arg Xaa Leu Phe Gln Thr Ala Leu Ser Ala 50 55 60

Asp Ser Ser Gly Gly Val Gln Ser Ser Phe Ser Leu Val Ser Pro Thr

65 70 75 80 Ser Ala Val Phe Val Val Val Ile Gly Gly Gly Gly Gly Gly Phe

85 90 95
Ala Ala Gly Glu Val Gln Leu Leu Glu Val Val Val Val Val Arg Leu
100 105 110

Pro Gln Pro Gln Arg Arg Lys Arg Arg Arg Arg Lys Asn Leu Lys Arg

Lys Arg Glu Thr Leu Asp Leu Ile Ser Leu Val Lys Arg Pro Lys Thr 130 135 140

Thr Leu Leu Val Phe

145

- (2) INFORMATION FOR SEQ ID NO:656:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

Met Gly Val Phe Ser Phe Val Cys Lys Ser Lys Gly Gly Glu Trp Thr 1 5 10 15

Ala Lys Gln His Glu Gly Asp Leu Glu Ala Ser Ala Ser Ser Thr Tyr
20 25 30

Asp Leu Gln Arg Xaa Leu Phe Gln Thr Ala Leu Ser Ala Asp Ser Ser 35 40 45

Gly Gly Val Gln Ser Ser Phe Ser Leu Val Ser Pro Thr Ser Ala Val 50 55 60

Phe Val Val Val Ile Gly Gly Gly Gly Gly Gly Phe Ala Ala Gly

Page 391 Client Docket No. 80146.003 65 70 7.5 Glu Val Gln Leu Leu Glu Val Val Val Val Arg Leu Pro Gln Pro 90 Gln Arg Arg Lys Arg Arg Arg Lys Asn Leu Lys Arg Lys Arg Glu 105 100 Thr Leu Asp Leu Ile Ser Leu Val Lys Arg Pro Lys Thr Thr Leu Leu 115 120 Val Phe 130 (2) INFORMATION FOR SEQ ID NO:657: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..437 (D) OTHER INFORMATION: / Ceres Seq. ID 1592855 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:657: acttctctct cttaggtttt ttttcccttc tcccaatctc atcttctccg aaaacctttc ttctctcaaa tttctgtgaa aacatgtctg acgacgagca ccactttgag gccagcgaat ccggagcttc caagacctat cctcaatcag ccggtaacat ccgtaaaggt ggtcacatcg tcatcaaaaa ccgtccctgc aagttgttga ggtttcgact tccaaaactg gcaagcacgg tcacgccaaa tgtcactttg ttgctattga tatcttcact gctaagaagc ttgaagatat 300 tgttccatct tcccacaatt gtgatgttcc acatgtgaac cgtgttgatt acsagttgat tgatatcact gaggatggct tcgtgagcct tctcactgac agtggtggca ccaaggatgt 420 taccggctga tttgagg (2) INFORMATION FOR SEQ ID NO:658: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..111 (D) OTHER INFORMATION: / Ceres Seq. ID 1592856 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658: Phe Ser Leu Leu Gly Phe Phe Ser Leu Leu Pro Ile Ser Ser Pro 10 Lys Thr Phe Leu Leu Ser Asn Phe Cys Glu Asn Met Ser Asp Asp Glu 25 His His Phe Glu Ala Ser Glu Ser Gly Ala Ser Lys Thr Tyr Pro Gln 40 Ser Ala Gly Asn Ile Arg Lys Gly Gly His Ile Val Ile Lys Asn Arg Pro Cys Lys Leu Leu Arg Phe Arg Leu Pro Lys Leu Ala Ser Thr Val 70 Thr Pro Asn Val Thr Leu Leu Leu Leu Ile Ser Ser Leu Leu Arg Ser 90 8.5

(2) INFORMATION FOR SEQ ID NO:659:

100

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids

Leu Lys Ile Leu Phe His Leu Pro Thr Ile Val Met Phe His Met

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..84 (D) OTHER INFORMATION: / Ceres Seq. ID 1592857 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:659: Met Ser Asp Asp Glu His His Phe Glu Ala Ser Glu Ser Gly Ala Ser 5 10 Lys Thr Tyr Pro Gln Ser Ala Gly Asn Ile Arg Lys Gly Gly His Ile 25 20 Val Ile Lys Asn Arg Pro Cys Lys Leu Leu Arg Phe Arg Leu Pro Lys 40 Leu Ala Ser Thr Val Thr Pro Asn Val Thr Leu Leu Leu Leu Ile Ser 55 60 Ser Leu Leu Arg Ser Leu Lys Ile Leu Phe His Leu Pro Thr Ile Val 70 Met Phe His Met (2) INFORMATION FOR SEQ ID NO:660: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 490 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..490 (D) OTHER INFORMATION: / Ceres Seq. ID 1592862 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:660: aaacattgtc ttttcgggtt aatttcttct tcttcttcct tttcttacta aattctctta 60 gggttttagt catatttaat ggcttccaat tcggagaaaa atcctcttct ttcagatgag 120 aaacccaaat cgacggagga gaataagagt tctaagccgg aatcagcttc tgggagttca 180 actteateag ctatgeetgg ettgaattte aatgettttg atttetetaa tatggetagt 240 atteteaacq atcetageat cagagaaatq tetgageaaa tagetaaaga teetgeettt 300 aaccaattgg ctgagcagct tcagagatct attcctaacg ctggccagga aggtggtttc 360 cctaactttq atcctcaaca qtatqtcaac acaatqcaac aqqttatqca taaccctqag 420 tttaagacaa tggccgagaa acttggtacc gccttagttc aggatccaca aatgtctcct 480 tttttqqatq (2) INFORMATION FOR SEQ ID NO:661: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..137 (D) OTHER INFORMATION: / Ceres Seq. ID 1592863 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:661: Met Ala Ser Asn Ser Glu Lys Asn Pro Leu Leu Ser Asp Glu Lys Pro 10 Lys Ser Thr Glu Glu Asn Lys Ser Ser Lys Pro Glu Ser Ala Ser Gly 25 20 Ser Ser Thr Ser Ser Ala Met Pro Gly Leu Asn Phe Asn Ala Phe Asp

35 40 45 Phe Ser Asn Met Ala Ser Ile Leu Asn Asp Pro Ser Ile Arg Glu Met

Ser Glu Gln Ile Ala Lys Asp Pro Ala Phe Asn Gln Leu Ala Glu Gln

75

Leu Gln Arg Ser Ile Pro Asn Ala Gly Gln Glu Gly Gly Phe Pro Asn 85 90 95

Phe Asp Pro Gln Gln Tyr Val Asn Thr Met Gln Gln Val Met His Asn 100 105 110

Pro Glu Phe Lys Thr Met Ala Glu Lys Leu Gly Thr Ala Leu Val Gln 115 120 125

Asp Pro Gln Met Ser Pro Phe Leu Asp 130 135

- (2) INFORMATION FOR SEQ ID NO:662:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592864
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met Pro Gly Leu Asn Phe Asn Ala Phe Asp Phe Ser Asn Met Ala Ser 1 5 10 15

Ile Leu Asn Asp Pro Ser Ile Arg Glu Met Ser Glu Gln Ile Ala Lys
20 25 30

Asp Pro Ala Phe Asn Gln Leu Ala Glu Gln Leu Gln Arg Ser Ile Pro 35 40 45

Asn Ala Gly Gln Glu Gly Gly Phe Pro Asn Phe Asp Pro Gln Gln Tyr 50 55 60

Val Asn Thr Met Gln Gln Val Met His Asn Pro Glu Phe Lys Thr Met 65 70 75 80

Ala Glu Lys Leu Gly Thr Ala Leu Val Gln Asp Pro Gln Met Ser Pro

Phe Leu Asp

- (2) INFORMATION FOR SEQ ID NO:663:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met Ala Ser Ile Leu Asn Asp Pro Ser Ile Arg Glu Met Ser Glu Gln
1 5 10 15

Ile Ala Lys Asp Pro Ala Phe Asn Gln Leu Ala Glu Gln Leu Gln Arg

Ser Ile Pro Asn Ala Gly Gln Glu Gly Gly Phe Pro Asn Phe Asp Pro 35 40 45

Gln Gln Tyr Val Asn Thr Met Gln Gln Val Met His Asn Pro Glu Phe 50 55 60

Lys Thr Met Ala Glu Lys Leu Gly Thr Ala Leu Val Gln Asp Pro Gln 65 70 75 80

Met Ser Pro Phe Leu Asp

- (2) INFORMATION FOR SEQ ID NO:664:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..414
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592866
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

 accaacaca catetetee tatetatga agcattagga aactttgatt acgaaageta 60

 caccaatttt acaaaattge catecteeca atggggtgat cagtteetea agttteeat 120

 tgetgatteg gattttgatg teettgaaag agagattgaa gtaetaaage etaaagtaag 180

 agagaacata ttegtgtegt ettecacaga caaagaegeg atgaaaaaga eaattette 240

 tatteatttt etggacagte ttggtetet ettateatttt gagaaggaaa tegaaggag 300

 cetaaaacat gstttegaga agatagaaga tttgateget gatgaaaata aaattgeaca 360

 caatstseas satetteega gtttteagga cataeggkta etacatgete tegg
- (2) INFORMATION FOR SEQ ID NO:665:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592867
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:
- Pro Thr Pro His Leu Ser Leu Ser Met Glu Ala Leu Gly Asn Phe Asp 1 5 10 15
- Tyr Glu Ser Tyr Thr Asn Phe Thr Lys Leu Pro Ser Ser Gln Trp Gly 20 25 30
- Asp Gln Phe Leu Lys Phe Ser Ile Ala Asp Ser Asp Phe Asp Val Leu 35 40 45
- Glu Arg Glu Ile Glu Val Leu Lys Pro Lys Val Arg Glu Asn Ile Phe 50 55 60
- Val Ser Ser Ser Thr Asp Lys Asp Ala Met Lys Lys Thr Ile Leu Ser 65 70 75 80
- Ile His Phe Leu Asp Ser Leu Gly Leu Ser Tyr His Phe Glu Lys Glu
 85
 90
 95
- Ile Glu Glu Ser Leu Lys His Xaa Phe Glu Lys Ile Glu Asp Leu Ile 100 105 110
- Ala Asp Glu Asn Lys Ile Ala His Asn Xaa Xaa Xaa Leu Pro Ser Phe 115 120 125
- Gln Asp Ile Arg Xaa Leu His Val Phe 130 135
- (2) INFORMATION FOR SEQ ID NO:666:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592868
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:
- Met Glu Ala Leu Gly Asn Phe Asp Tyr Glu Ser Tyr Thr Asn Phe Thr 1 5 10 15

 Lys Leu Pro Ser Ser Gln Trp Gly Asp Gln Phe Leu Lys Phe Ser Ile

30 25 20 Ala Asp Ser Asp Phe Asp Val Leu Glu Arg Glu Ile Glu Val Leu Lys 45 40 Pro Lys Val Arg Glu Asn Ile Phe Val Ser Ser Ser Thr Asp Lys Asp Ala Met Lys Lys Thr Ile Leu Ser Ile His Phe Leu Asp Ser Leu Gly 75 70 Leu Ser Tyr His Phe Glu Lys Glu Ile Glu Glu Ser Leu Lys His Xaa 90 85 Phe Glu Lys Ile Glu Asp Leu Ile Ala Asp Glu Asn Lys Ile Ala His 100 105 Asn Xaa Xaa Xaa Leu Pro Ser Phe Gln Asp Ile Arg Xaa Leu His Val 125 120 Phe

- (2) INFORMATION FOR SEQ ID NO:667:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..383
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592877
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

 aaaaaagtcc attgtttcaa gcaatactct caagtctaaa gaagaataaa aaaaatggat 60
 gaagaagttg agaacaaagt rttactccat ggatcattcg cgagtcctta cagcaaaagg 120
 attgagttag ccctaaggct taaatccata ccttacmaat tcgtgcaaga rgatctccag 180
 aacaagggcc aaaccctgct ccggtataac ccggttcaca agaagatccc ggttcttgtc 240
 cacaacggta aacccatctc tgaatcactg tttatcattg aatasatcga cgaaacgtgg 300
 agacacggtc cacatattt gccacaagac ccttatagaa gatctaaagt ccggttttrk 360
 gctaactaca tccaattaca tct
- (2) INFORMATION FOR SEQ ID NO:668:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592878
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:
- Met Asp Glu Glu Val Glu Asn Lys Xaa Leu Leu His Gly Ser Phe Ala

 1 5 10 15
- Ser Pro Tyr Ser Lys Arg Ile Glu Leu Ala Leu Arg Leu Lys Ser Ile
 20 25 30
- Pro Tyr Xaa Phe Val Gln Xaa Asp Leu Gln Asn Lys Ser Gln Thr Leu 35 40 45
- Leu Arg Tyr Asn Pro Val His Lys Lys Ile Pro Val Leu Val His Asn
 50 55 60
- Gly Lys Pro Ile Ser Glu Ser Leu Phe Ile Ile Glu Xaa Ile Asp Glu 65 70 75 80
- Thr Trp Arg His Gly Pro His Ile Leu Pro Gln Asp Pro Tyr Arg Arg 85 90 95
- Ser Lys Val Arg Phe Xaa Ala Asn Tyr Ile Gln Leu His
- (2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..514
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592898
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669: atcaacagtt ttaaaaaaag acataactca accaatctca ctttgaaaaa gacatgaaca 60 aaaccegeet tegtgetete teeccacett eeggtatgea acacegtaag agatgtegat 120 tgagaggtcg aaactacgta aggccagaag ttaaacaacg caactictca aaagatgaag 180 acgateteat ecteaagett catgeactte ttggcaatag atggteattg atagegggaa 240 gnttgccagg acgaaccgac aacgaavwta ggatccattg ggaaacttac ctaaaaagga 300 agetegtaaa aatgggaate gacceaacca atcategtet ceaceateae accaactaca 360 tttctagacg tcacctccat tcttcacata aggaacatga aaccaagatt attagtgatc 420 aatcttcttc ggtatccgaa tcatgtggtg taacaatttc gttggtctgg tattggagaa 480 ttgcgaactc ccgtttccga accacgggca cgtt
- (2) INFORMATION FOR SEQ ID NO:670:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592899
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:
- Met Asn Lys Thr Arg Leu Arg Ala Leu Ser Pro Pro Ser Gly Met Gln 10 5
- His Arg Lys Arg Cys Arg Leu Arg Gly Arg Asn Tyr Val Arg Pro Glu 25 30
- Val Lys Gln Arg Asn Phe Ser Lys Asp Glu Asp Asp Leu Ile Leu Lys 4.0
- Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Xaa Leu 60 55
- Pro Gly Arg Thr Asp Asn Glu Xaa Arg Ile His Trp Glu Thr Tyr Leu 75 70
- Lys Arg Lys Leu Val Lys Met Gly Ile Asp Pro Thr Asn His Arg Leu 90 His His His Thr Asn Tyr Ile Ser Arg Arg His Leu His Ser Ser His
- 110 105 100 Lys Glu His Glu Thr Lys Ile Ile Ser Asp Gln Ser Ser Ser Val Ser 125 120
- Glu Ser Cys Gly Val Thr Ile Ser Leu Val Trp Tyr Trp Arg Ile Ala 140 135
- Asn Ser Arg Phe Arg Thr Thr Gly Thr 150 145
- (2) INFORMATION FOR SEQ ID NO:671:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592900
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

 Met Gln His Arg Lys Arg Cys Arg Leu Arg Gly Arg Asn Tyr Val Arg

 1 5 10 15
- Pro Glu Val Lys Gln Arg Asn Phe Ser Lys Asp Glu Asp Asp Leu Ile
 20 25 30
- Leu Lys Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly
 35 40 45
- Xaa Leu Pro Gly Arg Thr Asp Asn Glu Xaa Arg Ile His Trp Glu Thr 50 55 60
- Tyr Leu Lys Arg Lys Leu Val Lys Met Gly Ile Asp Pro Thr Asn His 65 70 75 80
- Arg Leu His His His Thr Asn Tyr Ile Ser Arg Arg His Leu His Ser 85 90 95
- Ser His Lys Glu His Glu Thr Lys Ile Ile Ser Asp Gln Ser Ser Ser 100 105 110
- Val Ser Glu Ser Cys Gly Val Thr Ile Ser Leu Val Trp Tyr Trp Arg 115 120 125
- Ile Ala Asn Ser Arg Phe Arg Thr Thr Gly Thr 130
- (2) INFORMATION FOR SEQ ID NO:672:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..498
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592920
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672: gctttcaaaa tctcattcta tcactttgtg ccttttttag ccatcgcgaa aaacctctga 60 atcgcatccc ttgattttct gggtttgtga ctttgtgtag tggaaattag gcttgttgtt 120 tgatttcgct acgagaaaat ggacaagtac gagcttgtta aagacatcgg tgctgggaat 180 tttggagtgg cgaggctcat gagagtcaaa aactccaagg aacttgttgc tatgaagtac 240 atcgagcgtg gccctaagat tgatgagaac gtggcgagag agattattaa ccacagatca tttcgtcatc ccaatattat ccgctttaag gaggtggttt tgacaccaac gcacatcgcc 360 attgctatgg aatatgctgc tggtggtgag ctatttgagc gtatatgtag cgctggaaga 420 ttcagtgagg atgaggcaag atactttttc cagcagctta tctcaggagt cagctattgc 480 catgctatgc aaaatatg
- (2) INFORMATION FOR SEQ ID NO:673:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592921
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:
- Met Asp Lys Tyr Glu Leu Val Lys Asp Ile Gly Ala Gly Asn Phe Gly
 1 5 10 15
- Val Ala Arg Leu Met Arg Val Lys Asn Ser Lys Glu Leu Val Ala Met 20 25 30
- Lys Tyr Ile Glu Arg Gly Pro Lys Ile Asp Glu Asn Val Ala Arg Glu 35 40 45
- Ile Ile Asn His Arg Ser Phe Arg His Pro Asn Ile Ile Arg Phe Lys

50 55 Glu Val Val Leu Thr Pro Thr His Ile Ala Ile Ala Met Glu Tyr Ala 75 70 Ala Gly Glu Leu Phe Glu Arg Ile Cys Ser Ala Gly Arg Phe Ser 85 90 Glu Asp Glu Ala Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly Val Ser 100 105 110 Tyr Cys His Ala Met Gln Asn Met 115 (2) INFORMATION FOR SEQ ID NO:674: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..100 (D) OTHER INFORMATION: / Ceres Seq. ID 1592922 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674: Met Arg Val Lys Asn Ser Lys Glu Leu Val Ala Met Lys Tyr Ile Glu 10 Arg Gly Pro Lys Ile Asp Glu Asn Val Ala Arg Glu Ile Ile Asn His 25 20 Arg Ser Phe Arg His Pro Asn Ile Ile Arg Phe Lys Glu Val Val Leu 4.0 Thr Pro Thr His Ile Ala Ile Ala Met Glu Tyr Ala Ala Gly Gly Glu 55 60 Leu Phe Glu Arg Ile Cys Ser Ala Gly Arg Phe Ser Glu Asp Glu Ala 75 70 Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly Val Ser Tyr Cys His Ala 90 Met Gln Asn Met 100 (2) INFORMATION FOR SEQ ID NO:675: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..89 (D) OTHER INFORMATION: / Ceres Seq. ID 1592923 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675: Met Lys Tyr Ile Glu Arg Gly Pro Lys Ile Asp Glu Asn Val Ala Arg 10 Glu Ile Ile Asn His Arg Ser Phe Arg His Pro Asn Ile Ile Arg Phe 25 Lys Glu Val Val Leu Thr Pro Thr His Ile Ala Ile Ala Met Glu Tyr 40 Ala Ala Gly Gly Glu Leu Phe Glu Arg Ile Cys Ser Ala Gly Arg Phe 55 60 Ser Glu Asp Glu Ala Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly Val 75 70 Ser Tyr Cys His Ala Met Gln Asn Met 8.5

(2) INFORMATION FOR SEQ ID NO:676: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..482
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592924
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676: ataaaccata ttaagaacta gcttatagat aaggatatgg cctttacgaa cgtttgccta 60 tggacgctac tcgccttcat gctgacttgg acagtgttct acgtcacaaa cagggggaag 120 aaggcgacgc agttggcgga tgcggtggtt gaagagcgag aagacggtgc tactgacgtt 180 atcatcgttg gggctggagt aggcggctcg gctctcgcat atgctcttgc taaggacggg 240 cgtcgagtcc atgtaataga gagggacctg agagaaccag agagaatcat gggtgagttt 300 atgcaaccag gaggacgact catgctctct aagcttggtc ttgaagattg tttggaggga 360 atagatgccc aaaaagccac gggcatgaca gtttataagg acggaaaaga agcagtcgca 420 tetttteceg tggacaacaa caatttteet tatgateett eggetegate titteacaat 480
- (2) INFORMATION FOR SEQ ID NO:677:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592925
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:
- Met Ala Phe Thr Asn Val Cys Leu Trp Thr Leu Leu Ala Phe Met Leu 1 5 15 15
- Thr Trp Thr Val Phe Tyr Val Thr Asn Arg Gly Lys Lys Ala Thr Gln 20 25 30
- Leu Ala Asp Ala Val Val Glu Glu Arg Glu Asp Gly Ala Thr Asp Val 35 40
- Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ala Leu 50 55 60
- Ala Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Leu Arg Glu 65 70 75 80
- Pro Glu Arg Ile Met Gly Glu Phe Met Gln Pro Gly Gly Arg Leu Met 85 85 90 95 Leu Ser Lys Leu Gly Leu Glu Asp Cys Leu Glu Gly Ile Asp Ala Gln
- 100 105 110 Lys Ala Thr Gly Met Thr Val Tyr Lys Asp Gly Lys Glu Ala Val Ala
- 115 120 125
 Ser Phe Pro Val Asp Asn Asn Phe Pro Tyr Asp Pro Ser Ala Arg
 130 135 140
- Ser Phe His Asn
- 145
- (2) INFORMATION FOR SEQ ID NO:678:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134

```
(D) OTHER INFORMATION: / Ceres Seq. ID 1592926
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:
Met Leu Thr Trp Thr Val Phe Tyr Val Thr Asn Arg Gly Lys Lys Ala
                                    10
Thr Gln Leu Ala Asp Ala Val Val Glu Glu Arg Glu Asp Gly Ala Thr
          20
                                25
Asp Val Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr
                            40
Ala Leu Ala Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Leu
                        55
                                            60
Arg Glu Pro Glu Arg Ile Met Gly Glu Phe Met Gln Pro Gly Gly Arg
                                        75
                    70
Leu Met Leu Ser Lys Leu Gly Leu Glu Asp Cys Leu Glu Gly Ile Asp
                                    90
                8.5
Ala Gln Lys Ala Thr Gly Met Thr Val Tyr Lys Asp Gly Lys Glu Ala
                             105
                                                    110
Val Ala Ser Phe Pro Val Asp Asn Asn Phe Pro Tyr Asp Pro Ser
                                                125
                            120
        115
Ala Arg Ser Phe His Asn
    130
(2) INFORMATION FOR SEQ ID NO:679:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 499 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..499
           (D) OTHER INFORMATION: / Ceres Seq. ID 1592932
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:
attaaattat gtgcatatgt aaaatgattg ttggttataa tactaaataa taaagtttat
                                                                        60
aacaatattt tacaaatttg gaagttgcaa ctataaatgg taaattcggt ccttaagatt
                                                                       120
agaagacaaa gaagagtogt gttggtgago taactaccca acctgtgaag ctacccccat
                                                                       180
tctctctcaa cgttttcgtt ttgaaatggc gaggaagaag atcagagagt atgactcaaa
                                                                       240
gaggttggtg aaggaacatt tcaaaaggct ttctggcaaa gagcttccta tcagatccgt
                                                                       300
teagattaat gaaacaactg atctaaatga gctagttgaa aaggaacctt ggctctcgtc
                                                                       360
 tgagaagctg gtggtgaaac ctgacatgtt gtttggaaag cgtggcaaga gtggtttggt
                                                                       420
 tgccttgaaa ttagattttg ctgatgttgc cacttttgtt aaagaacgtt tgggaaaaga
                                                                       480
 ggtagagatg agtggatgc
 (2) INFORMATION FOR SEQ ID NO:680:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 98 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..98
           (D) OTHER INFORMATION: / Ceres Seq. ID 1592933
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:
 Met Ala Arg Lys Lys Ile Arg Glu Tyr Asp Ser Lys Arg Leu Val Lys
                                     10
                 5
 Glu His Phe Lys Arg Leu Ser Gly Lys Glu Leu Pro Ile Arg Ser Val
                                  25
             20
 Gln Ile Asn Glu Thr Thr Asp Leu Asn Glu Leu Val Glu Lys Glu Pro
                                                  45
 Trp Leu Ser Ser Glu Lys Leu Val Val Lys Pro Asp Met Leu Phe Gly
                                              60
                          55
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Lys Arg Gly Lys Ser Gly Leu Val Ala Leu Lys Leu Asp Phe Ala Asp 65 70 70 75 80

Val Ala Thr Phe Val Lys Glu Arg Leu Gly Lys Glu Val Glu Met Ser 85 90 95

Gly Cys
```

- (2) INFORMATION FOR SEQ ID NO:681:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..467
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592963
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

aaaattgaaa ttcgaaaaca gaacaaaaaa aaaaatctct ctcaatctct ctcagatctg aatccatcca tcaccgatct ctaatggcgg caccaccagc atcatcctcg gcgagggaag 120 agttcgtgta cctcgcaaag ctcgcagasa agcggaacgt tacgaagaaa tggttgaatt 180 catggaaaaa gtcgctgaag ccgttgacaa agacgaactc accgtcgaag aacgtaatct 240 cctctccgtc gcttacaaaa acgtaatcgg tgctcgtcgt gcttcctgga gaatcatctc 300 ttccattgaa caaaaagaag agagtcgtgg taacgatgac catgtgacca cgatccgtga 360 ttacagaagc aagatcgaat ctgagttatc gaaaatctgt gacggtattc ttaagcttct 420 tgatactaga cttgttcctg cttctgctaa tggagattct aaggttt

- (2) INFORMATION FOR SEQ ID NO:682:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592964
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

Met Ala Ala Pro Pro Ala Ser Ser Ser Ala Arg Glu Glu Phe Val Tyr 1 $$ 5 $$ 10 $$ 15

Leu Ala Lys Leu Ala Xaa Lys Arg Asn Val Thr Lys Lys Trp Leu Asn 20 25 30

Ser Trp Lys Lys Ser Leu Lys Pro Leu Thr Lys Thr Asn Ser Pro Ser 35 40 45

Lys Asn Val Ile Ser Ser Pro Ser Leu Thr Lys Thr
50 60

- (2) INFORMATION FOR SEQ ID NO:683:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592965
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

Met Val Glu Phe Met Glu Lys Val Ala Glu Ala Val Asp Lys Asp Glu 1 5 10 15

Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val

- (2) INFORMATION FOR SEQ ID NO:684:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592966
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Met Glu Lys Val Ala Glu Ala Val Asp Lys Asp Glu Leu Thr Val Glu 1 5 10 15

Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala Arg 20 25 30

Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Glu Lys Glu Glu Ser 35 40 \cdot 45

Arg Gly Asn Asp Asp His Val Thr Thr Ile Arg Asp Tyr Arg Ser Lys 50 55 60

Ile Glu Ser Glu Leu Ser Lys Ile Cys Asp Gly Ile Leu Lys Leu 65 70 75 80

Asp Thr Arg Leu Val Pro Ala Ser Ala Asn Gly Asp Ser Lys Val 85 90 95

- (2) INFORMATION FOR SEQ ID NO:685:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..496
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1592975
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

actttcaact taatcacaca caaggagaga agagagaaag agagaaagag agacagagat 60 aatggcgtac agtgcgtgtt tcctacacca gagcgcattg gcttcatcag ccgcacgatc 120 atcatctcc tcctcatccc agcgtcacgt gtcgctctcc aaacctgttc agatcatctg taaagctcaa cagtctcatg aagacgataa ctccgccgtc tcccgccgtc ttgctctcac 240 tctcctcgtc ggcgccgctg ctgttggttc caaagtatct cctgctgatg ccgcctacgg 300 tgaagctgca aacgtgtttg ggaagccaaa gacgacacaa gacttcttgc catacaatgg 360 agatgggttc aaagtgcagg ttccagcaaa atggaaccca agcaaagaga ttgagtatcc 420 aggacaagtc cttaggttcg aagacaactt cgatgctact agcaatctca atgtcatggt 480 cactcctacc gacaag

- (2) INFORMATION FOR SEQ ID NO:686:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..145 (D) OTHER INFORMATION: / Ceres Seq. ID 1592976 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:686: Met Ala Tyr Ser Ala Cys Phe Leu His Gln Ser Ala Leu Ala Ser Ser 10 Ala Ala Arg Ser Ser Ser Ser Ser Ser Gln Arg His Val Ser Leu 20 25 Ser Lys Pro Val Gln Ile Ile Cys Lys Ala Gln Gln Ser His Glu Asp 40 Asp Asn Ser Ala Val Ser Arg Arg Leu Ala Leu Thr Leu Leu Val Gly 55 Ala Ala Val Gly Ser Lys Val Ser Pro Ala Asp Ala Ala Tyr Gly 70 75 Glu Ala Ala Asn Val Phe Gly Lys Pro Lys Thr Asn Thr Asp Phe Leu Pro Tyr Asn Gly Asp Gly Phe Lys Val Gln Val Pro Ala Lys Trp Asn 100 105 Pro Ser Lys Glu Ile Glu Tyr Pro Gly Gln Val Leu Arg Phe Glu Asp 115 120 125 Asn Phe Asp Ala Thr Ser Asn Leu Asn Val Met Val Thr Pro Thr Asp 130 135 Lys 145 (2) INFORMATION FOR SEQ ID NO:687: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..99 (D) OTHER INFORMATION: / Ceres Seq. ID 1592977 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:687: Met Lys Thr Ile Thr Pro Pro Ser Pro Ala Val Leu Leu Ser Leu Ser 5 10 Ser Ser Ala Pro Leu Leu Val Pro Lys Tyr Leu Leu Met Pro 20 25 Pro Thr Val Lys Leu Gln Thr Cys Leu Gly Ser Gln Arg Arg Thr Gln 40 Thr Ser Cys His Thr Met Glu Met Gly Ser Lys Cys Arg Phe Gln Gln 55 Asn Gly Thr Gln Ala Lys Arg Leu Ser Ile Gln Asp Lys Ser Leu Gly 70 75 Ser Lys Thr Thr Ser Met Leu Leu Ala Ile Ser Met Ser Trp Ser Leu 90 Leu Pro Thr (2) INFORMATION FOR SEQ ID NO:688: (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

120

- (A) NAME/KEY: -
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593000
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:688: attcactcac caaagcatca cataacactc acacasacac tttbncttct cttatttct cagttcttt aactctttc tctacctata ttcaaatggc caccgtcgag gttgaacaag tgactccagt agcagctgag aacatcgagg tgccaccacc aaaggctgtg gagtcggagg
- aagtcaccac cgtctccgag tctcttccag ctccggtaac agaatctcaa gcgcctgtcg
 aagtaacaac taaagatttg gtcgtggaag agacagagaa accaatcgaa gaaacagagg
 aagctcaagt tgaaactccg gagttgtgga gatcaagaaa gatgaagaag ctccggagtt
 tcaacttgag ctt
- (2) INFORMATION FOR SEQ ID NO:689:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593001
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:
- Ser Leu Thr Lys Ala Ser His Asn Thr His Thr Xaa Thr Xaa Xaa Ser 1 5 10 15
- Leu Ile Phe Ser Val Leu Leu Thr Leu Phe Ser Thr Tyr Ile Gln Met 20 25 30
- Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$
- Glu Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr Val
 50 55 60
- Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val Glu 65 70 75 80
- Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile Glu 85 90 95
- Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Leu Trp Arg Ser Arg 100 105 110
- Lys Met Lys Leu Arg Ser Phe Asn Leu Ser 115 120
- (2) INFORMATION FOR SEQ ID NO:690:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593002
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:
- Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn 1 5 10 15
- Ile Glu Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr 20 25 30
- Val Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val 35 40 45
- Glu Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile 50 60
- Glu Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Leu Trp Arg Ser 65 70 75 80

Arg Lys Met Lys Leu Arg Ser Phe Asn Leu Ser 85 90

- (2) INFORMATION FOR SEQ ID NO:691:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..443
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593014
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

accaataagc aatttgctca ttagagaaca gagaaaaaaa aaaacaatgg caactcaagc 60 cgccgggatc ttcaactccg ccataacaac cgccgcaagc ctccggsgtc aagaaactcc 120 actttttctc aacaaccac cgtcccaaat cmctctcctt caccaaaacc gcgatccgcg 180 ccgagaaaac agattcctcc gccgccgctg ctgcagcccc cgccacgaaa gaagctcccg 240 tgggattcac gccaccgcag ctagacccaa acacaccgtc tccgatcttc gctggaagca 300 ccggtggtct tctacgtaaa gcgcaagtgg aagagttcta cgttatcacg tggaactcac 360 cgaaagaaca gatctttgag atgccgacag gaggagcagc gatcatgaga gaagatgtct 420 gctttgtctt ctggtggtca gct

- (2) INFORMATION FOR SEQ ID NO:692:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593015
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

Pro Ile Ser Asn Leu Leu Ile Arg Glu Gln Arg Lys Lys Lys Thr Met

1 10 15

Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala Ala 20 25 30

Ser Leu Arg Xaa Gln Glu Thr Pro Leu Phe Leu Asn Asn Pro Pro Ser 35 40 45

Gln Ile Xaa Leu Leu His Gln Asn Arg Asp Pro Arg Arg Glu Asn Arg 50 55 60

Phe Leu Arg Arg Arg Cys Cys Ser Pro Arg His Glu Arg Ser Ser Arg 65 70 75 80

Gly Ile His Ala Thr Ala Ala Arg Pro Lys His Thr Val Ser Asp Leu 85 90 95

Arg Trp Lys His Arg Trp Ser Ser Thr 100 105

- (2) INFORMATION FOR SEQ ID NO:693:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..90
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593016
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala

240

300

360

```
5
                                    10
Ala Ser Leu Arg Xaa Gln Glu Thr Pro Leu Phe Leu Asn Asn Pro Pro
                                25
Ser Gln Ile Xaa Leu Leu His Gln Asn Arg Asp Pro Arg Arg Glu Asn
                            40
Arg Phe Leu Arg Arg Cys Cys Ser Pro Arg His Glu Arg Ser Ser
Arg Gly Ile His Ala Thr Ala Ala Arg Pro Lys His Thr Val Ser Asp
                                        75
                    70
Leu Arg Trp Lys His Arg Trp Ser Ser Thr
               85
(2) INFORMATION FOR SEQ ID NO:694:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 474 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..474
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593017
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:
aaqaaaqqtt ctqtqtttaq gqttctqqtt ctqqqaaqct cqttctcacc gqaaaaccqa
agaatatgat cggagtctgg aaaatgaaac agtactccaa cgtccttgac aagcctctca
qcaaaggcaa gcaagaggtg agcttgaccg catttgcttt cttattctcg gagctcgttc
agtacaatca aacccaggtt gacaatatag ctgaacttga aagaagacta gaggatgctg
ggtatgcagt tggatctagt tctagagctt ctttgcaacc gggaaaaggg aaacagaaga
qaqacacqqt tactqqqaat tctqtctttc qttcacaqta ctqtqtqqaa aqtqttqttt
                                                                       420
qqaaaqgttg ctgattcact tgaaaaagga acagaacatg aagatgcatg ctaaagcaaa
gtagcatctt tgagaatgaa ttggtcagct gcttgaaagg attgtgttga aaag
(2) INFORMATION FOR SEQ ID NO:695:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 102 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..102
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593018
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:
Met Ile Gly Val Trp Lys Met Lys Gln Tyr Ser Asn Val Leu Asp Lys
                5
                                    10
Pro Leu Ser Lys Gly Lys Gln Glu Val Ser Leu Thr Ala Phe Ala Phe
            20
                                25
Leu Phe Ser Glu Leu Val Gln Tyr Asn Gln Thr Gln Val Asp Asn Ile
                            40
                                                 45
Ala Glu Leu Glu Arg Arg Leu Glu Asp Ala Gly Tyr Ala Val Gly Ser
                        55
                                             60
Ser Ser Arg Ala Ser Leu Gln Pro Gly Lys Gly Lys Gln Lys Arg Asp
                                        75
                    70
Thr Val Thr Gly Asn Ser Val Phe Arg Ser Gln Tyr Cys Val Glu Ser
                                    90
                85
Val Val Trp Lys Gly Cys
```

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593019
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

Met Lys Gln Tyr Ser Asn Val Leu Asp Lys Pro Leu Ser Lys Gly Lys 1 5 10 15

Gln Glu Val Ser Leu Thr Ala Phe Ala Phe Leu Phe Ser Glu Leu Val 20 25 30

Gln Tyr Asn Gln Thr Gln Val Asp Asn Ile Ala Glu Leu Glu Arg Arg 35 40 45

Leu Glu Asp Ala Gly Tyr Ala Val Gly Ser Ser Ser Arg Ala Ser Leu 50 55 60

Gln Pro Gly Lys Gly Lys Gln Lys Arg Asp Thr Val Thr Gly Asn Ser 70 75 80

Val Phe Arg Ser Gln Tyr Cys Val Glu Ser Val Val Trp Lys Gly Cys 85 90 95

- (2) INFORMATION FOR SEQ ID NO:697:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593020
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

Met Leu Gly Met Gln Leu Asp Leu Val Leu Glu Leu Cys Asn Arg 1 5 10 15

Val His Ser Thr Val Trp Lys Val Leu Phe Gly Lys Val Ala Asp Ser 35 40 45

Leu Glu Lys Gly Thr Glu His Glu Asp Ala Cys 50 55

- (2) INFORMATION FOR SEQ ID NO:698:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..457
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593051
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

(XI) DECOUNCE DEDOUGETION, DEC ID NOTOTO							
	ccgacgaccg	tgaatcacca	gcaaaggatt	cgtgtcaatg	ttcttgtgag	atcgaacttt	60
	ctctgggttc	gtgcagaagc	tttgcttttt	tgagtatcgc	gtttaaggca	catcgaagaa	120
			tttgagttct				180
			gacatctcgc				240
			gtgctatatc				300
			tctccaagga				360
	caccctattt	ctcactgaaa	tggtcagggg	tttgtcactg	accctcaagt	acttctttga	420

tccaaaagtt acaatcaatt atccttttga gaagggt (2) INFORMATION FOR SEQ ID NO:699: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..101 (D) OTHER INFORMATION: / Ceres Seq. ID 1593052 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699: Met Ala Ser Leu Leu Ala Arg Arg Ser Phe Ser Ala Leu Arg Ala Arg 10 5 His Leu Ala Phe Ser Gly Gln Gly Leu Gln Gly Ser His Leu Cys Gly 20 25 Leu Gln Ser Arg Ala Ile Ser Tyr Gly Ser Asn Lys Asp Asp Glu Glu 40 4.5 Ala Glu Gln Leu Ala Lys Glu Ile Ser Lys Asp Trp Ser Thr Val Phe 60 55 Glu Arg Ser Met Asn Thr Leu Phe Leu Thr Glu Met Val Arg Gly Leu 75 70 Ser Leu Thr Leu Lys Tyr Phe Phe Asp Pro Lys Val Thr Ile Asn Tyr 90 85 Pro Phe Glu Lys Gly 100 (2) INFORMATION FOR SEQ ID NO:700: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 393 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..393 (D) OTHER INFORMATION: / Ceres Seq. ID 1593053 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700: gagagattga gatatctttt gggagaggag aaagaaaaag aaaatgggaa gagggagagt 60 agaattgaag aggatagaga acaagatcaa taggcaagtg acgtttgcaa agagaaggaa 120 tggtcttttg aagaaagcat acgagctttc agttctatgt gatgcagaag ttgctctcat 180 catcttctca aatagaggaa agctgtacga gttttgcagt agttcgagca tgcttcggac 240 actggagagg taccaaaagt gtaactatgg agcaccagaa cccaatgtgc cttcaagaga 300 ggccttagca gttgaactta gtagccagca ggagtatctc aagcttaagg agcgttatga 360 cgccttacag agaacccatt tttttttt ttt (2) INFORMATION FOR SEQ ID NO:701: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..116 (D) OTHER INFORMATION: / Ceres Seq. ID 1593054 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn

Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala

```
20
Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe
                            40
Ser Asn Arq Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Ser Met Leu
                        55
Arg Thr Leu Glu Arg Tyr Gln Lys Cys Asn Tyr Gly Ala Pro Glu Pro
                    70
                                        75
Asn Val Pro Ser Arg Glu Ala Leu Ala Val Glu Leu Ser Ser Gln Gln
                                    90
                85
Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg Thr His
                                105
            100
Phe Phe Phe Phe
        115
(2) INFORMATION FOR SEQ ID NO:702:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 382 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..382
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593057
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:
cagaaatttt cttccgccgt aaaagcaaaa aaagatgcag atcttcgtga aaaccctaac
                                                                        60
ggggaagacg atcactctcg aggtcgagtc ctctgacacc atcgacaatg tcaaggccaa
                                                                       120
gatccaagac aaggaaggaa tcccaccgga ccagcagcga ttgattttcg ccggaaagca
                                                                       180
gctcgaagac ggacgtacct tagccgatta caacatccag aaggaatcaa cgcttcacct
                                                                       240
                                                                       300
tgtccttcgt ctccgtggag gtgctaagaa gaggaagaag aagacctaca ccaagcctaa
gaagatcaag cacaagcaca agaaggtcaa gctcgctgtt cttcagttct acaaggttga
                                                                       360
tggttcaggt aaaccaaagt tt
(2) INFORMATION FOR SEQ ID NO:703:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 116 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..116
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593058
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
                                     10
                5
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
                             40
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
                         55
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ala Lys Lys Arg
                    70
                                         75
Lys Lys Lys Thr Tyr Thr Lys Pro Lys Lys Ile Lys His Lys
                85
                                     90
Lys Val Lys Leu Ala Val Leu Gln Phe Tyr Lys Val Asp Gly Ser Gly
                                 105
            100
Lys Pro Lys Phe
```

(2) INFORMATION FOR SEQ ID NO:704:

- Page 410 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..336 (D) OTHER INFORMATION: / Ceres Seq. ID 1593077 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704: atttttgaaa agtttctaac ctctaggcca cccactcatg gctactctgt tcatgaagct ggtgagcttc tttctaattc tatctacttt ttgtctcact actgtgaact cggagccaca 120 gtgccataat ttcaaatcga tcattagttt cggtgattct attgccgaca ctggaaactt 180 240 qctcqccctc tccgatccta ccaatctccc taaggtcgcg tttctaccgt acggagaaac 300 cttcttccac catccgaccg gccgtttctc aaacggcgcc tcatcatcga tttcattgct qaatttttgg gttttccgct tgtgsctcmt ttttat (2) INFORMATION FOR SEQ ID NO:705: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..99 (D) OTHER INFORMATION: / Ceres Seq. ID 1593078 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705: Met Ala Thr Leu Phe Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser 10 5 Thr Phe Cys Leu Thr Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe 30 25 20 Lys Ser Ile Ile Ser Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu 45 40 Leu Ala Leu Ser Asp Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro 55 60 Tyr Gly Glu Thr Phe Phe His His Pro Thr Gly Arg Phe Ser Asn Gly 75 70 Ala Ser Ser Ser Ile Ser Leu Leu Asn Phe Trp Val Phe Arg Leu Xaa 85 90 Leu Xaa Phe (2) INFORMATION FOR SEQ ID NO:706: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..94 (D) OTHER INFORMATION: / Ceres Seq. ID 1593079
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser Thr Phe Cys Leu Thr 10

Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe Lys Ser Ile Ile Ser 25

Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu Leu Ala Leu Ser Asp

- (2) INFORMATION FOR SEQ ID NO:707:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..410
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593101
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707: acgccgctca tttttagggt ttcagatata ggcagattct cacatttgca aacatgacga

ctcagatcag caagaagaga aagtttgtag cggacggtgt gttctacgct gaattgaatg 120 aggttcttac aagagagcta gcagaggatg gttactctgg tgttgaggtt agggttactc 180 ctatgaggac tgagattatc atcagagcta cacgtactca gaatgttctc ggtgagaagg 240 ggaggagaat tagggaattg acttcccttg ttcagaagag attcaagttt ccagttgaca 300 gtgttgagct ttatgccgag aaggttaaca acagaggtct ctgtgccatc gctcaggctg 360

- agtetttacg ttacaagett ettggeataa ageteaacae tgteaactgg (2) INFORMATION FOR SEQ ID NO:708:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

Phe Tyr Ala Glu Leu Asn Glu Val Leu Thr Arg Glu Leu Ala Glu Asp 20 25 30

Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile 35 40 45

Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
50 55 60

Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys Arg Phe Lys Phe Pro 65 70 75 80
Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val Asn Asn Arg Gly Leu

85 90 95

Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Ile
100 105 110

Lys Leu Asn Thr Val Asn Trp

- (2) INFORMATION FOR SEQ ID NO:709:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys 20 25 30

Arg Phe Lys Phe Pro Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val 35 40 45

Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr 50 55 60

Lys Leu Leu Gly Ile Lys Leu Asn Thr Val Asn Trp 65 70 75

- (2) INFORMATION FOR SEQ ID NO:710:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..487
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:710: atgaacatta gggtgagaag agatcgagag aagaatagtt tgatcatctt gtgagaaaaa

- (2) INFORMATION FOR SEQ ID NO:711:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

agaaccc

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Met Ala Ala Ser Val Met Leu Ser Ser Val Thr Leu Lys Pro Ala Gly
1 5 10 15

Phe Thr Val Glu Lys Thr Ala Ala Arg Gly Leu Pro Ser Leu Thr Arg 20 25 30

Ala Arg Pro Ser Phe Lys Ile Val Ala Ser Xaa Ser Arg Arg Ser Arg 35 40 45

Pro Thr Ser Pro Ser Glu Leu Thr Ala Ala Trp Thr 50 55 60

- (2) INFORMATION FOR SEQ ID NO:712:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

Table 2 Page 413 (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..55 (D) OTHER INFORMATION: / Ceres Seq. ID 1593106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712: Met Leu Ser Ser Val Thr Leu Lys Pro Ala Gly Phe Thr Val Glu Lys 10 5 Thr Ala Ala Arg Gly Leu Pro Ser Leu Thr Arg Ala Arg Pro Ser Phe 25 20 Lys Ile Val Ala Ser Xaa Ser Arg Arg Ser Arg Pro Thr Ser Pro Ser 40 Glu Leu Thr Ala Ala Trp Thr 50 55 (2) INFORMATION FOR SEQ ID NO:713: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..84 (D) OTHER INFORMATION: / Ceres Seq. ID 1593107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:713: Met Asp Leu Arg Asp Gly Val Asp Ala Ser Gly Arg Lys Gly Lys Gly 5 10 Tyr Gly Val Tyr Lys Tyr Val Asp Lys Tyr Gly Ala Asn Val Asp Gly 20 25 Tyr Ser Pro Ile Tyr Asn Glu Asn Glu Trp Ser Ala Ser Gly Asp Val 40 Tyr Lys Gly Gly Val Thr Gly Leu Ala Ile Trp Ala Val Thr Leu Ala 55 60 Gly Ile Leu Leu Gln Pro Ile Leu Leu Leu Ala Ala Met Val Lys Tyr 8.0 Ser Gln Glu Pro (2) INFORMATION FOR SEQ ID NO:714: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..472 (D) OTHER INFORMATION: / Ceres Seq. ID 1593153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

aaaaaaattc gagctctctt gaagcaaaaa gctatccgcc gtcgactcga gcttcgttcg 60 tctctctgca aatatggcga casgtatcaa ccaatgaaac caggaaaggc tggtttggaa 120 gagccactcg agcagattca caagatcagg attactctct cctccaagaa tgtcaagaac 180 cttgagaaag tgtgcactga tttggttcgt ggagctaagg acaagagact tagagtcaag 240 qqaccaqtga gaatgcccac taaggttctc aagatcacta cccgaaaaagc tccctgtggt qaaqqaccaa tacatgggac agatttgaac ttagggtgca caagcgagtg attgatctct tcagctctcc tgatgtggtc aagcmaatca catccatcac cattgaacct ggtgttgagg 420 ttgaggtcac categocgne tegtngateg actetettac ttetgttttt ge

- (2) INFORMATION FOR SEQ ID NO:715:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593154
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Lys Lys Ile Arg Ala Leu Leu Lys Gln Lys Ala Ile Arg Arg Leu 1 5 10 15

Glu Leu Arg Ser Ser Leu Cys Lys Tyr Gly Asp Xaa Tyr Gln Pro Met 20 25 30

Lys Pro Gly Lys Ala Gly Leu Glu Glu Pro Leu Glu Gln Ile His Lys 35 40 45

Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys Asn Leu Glu Lys Val 50 55 60

Cys Thr Asp Leu Val Arg Gly Ala Lys Asp Lys Arg Leu Arg Val Lys 65 70 75 80

Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys Ile Thr Thr Arg Lys 85 90 95

Ala Pro Cys Gly Glu Gly Pro Ile His Gly Thr Asp Leu Asn Leu Gly 100 105 110

Cys Thr Ser Glu

115

- (2) INFORMATION FOR SEQ ID NO:716:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

Lys Asn Ser Ser Ser Leu Glu Ala Lys Ser Tyr Pro Pro Ser Thr Arg 1 5 10 15

Ala Ser Phe Val Ser Leu Gln Ile Trp Arg Xaa Val Ser Thr Asn Glu 20 25 30

Thr Arg Lys Gly Trp Phe Gly Arg Ala Thr Arg Ala Asp Ser Gln Asp 35 40 45

- Gln Asp Tyr Ser Leu Leu Gln Glu Cys Gln Glu Pro 50 55 60
- (2) INFORMATION FOR SEQ ID NO:717:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

Met Lys Pro Gly Lys Ala Gly Leu Glu Glu Pro Leu Glu Gln Ile His 1 5 10 15

Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys Asn Leu Glu Lys 20 25 30

- 85
 (2) INFORMATION FOR SEQ ID NO:718:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..430
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

 acacaatacc atttgcaaaa aacttctctc tgaatctcag tgagttctca taaaatgaga 60
 gggatggtga gttttgccgt ttgggctctc tttgctgctt tactctcaca gcagctcttt 120
 gcttctgttg cttccgtaag tttgaggatg ccaaaacata ctacttatct cctccctctg 180
 gctcacatgg aactcctcca tcacacacgc ctccttcttc taactgtgga agtccacctt 240
 acgacccttc tccttcaact ccttctcacc cttcacctcc atcacatact ccaactcctt 300
 ccgactccat cacacactcc aactccacac actccatcac acacgccaac tcsacacac 360
 cctccttgta actgtggaag tccaccttcc cagttaaaga aggtgttttg agcatcgagc 420
- (2) INFORMATION FOR SEQ ID NO:719:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

agtttagctt

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593184
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

Met Arg Gly Met Val Ser Phe Ala Val Trp Ala Leu Phe Ala Ala Leu 1 5 10 15

Leu Ser Gln Gln Leu Phe Ala Ser Val Ala Ser Val Ser Leu Arg Met 20 25 30

Pro Lys His Thr Thr Tyr Leu Leu Pro Leu Ala His Met Glu Leu Leu 35 40 45

His His Thr Arg Leu Leu Leu Thr Val Glu Val His Leu Thr Thr 50 55 60

Leu Leu Gln Leu Leu Thr Leu His Leu His His Ile Leu Gln 65 70 75 80

Leu Leu Pro Thr Pro Ser His Thr Pro Thr Pro His Thr Pro Ser His

85

90

95

Thu Dro Thr Yes His Thr Pro Pro Cus Asp Cus Cly Ser Pro Pro Ser

Thr Pro Thr Xaa His Thr Pro Pro Cys Asn Cys Gly Ser Pro Pro Ser 100 105 110

Gln Leu Lys Lys Val Phe 115

- TT3
- (2) INFORMATION FOR SEQ ID NO:720:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593185
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

Met Val Ser Phe Ala Val Trp Ala Leu Phe Ala Ala Leu Leu Ser Gln 1 5 10 15

Gln Leu Phe Ala Ser Val Ala Ser Val Ser Leu Arg Met Pro Lys His 20 25 30

Thr Thr Tyr Leu Leu Pro Leu Ala His Met Glu Leu Leu His His Thr 35 40 45

Arg Leu Leu Leu Thr Val Glu Val His Leu Thr Thr Leu Leu Leu 50 55 60

Gln Leu Leu Thr Leu His Leu His Ile Leu Gln Leu Leu Pro 70 75 80

Thr Pro Ser His Thr Pro Thr Pro His Thr Pro Ser His Thr Pro Thr 85 90 95

Xaa His Thr Pro Pro Cys Asn Cys Gly Ser Pro Pro Ser Gln Leu Lys 100 105 110

Lys Val Phe

115

- (2) INFORMATION FOR SEQ ID NO:721:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

Met Pro Lys His Thr Thr Tyr Leu Leu Pro Leu Ala His Met Glu Leu 1 5 10 15

Leu His His Thr Arg Leu Leu Leu Leu Thr Val Glu Val His Leu Thr 20 25 30

Thr Leu Leu Gln Leu Leu Leu Thr Leu His Leu His His Ile Leu 35 40 45

Gln Leu Leu Pro Thr Pro Ser His Thr Pro Thr Pro His Thr Pro Ser 50 55 60

His Thr Pro Thr Xaa His Thr Pro Pro Cys Asn Cys Gly Ser Pro Pro 65 70 75 80

Ser Gln Leu Lys Lys Val Phe 85

- (2) INFORMATION FOR SEQ ID NO:722:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..524
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593202
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:722: tcacatctct ctctattct cttccacaaa gagtcctaac ttcgagttga aacaaacacc attctcatc tctatctcag aaagaacaaa ccatttcgtg ttctttcttt ctctattctc

ataaggaaat ataattcctg aaactgttga gttcttgtga aaggaaataa aaaacatgat 180 gatgggcaaa gaagatctag gtttgagcct aagcttaggg ttttcacaaa atcacaatcc 240 tcttcagatg aatctgaatc ctaactcttc attacaaac aatctccaga gactcccatg gaaccaaaca ttcgatccta catcagatct tcgcaagata gacgtgaaca gttttccatc 360 aacggttaac tgggaggaag acacaggagt ttcgtcacca nacagtacga tttcaagcac 420 cattagcggg aagagaagtg agagagaagg aatctccgga accggcgttg gctccggcga 480 acgatcacga cgagatcact ccgggatcga gggtactcac gtgg

- (2) INFORMATION FOR SEQ ID NO:723:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593203
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Met Met Met Gly Lys Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe 1 5 10 15

Ser Gln Asn His Asn Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser 20 25 30

Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro 35 40 45

Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val 50 55 60

Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Xaa Ser Thr Ile Ser 65 70 75 80

Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr
85 90 95

Gly Val Gly Ser Gly Glu Arg Ser Arg Arg Asp His Ser Gly Ile Glu 100 105 110

Gly Thr His Val

115

- (2) INFORMATION FOR SEQ ID NO:724:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593204
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

Met Met Gly Lys Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser 1 5 10 15

Gln Asn His Asn Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu 20 25 30

Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr 35 40 45

Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn 50 55 60 .

Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Xaa Ser Thr Ile Ser Ser 65 70 75 80

Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly 85 90 95

Val Gly Ser Gly Glu Arg Ser Arg Arg Asp His Ser Gly Ile Glu Gly
100 105 110

Thr His Val

115

- (2) INFORMATION FOR SEQ ID NO:725:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593205
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Met Gly Lys Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln 1 5 10 15

Asn His Asn Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu Ser 20 25 30

Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser

Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn Cys 50 55 60

Glu Glu Asp Thr Gly Val Ser Ser Pro Xaa Ser Thr Ile Ser Ser Thr 65 70 75 80

Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly Val 85 90 95

Gly Ser Gly Glu Arg Ser Arg Arg Asp His Ser Gly Ile Glu Gly Thr $100 \hspace{1cm} 105 \hspace{1cm} 105 \hspace{1cm} 110 \hspace{1cm}$

His Val

- (2) INFORMATION FOR SEQ ID NO:726:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..529
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593228
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

aagaatcaac aaaagaaaaa acattcacct tctcttacgc gactctcgcc ggaaacagat 60 cgctccgccg tgaactcgga agccatgggg tcacttttgc agggttttac taaatcactc 120 gccatgactt tcctctccga gattggtgac aaaacgttct tcgctgctgc tattttggcg 180 atgeggtate etaggagget tgtattaget ggttgtttat eagetttgat tgtvatgaet 240 atattatctg ctacacttgg ttgggctgct ccaaatctga tctctcggaa atggactcat 300 360 catataacaa cattettgtt etttggettt gggttatggt etttgtggga tggttttaaa 420 gaaggaggag gttctgaaga attggcagaa gttgaagcag aactggattc tgatttgaag aagactaatg atcaatcgaa aaacagtaag attgaagatg aacagaaaaa gcagaaaaga 480 ccattcctta ctgcattctt ctctcccatt tttctcaagg cgtttttcg

- (2) INFORMATION FOR SEQ ID NO:727:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids(B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1593229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:727: Lys Asn Gln Gln Lys Lys Lys His Ser Pro Ser Leu Thr Arg Leu Ser 10 Pro Glu Thr Asp Arg Ser Ala Val Asn Ser Glu Ala Met Gly Ser Leu 20 25 Leu Gln Gly Phe Thr Lys Ser Leu Ala Met Thr Phe Leu Ser Glu Ile 40 Gly Asp Lys Thr Phe Phe Ala Ala Ala Ile Leu Ala Met Arg Tyr Pro 55 Arg Arg Leu Val Leu Ala Gly Cys Leu Ser Ala Leu Ile Xaa Met Thr 70 75 Ile Leu Ser Ala Thr Leu Gly Trp Ala Ala Pro Asn Leu Ile Ser Arg 90 8.5 Lys Trp Thr His His Ile Thr Thr Phe Leu Phe Phe Gly Phe Gly Leu 100 105 Trp Ser Leu Trp Asp Gly Phe Lys Glu Gly Gly Ser Glu Glu Leu 115 120 125 Ala Glu Val Glu Ala Glu Leu Asp Ser Asp Leu Lys Lys Thr Asn Asp 130 135 140 Gln Ser Lys Asn Ser Lys Ile Glu Asp Glu Gln Lys Lys Gln Lys Arg 145 150 155 Pro Phe Leu Thr Ala Phe Phe Ser Pro Ile Phe Leu Lys Ala Phe Phe 165 170

- (2) INFORMATION FOR SEQ ID NO:728:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593230
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:
- Met Gly Ser Leu Leu Gln Gly Phe Thr Lys Ser Leu Ala Met Thr Phe

 1 10 15

 15
- Leu Ser Glu Ile Gly Asp Lys Thr Phe Phe Ala Ala Ala Ile Leu Ala 20 25 30
- Met Arg Tyr Pro Arg Arg Leu Val Leu Ala Gly Cys Leu Ser Ala Leu 35 40 45
- Ile Xaa Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala Ala Pro Asn 50 55 60
- Leu Ile Ser Arg Lys Trp Thr His His Ile Thr Thr Phe Leu Phe Phe 65 70 75 80
- Gly Phe Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu Gly Gly 85 90 95
- Ser Glu Glu Leu Ala Glu Val Glu Ala Glu Leu Asp Ser Asp Leu Lys 100 105 110
- Lys Thr Asn Asp Gln Ser Lys Asn Ser Lys Ile Glu Asp Glu Gln Lys 115 120 125
- Lys Gln Lys Arg Pro Phe Leu Thr Ala Phe Phe Ser Pro Ile Phe Leu 130 135 140
- Lys Ala Phe Phe
- 145
- (2) INFORMATION FOR SEQ ID NO:729:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids

(B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..135 (D) OTHER INFORMATION: / Ceres Seq. ID 1593231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729: Met Thr Phe Leu Ser Glu Ile Gly Asp Lys Thr Phe Phe Ala Ala Ala 10 5 Ile Leu Ala Met Arg Tyr Pro Arg Arg Leu Val Leu Ala Gly Cys Leu 25 30 2.0 Ser Ala Leu Ile Xaa Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala 40 45 Ala Pro Asn Leu Ile Ser Arg Lys Trp Thr His His Ile Thr Thr Phe 60 55 Leu Phe Phe Gly Phe Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu 75 70 Gly Gly Ser Glu Glu Leu Ala Glu Val Glu Ala Glu Leu Asp Ser 90 85 Asp Leu Lys Lys Thr Asn Asp Gln Ser Lys Asn Ser Lys Ile Glu Asp 110 105 100 Glu Gln Lys Lys Gln Lys Arg Pro Phe Leu Thr Ala Phe Phe Ser Pro 125 120 Ile Phe Leu Lys Ala Phe Phe (2) INFORMATION FOR SEQ ID NO:730: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 457 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..457 (D) OTHER INFORMATION: / Ceres Seq. ID 1593275 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730: gtttcaacag attgaaggta agggaaccag tgattgagcc ggttgtggag gatgttgagg 60 acagtactga ctcgagcgta ggagaagaag aagaagagga tgatttgatc aaggagattg 120 tccgtaccaa gactttcgag atgccaccat tgactgtcgc tgaggcagtc gagcagctgg 180 aactagtcag tcacgacttc tatggcttcc aaaatgaaga aactggtgag ataaacatag 240 tgtacaagag aaaagaagga ggttacggtc tgataatccc aaagaaagac gggaaggccg 300 agaaggttga gccgcttcca accgagcaat tgaatgaaca ctctttcgcc gagtagactg 360 cctctgctca caccaaaacc gataagctca tctctcctta cagtttacct gtgtaggagt 420 tagggttctt gaataaacaa tgcaacaaag attgtag (2) INFORMATION FOR SEQ ID NO:731: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..117 (D) OTHER INFORMATION: / Ceres Seq. ID 1593276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

Phe Asn Arg Leu Lys Val Arg Glu Pro Val Ile Glu Pro Val Val Glu

5

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Client Docket No. 80146.003
Asp Val Glu Asp Ser Thr Asp Ser Ser Val Gly Glu Glu Glu Glu
                               25
          20
Asp Asp Leu Ile Lys Glu Ile Val Arg Thr Lys Thr Phe Glu Met Pro
                                               45
                         4.0
Pro Leu Thr Val Ala Glu Ala Val Glu Gln Leu Glu Leu Val Ser His
                                          60
                      55
Asp Phe Tyr Gly Phe Gln Asn Glu Glu Thr Gly Glu Ile Asn Ile Val
               70
                                       75
Tyr Lys Arg Lys Glu Gly Gly Tyr Gly Leu Ile Ile Pro Lys Lys Asp
                            90
              85
Gly Lys Ala Glu Lys Val Glu Pro Leu Pro Thr Glu Gln Leu Asn Glu
          100 105
                                                  110
His Ser Phe Ala Glu
       115
(2) INFORMATION FOR SEQ ID NO:732:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 71 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
          (B) LOCATION: 1..71
         (D) OTHER INFORMATION: / Ceres Seq. ID 1593277
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:
Met Pro Pro Leu Thr Val Ala Glu Ala Val Glu Gln Leu Glu Leu Val
   5
                                   10
Ser His Asp Phe Tyr Gly Phe Gln Asn Glu Glu Thr Gly Glu Ile Asn
                              25
Ile Val Tyr Lys Arg Lys Glu Gly Gly Tyr Gly Leu Ile Ile Pro Lys
                                     4.5
                       40
Lys Asp Gly Lys Ala Glu Lys Val Glu Pro Leu Pro Thr Glu Gln Leu
                       55
Asn Glu His Ser Phe Ala Glu
                   70
(2) INFORMATION FOR SEQ ID NO:733:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 462 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..462
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593331
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:
ctcctctaaa aaaccaaaat aaaaaccttt tttctctctt catgcttagc ctatcatgag
                                                                     60
caacatecet agatetetea eegacteaga tettteteta titaetetea taatetette
                                                                     120
tgctgttgat ccttggcctt tttctatcac cgttttttag catcaacaaa actcaccgga
                                                                     180
aaatctctaa caaccaccgt ttaacacttc tcttcctcct cgtcgatcgt ttttaaacca
                                                                     240
                                                                     300
atctttgtgt ttcttgtttg gtttttcggt gaaaaagatt ccttccttct taatgggttt
tgaagaaaac caaaaacaga gtccaaaaca gagtccgaat catatcaagc atatggtgtt
                                                                     360
caagtttcac ttccatgttc ctcatcttca catactccct catcaccacc accaccacca
                                                                     420
ccatgatgtt cctaaaggct gtgtagcgat tatggtggga ca
```

- (2) INFORMATION FOR SEQ ID NO:734:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..34 (D) OTHER INFORMATION: / Ceres Seq. ID 1593332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:734: Met Ser Asn Ile Pro Arg Ser Leu Thr Asp Ser Asp Leu Ser Leu Phe 10 5 Thr Leu Ile Ile Ser Ser Ala Val Asp Pro Trp Pro Phe Ser Ile Thr 25 20 Val Phe (2) INFORMATION FOR SEQ ID NO:735: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..56 (D) OTHER INFORMATION: / Ceres Seq. ID 1593333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:735: Met Gly Phe Glu Glu Asn Gln Lys Gln Ser Pro Lys Gln Ser Pro Asn 5 10 His Ile Lys His Met Val Phe Lys Phe His Phe His Val Pro His Leu 20 25 His Ile Leu Pro His His His His His His His Asp Val Pro Lys 40 Gly Cys Val Ala Ile Met Val Gly (2) INFORMATION FOR SEQ ID NO:736: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..36 (D) OTHER INFORMATION: / Ceres Seq. ID 1593334 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:736: Met Val Phe Lys Phe His Phe His Val Pro His Leu His Ile Leu Pro 10 His His His His His His His Asp Val Pro Lys Gly Cys Val Ala 25 20 Ile Met Val Gly 35 (2) INFORMATION FOR SEQ ID NO:737: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 404 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1593344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:									
aactactgtc t	tcgatctct	ctttcatata	caccatataa	aacgaaccag	ttaattatgg	60			
gtttaatttc c	gggaaggtg	tgtgtgttta	tctttgtatt	cgctctagtc	gctgaatttt	120			
cgttcggaaa t	gttgaggtt	aacqacqaca	aacacttttt	ccacaaacct	cgtccatttt	180			
tacacaaacc t	catccattc	ctccacaagc	atggcattta	caagaaaggt	ttcggtaagg	240			
gtttgggcgg t	agaaacaat	ctaggcggcg	gaggtggtct	aggaggcggt	ggtggaggtt	300			
taggcggcgg t	ggtggtcta	ggaggcggta	gcggtttggg	aggaggaggg	ggtctaggag	360			
gcggtagcgg t									

- (2) INFORMATION FOR SEQ ID NO:738:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

Leu Leu Ser Ser Ile Ser Leu Ser Tyr Thr Pro Tyr Lys Thr Asn Gln
1 5 10 15

Leu Ile Met Gly Leu Ile Ser Gly Lys Val Cys Val Phe Ile Phe Val 20 25 30

Phe Ala Leu Val Ala Glu Phe Ser Phe Gly Asn Val Glu Val Asn Asp 35 40 45

Asp Lys His Phe Phe His Lys Pro Arg Pro Phe Leu His Lys Pro Arg 50 55 60

Pro Phe Leu His Lys His Gly Ile Tyr Lys Lys Gly Phe Gly Lys Gly 65 70 75 80

Gly Gly Gly Gly Leu Gly Gly Gly Ser Gly Leu Gly Gly Gly 115 120 125

- Gly Phe Gly Gly Gly Gly 130
- (2) INFORMATION FOR SEQ ID NO:739:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593346
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

Met Gly Leu Ile Ser Gly Lys Val Cys Val Phe Ile Phe Val Phe Ala
1 5 10 15

Leu Val Ala Glu Phe Ser Phe Gly Asn Val Glu Val Asn Asp Asp Lys
20 25 30

His Phe Phe His Lys Pro Arg Pro Phe Leu His Lys Pro Arg Pro Phe 35 40 45

Leu His Lys His Gly Ile Tyr Lys Lys Gly Phe Gly Lys Gly Leu Gly 50 55 60

Gly Leu Gly Gly Gly Gly Leu Gly Gly Gly Ser Gly Leu Gly Gly 90 85 Gly Gly Gly Leu Gly Gly Gly Ser Gly Leu Gly Gly Gly Gly Phe 105 100 Gly Gly Gly Gly 115

- (2) INFORMATION FOR SEQ ID NO:740:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..498
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593394
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

60 aaaacttgcg actttttaac aatcgaccga cttatcaaaa ttagggatag ttttatatat aaagagagac gcatctcttt atttcattca tcgcttctcc aaaattttct tcaaagaaca 120 180 aatctcccaa atctaaaatc tttctcttct ctcttcgttt ccataaccat gtctgcgaag aagattgtgt tgaagagttc cgatggtgaa tctttcgagg ttgaggaggc ggtggctctc 240 gagtcacaaa ccatagcgca tatggttgaa gacggactgc gtsacaacgg agtccctctt 300 cctaacgtca cgagcaagat cctcgccaag gtgatcgagt attgcaagag gcacgtcgag 360 gctgctgcct ctaaggccga ggccgtcgag ggtgctgcta cctccgatka cgatcttaag 420 gcctgggacg ctgattttat gaagatcgat caagctactc tctttgaact cattctggct 480 gctaattacc tgaatatc

- (2) INFORMATION FOR SEQ ID NO:741:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593395
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Lys Thr Cys Asp Phe Leu Thr Ile Asp Arg Leu Ile Lys Ile Arg Asp 10

Ser Phe Ile Tyr Lys Glu Arg Arg Ile Ser Leu Phe His Ser Ser Leu 20 25 30

Leu Gln Asn Phe Leu Gln Arg Thr Asn Leu Pro Asn Leu Lys Ser Phe 40

Ser Ser Leu Phe Val Ser Ile Thr Met Ser Ala Lys Lys Ile Val Leu 55

Lys Ser Ser Asp Gly Glu Ser Phe Glu Val Glu Glu Ala Val Ala Leu 70 75

Glu Ser Gln Thr Ile Ala His Met Val Glu Asp Gly Leu Arg Xaa Asn 90 85

Gly Val Pro Leu Pro Asn Val Thr Ser Lys Ile Leu Ala Lys Val Ile 105 100

Glu Tyr Cys Lys Arg His Val Glu Ala Ala Ala Ser Lys Ala Glu Ala 120 115

Val Glu Gly Ala Ala Thr Ser Asp Xaa Asp Leu Lys Ala Trp Asp Ala 140 135

Asp Phe Met Lys Ile Asp Gln Ala Thr Leu Phe Glu Leu Ile Leu Ala 155 150

Ala Asn Tyr Leu Asn Ile

(2) INFORMATION FOR SEQ ID NO:742: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..110 (D) OTHER INFORMATION: / Ceres Seq. ID 1593396 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742: Met Ser Ala Lys Lys Ile Val Leu Lys Ser Ser Asp Gly Glu Ser Phe 5 10 Glu Val Glu Glu Ala Val Ala Leu Glu Ser Gln Thr Ile Ala His Met 25 30 20 Val Glu Asp Gly Leu Arg Xaa Asn Gly Val Pro Leu Pro Asn Val Thr 45 40 Ser Lys Ile Leu Ala Lys Val Ile Glu Tyr Cys Lys Arg His Val Glu 60 55 Ala Ala Ala Ser Lys Ala Glu Ala Val Glu Gly Ala Ala Thr Ser Asp 75 70 Xaa Asp Leu Lys Ala Trp Asp Ala Asp Phe Met Lys Ile Asp Gln Ala 85 90 Thr Leu Phe Glu Leu Ile Leu Ala Ala Asn Tyr Leu Asn Ile 105 100 (2) INFORMATION FOR SEQ ID NO:743: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 367 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..367 (D) OTHER INFORMATION: / Ceres Seq. ID 1593424 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743: 60 ttctcagacc tcaatttcca agcagagatg acggtgaaga taaggctcgc gcgtcttggt tgtaaacacc gacccttcta tcgtgtagtt gtcgccgatg aaaaatcgcg cagggacggt 120 aaacaaatcg aggtgttagg cttttatgat ccactccaag gcaaagaaga tgcggatara 180 gtgagcctca aattcgacag aatcaagtac tggttatctg ttggagctca accaacagac 240 acagtggaaa gcatgctttt cagggccggt ttgataccac caaagcctat ggtagtggtc 300 ggttcaaawa atgggcagaa gtggtttttg tggctttcga ccacttgtgc ttatcgacca 360 ttatqct (2) INFORMATION FOR SEQ ID NO:744: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..122 (D) OTHER INFORMATION: / Ceres Seq. ID 1593425 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744: Phe Ser Asp Leu Asn Phe Gln Ala Glu Met Thr Val Lys Ile Arg Leu 10 5 Ala Arg Leu Gly Cys Lys His Arg Pro Phe Tyr Arg Val Val Ala

Ser Thr Thr Cys Ala Tyr Arg Pro Leu Cys 115 120

- (2) INFORMATION FOR SEQ ID NO:745:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593426
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly Cys Lys His Arg Pro

1 10 15

15 10 15

Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser Arg Arg Asp Gly Lys 20 25 30

Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu Gln Gly Lys Glu Asp 35 40 45

Ala Asp Xaa Val Ser Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser
50 55 60

Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser Met Leu Phe Arg Ala 65 70 75 80
Gly Leu Ile Pro Pro Lys Pro Met Val Val Gly Ser Xaa Asn Gly

85 90 95

Gloung Tro Phe Leu Tro Leu Ser Thr Thr Cvs Ala Tvr Arg Pro Leu

Gln Lys Trp Phe Leu Trp Leu Ser Thr Thr Cys Ala Tyr Arg Pro Leu 100 105 110

Cys

- (2) INFORMATION FOR SEQ ID NO:746:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

teccageete tete

- (A) NAME/KEY: -
- (B) LOCATION: 1..494
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:746: attcttttta gctaggtcat atataaaaaa aagccgcaag aatagagctt gcgattatcg 60 gaggattcaa tcatcggcgg aggacgaaaa tgagtgttat caggcttcac cagtaccaag 120 tcgtaggacg agctctcccg acggagaaag atgagcaacc aaagatttac aggatgaagc 180 tctgggcaac gaacgaggtt cttgccaaat ccaagttctg gtactactta aggaggcaaa 240 agaaggtgaa gaagagtaat ggacagatgc tagccatcaa cgagatcttt gagaagaacc 300 caacaacgat caagaatttt ggaatctggt tgagatacca gagccgtaca ggttaccata 360 420 acatgtacaa agagtaccgt gacactactt tgaatggagc agtggagcaa atgtacactg agatggcgtc aagacacaga gtaaggttcc cttgcattca gattattaag acagcaacag 480

- Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:747: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..135 (D) OTHER INFORMATION: / Ceres Seq. ID 1593442 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:747: Met Ser Val Ile Arg Leu His Gln Tyr Gln Val Val Gly Arg Ala Leu 5 10 Pro Thr Glu Lys Asp Glu Gln Pro Lys Ile Tyr Arg Met Lys Leu Trp 25 20 Ala Thr Asn Glu Val Leu Ala Lys Ser Lys Phe Trp Tyr Tyr Leu Arg 40 Arg Gln Lys Lys Val Lys Lys Ser Asn Gly Gln Met Leu Ala Ile Asn 55 Glu Ile Phe Glu Lys Asn Pro Thr Thr Ile Lys Asn Phe Gly Ile Trp 75 70 Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn Met Tyr Lys Glu Tyr 90 Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln Met Tyr Thr Glu Met 100 105 110 Ala Ser Arg His Arg Val Arg Phe Pro Cys Ile Gln Ile Ile Lys Thr 115 120 Ala Thr Val Pro Ala Ser Leu 130 (2) INFORMATION FOR SEQ ID NO:748: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1593443 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:748: Met Lys Leu Trp Ala Thr Asn Glu Val Leu Ala Lys Ser Lys Phe Trp 5 10 Tyr Tyr Leu Arg Arg Gln Lys Lys Val Lys Lys Ser Asn Gly Gln Met Leu Ala Ile Asn Glu Ile Phe Glu Lys Asn Pro Thr Thr Ile Lys Asn 40 Phe Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn Met 55 Tyr Lys Glu Tyr Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln Met 75 70 Tyr Thr Glu Met Ala Ser Arg His Arg Val Arg Phe Pro Cys Ile Gln 90 85 Ile Ile Lys Thr Ala Thr Val Pro Ala Ser Leu
 - (2) INFORMATION FOR SEQ ID NO:749:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..76 (D) OTHER INFORMATION: / Ceres Seq. ID 1593444 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:749: Met Leu Ala Ile Asn Glu Ile Phe Glu Lys Asn Pro Thr Thr Ile Lys 10 5 Asn Phe Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn 25 20 Met Tyr Lys Glu Tyr Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln 40 Met Tyr Thr Glu Met Ala Ser Arg His Arg Val Arg Phe Pro Cys Ile 60 55 Gln Ile Ile Lys Thr Ala Thr Val Pro Ala Ser Leu 70 (2) INFORMATION FOR SEQ ID NO:750: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..527 (D) OTHER INFORMATION: / Ceres Seq. ID 1593459 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:750: atcaaacaat acacttaaca atggattett etetgaaaac teaggaacet caagtagtgg aaacttctcc ttctccggta gctcaggagc ctcctcaagt agctgacaaa cctgcgattg 120 180 ttccttctcc gatagctcaa gagccagaca acgatgtccc ggcgccggga aacgagtttg ctgagttcgc cgccggttgt ttctggggag tggagcttgc tttccagaga atccctggcg 240 tgaccgtgac tgaggtcggt tacactcatg ggatctctca caatccgtct tatgaagatg tctgtacgaa caccacgaac catgcagaag ttgtcagggt tcaatatgat cctaangaat gcacttatga gacacttctt gatttgtttt ggtctagaca taatcctacc accttgaatc 420 gtcagggaga acttttagga gcacaatacc gatcaggtat atacttctac acaccggagc aagagaaact agcacgcgag tototagaga agagcagaaa aaactgg (2) INFORMATION FOR SEQ ID NO:751: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 175 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..175 (D) OTHER INFORMATION: / Ceres Seq. ID 1593460 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:751: Gln Thr Ile His Leu Thr Met Asp Ser Ser Leu Lys Thr Gln Glu Pro 10 5 Gln Val Val Glu Thr Ser Pro Ser Pro Val Ala Gln Glu Pro Pro Gln 25 20 Val Ala Asp Lys Pro Ala Ile Val Pro Ser Pro Ile Ala Gln Glu Pro 40 Asp Asn Asp Val Pro Ala Pro Gly Asn Glu Phe Ala Glu Phe Ala Ala 55 Gly Cys Phe Trp Gly Val Glu Leu Ala Phe Gln Arg Ile Pro Gly Val 75 70

Thr Val Thr Glu Val Gly Tyr Thr His Gly Ile Ser His Asn Pro Ser

180

240

85 90 Tyr Glu Asp Val Cys Thr Asn Thr Thr Asn His Ala Glu Val Val Arg 105 100 Val Gln Tyr Asp Pro Xaa Glu Cys Thr Tyr Glu Thr Leu Leu Asp Leu 120 125 115 Phe Trp Ser Arg His Asn Pro Thr Thr Leu Asn Arg Gln Gly Glu Leu 135 140 Leu Gly Ala Gln Tyr Arg Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln 150 155 Glu Lys Leu Ala Arg Glu Ser Leu Glu Lys Ser Arg Lys Asn Trp 165 170 (2) INFORMATION FOR SEQ ID NO:752: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..169 (D) OTHER INFORMATION: / Ceres Seq. ID 1593461 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:752: Met Asp Ser Ser Leu Lys Thr Gln Glu Pro Gln Val Val Glu Thr Ser 5 10 Pro Ser Pro Val Ala Gln Glu Pro Pro Gln Val Ala Asp Lys Pro Ala 30 25 Ile Val Pro Ser Pro Ile Ala Gln Glu Pro Asp Asn Asp Val Pro Ala 40 45 Pro Gly Asn Glu Phe Ala Glu Phe Ala Ala Gly Cys Phe Trp Gly Val 55 60 Glu Leu Ala Phe Gln Arg Ile Pro Gly Val Thr Val Thr Glu Val Gly 70 75 Tyr Thr His Gly Ile Ser His Asn Pro Ser Tyr Glu Asp Val Cys Thr 90 Asn Thr Thr Asn His Ala Glu Val Val Arg Val Gln Tyr Asp Pro Xaa 110 100 105 Glu Cys Thr Tyr Glu Thr Leu Leu Asp Leu Phe Trp Ser Arg His Asn 120 125 Pro Thr Thr Leu Asn Arg Gln Gly Glu Leu Leu Gly Ala Gln Tyr Arg 135 140 Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu 150 155 Ser Leu Glu Lys Ser Arg Lys Asn Trp 165 (2) INFORMATION FOR SEQ ID NO:753: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..533 (D) OTHER INFORMATION: / Ceres Seq. ID 1593489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753: ctagtctagt catttctcag actctgacct cactgatctc caatggcgaa aaccctagct cgctccacag cgtcacgcat caccaagcgc ttattctcca cctccggagc caccactcct tccccttctt atatcctctc ccgtcgatca accccggtgt tctcccatgc cgtcggatca atctcttcct tgaatcgttt cacaacgatt cgaactcgaa tggataggtc cggtggatcg

tactctcctc taaaatccgg ttcgaatttc agcgaccgag cacccactga gatggcgccg 300 ttgtttcctg gctgcgatta tgagcattgg ttgattgtaa tggacaaacc tggaggcgaa 360 aacgctacta agcagcaaat gattgattgt tatgttcaaa ccctagctaa aattatcggc agtgaggaag aagctaagaa gaagatttat aatgtatcgt gtgaaaggta ttttggattt 480 ggttgtgaga ttgatgaaga gacatcaaac aaaacttgaa ggacttcctg gtg

- (2) INFORMATION FOR SEQ ID NO:754:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..158
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593490
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

Met Ala Lys Thr Leu Ala Arg Ser Thr Ala Ser Arg Ile Thr Lys Arg 1 10 15

Leu Phe Ser Thr Ser Gly Ala Thr Thr Pro Ser Pro Ser Tyr Ile Leu 20 25 30

Ser Arg Arg Ser Thr Pro Val Phe Ser His Ala Val Gly Phe Ile Ser

Ser Leu Asn Arg Phe Thr Thr Ile Arg Thr Arg Met Asp Arg Ser Gly 50 60

Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn Phe Ser Asp Arg Ala 65 70 75 80

Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys Asp Tyr Glu His Trp 85 90 95

Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn Ala Thr Lys Gln Gln
100 105 110

Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys Ile Ile Gly Ser Glu 115 120 125

Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser Cys Glu Arg Tyr Phe 130 135 140

Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser Asn Lys Thr 145 150 155

- (2) INFORMATION FOR SEQ ID NO:755:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

Met Asp Arg Ser Gly Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn 1 5 10

Phe Ser Asp Arg Ala Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys 20 25 30

Asp Tyr Glu His Trp Leu Ile Val Met Asp Lys Pro Gly Glu Asn 35 40 45

Ala Thr Lys Gln Gln Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys 50 55 60

Ile Ile Gly Ser Glu Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser 65 70 75 80

Cys Glu Arg Tyr Phe Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser 85 90 95

Asn Lys Thr

- (2) INFORMATION FOR SEQ ID NO:756:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..498
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593502
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

atggaattgg atcttacctc ttttgatctc ttctctcctc atctccttcg tcgctttcta 60 tggattette ttgaaacega ageggaatag teteegteae gateggaaaa etgtttetae 120 cgtcacttcc gacgtcggat ctgttaatat taccggagat accgtcgctg atgtcattgt 180 tgttggaget ggtgttgctg gttctgctct tgcttatact cttggaaagg ataaacgccg 240 300 agttcatgtg attgaaagag atttatcgga gcctgatcgt atcgttgggg agttgttaca gcctgggggt tatctcaagt tactggagtt gggaattgaa ggtaaggaag attttgtaga 360 gaatccgtag gggactattc tcacctctat tgtgctctgt agttatttac tagataatga 420 cattaaggta aaagacagta cetgtgagaa aacagacgca tgtgctcatt gtttttcttc 480 attagtcatt ctaatctc

- (2) INFORMATION FOR SEQ ID NO:757:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593503
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

Trp Asn Trp Ile Leu Pro Leu Leu Ile Ser Ser Leu Leu Ile Ser Phe 10

Val Ala Phe Tyr Gly Phe Phe Leu Lys Pro Lys Arg Asn Ser Leu Arg 25 20

His Asp Arg Lys Thr Val Ser Thr Val Thr Ser Asp Val Gly Ser Val 40

Asn Ile Thr Gly Asp Thr Val Ala Asp Val Ile Val Val Gly Ala Gly 55

Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly Lys Asp Lys Arg Arg 75 70

Val His Val Ile Glu Arg Asp Leu Ser Glu Pro Asp Arg Ile Val Gly 90 85

Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Leu Glu Leu Gly Ile 105 100

Glu Gly Lys Glu Asp Phe Val Glu Asn Pro 120 115

- (2) INFORMATION FOR SEQ ID NO:758:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501

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(xi) SEQUENCE atggcggaaa ggttct accaccaccg ttagca ccaacatcct cgcagc ttcctccttg gtgtaa atcatcatct cgagtc gtctccggat ttcttg ggaatgcacc cggttg gcatctcacg tcaaag gatgcggcc ctggtg (2) INFORMATION F	OR SEQ ID NO:759:	attca 120 acctc 180 cattg 240 aacg 300 accgg 360 acacg 420							
<pre>(i) SEQUENCE CHARACTERISTICS:</pre>									
1 Ser Thr Ala T	The Ser Ser Gly Glu Ala Gln Tyr Trp Pro Asn To 10 15 Thr Thr Thr Val Ser Asn Ser Pro Ile Ser Ser For 30								
20 Phe His Gln Leu A 35	25 30 arg Ser His Ser Pro Thr Ser Ser Gln Leu Phe (40 45	Gly							
50	he Ile Ser Thr Gly Ile Leu Leu Phe Leu Leu 6 55 60								
65	Ala Ala Val Leu Gly Phe Ile Val Phe Leu Pro I 70 75 Ser Pro Ile Trp Ile Pro Val Phe Val Val Val	80							
8	95 Val Ser Gly Phe Leu Val Gly Thr Val Ala Leu V								
100	110 Arg Tyr Phe Arg Gly Met His Pro Val Gly Ser A								
115 Gln Met Asp Tyr A	120 125 Ala Arg Ser Arg Ile Tyr Asp Thr Ala Ser His ' 135 140								
145 Asp Ala Ala Pro (Arg Glu Tyr Gly Gly Tyr Phe His Gly Arg Ala 150 155 Gly Ala	Lys 160							
(2) INFORMATION 1	165 FOR SEQ ID NO:760: E CHARACTERISTICS:								

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..693
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593608
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

 cggttttaat cggtgccttg tgtttcacgg cctacaagaa gaaacaagga tatcaaggag
 gcgactctca cacatcaagt tggcttccta tatatggaaa ctctaccaca tcaggaacca
 aatcaaccat ctcagggaag agcaacaatg gaagtcacct atccaatctc gcagcaggtt
 tatgccgtag attctcttta ccagaaatca aacacggaac acaaaacttc gatgattcca
 240

acgtcattgg agttggaggg tttggtaaag tctacaaagg agttatagac ggcacaacta 300 aagtagcggt aaaaaatca aacccaaatt cagaacaagg actcaacgaa ttcgagacag 360 aaatcgaact cctctcaaga ctaagacaca aacacttagt ctccttgata ggatactgcg 420 acgagggagg agaaatgtgt ctcgtatacg attacatggc atttggaaca ctccgtgagc atctatacaa cacaaagaaa ccacaattaa cttggaaacg aaggctagag atagctattg 340 gagcagcaag aggattacat taccttcaca caggagcaaa gtacacgatt atacacagag 600 acgttaaaac aactagacct aacatgaatg gag

- (2) INFORMATION FOR SEQ ID NO:761:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..230
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593609
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:
- Val Leu Ile Gly Ala Leu Cys Phe Thr Ala Tyr Lys Lys Gln Gly
 1 5 10 15
- Tyr Gln Gly Gly Asp Ser His Thr Ser Ser Trp Leu Pro Ile Tyr Gly
 20 25 30
- Asn Ser Thr Thr Ser Gly Thr Lys Ser Thr Ile Ser Gly Lys Ser Asn 35 40 45
- Asn Gly Ser His Leu Ser Asn Leu Ala Ala Gly Leu Cys Arg Arg Phe 50 55 60
- Ser Leu Pro Glu Ile Lys His Gly Thr Gln Asn Phe Asp Asp Ser Asn 65 70 75 80
- Val Ile Gly Val Gly Gly Phe Gly Lys Val Tyr Lys Gly Val Ile Asp 85 90 95
- Gly Thr Thr Lys Val Ala Val Lys Lys Ser Asn Pro Asn Ser Glu Gln 100 105 110
- Gly Leu Asn Glu Phe Glu Thr Glu Ile Glu Leu Leu Ser Arg Leu Arg 115 120 125
- His Lys His Leu Val Ser Leu Ile Gly Tyr Cys Asp Glu Gly Glu 130 135 140
- Met Cys Leu Val Tyr Asp Tyr Met Ala Phe Gly Thr Leu Arg Glu His 145 . 150 . 150 . 155 . 160 Leu Tyr Asn Thr Lys Lys Pro Gln Leu Thr Trp Lys Arg Arg Leu Glu
- 165 170 175

 Ile Ala Ile Gly Ala Ala Arg Gly Leu His Tyr Leu His Thr Gly Ala
- Ile Ala Ile Gly Ala Ala Arg Gly Leu His Tyr Leu His Thr Gly Ala 180 185 190 Lys Tyr Thr Ile Ile His Arg Asp Val Lys Thr Thr Asn Ile Leu Val
- 195 200 205
 Asp Glu Asn Trp Val Ala Lys Val Ser Asp Phe Gly Leu Ser Lys Thr

220

- Gly Pro Asn Met Asn Gly
- 225 230
- (2) INFORMATION FOR SEQ ID NO:762:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1139 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1139
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762: tctcaaaaca aacttcttta acttccctaa aggtaaacct tttactgatc ttcttggtga 60 tcttctcggt ggaggcatat tcaatgtcga cggtcactca tggagctcgc agcgcaaact 120 cgctagccac gagttctcca ctcgctcgct taggagtttt gcttttgagg ttcttaaaga 180 cgaagtggag aaccgtctag tcccggttct atccacggcg gctgatgttg gtacgaccgt 240 ggatttgcaa gatgttttga aacgttttgc ttttgatgtt gtttgtaaag tctcgttggg 300 ttgggatccg gattgtttgg atctaacccg acccgttaat ccacttgtgg aggcttttga 360 caccgctgct gagattagtg ctcgccgtgc cacggagcct atttacgctg tttggaaaac 420 gaaacgtgtg ttgaacgtgg gaagcgagag gacgcttagg gaagcgatca ggaccgtaca 480 540 cgtgttggtc tctgagattg tcagagctaa gaagaaaagt cttgagatcg gaaccggagc 600 agaagcaaag caagatettt tgtegaggtt tetaneegee ggeeacaaeg gegaageagt 660 gagggacatg gttattagtt ttatcatggc gggaagagat acaacgtcag cagcgatgac gtggctgttt tggttgttga ctgagaacga tgacgtggag aggaagattt tagaagaagt 720 gaacccgttg ctgagtttag ggttagagtt tgaggatttg aaagagatga cttacacgaa 780 840 ggcttgtcta tgtgaagcca tgaggcttta tcctcctgtg tcgtgggact caaagcatgc 900 tgcaaacgac gacgttttac cagatgggac acatgtcaag aaaggagaca aagtgacata 960 tttcccatac ggtatgggga ggatggagac gctatggggg gcggattcag aagaatttaa accgaaccgg tggtttgatt ctgaaccggg gtgtacacga ccggttttga aacctattag 1020 1080 tccttacaaa ttttctgttt ttcaagccgg accaagagtt tgtgtaggga aagagatggc gtttatgcag atgaaattcg tcgttggttc tgttttgagt cggtttgaga ttaagccgg

- (2) INFORMATION FOR SEQ ID NO:763:
 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..379
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593623
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

Leu Lys Thr Asn Phe Phe Asn Phe Pro Lys Gly Lys Pro Phe Thr Asp 1 10 15

Leu Leu Gly Asp Leu Leu Gly Gly Gly Ile Phe Asn Val Asp Gly His 20 25 30

Ser Trp Ser Ser Gln Arg Lys Leu Ala Ser His Glu Phe Ser Thr Arg 35 40 45

Ser Leu Arg Ser Phe Ala Phe Glu Val Leu Lys Asp Glu Val Glu Asn 50 55 60

Arg Leu Val Pro Val Leu Ser Thr Ala Ala Asp Val Gly Thr Thr Val 65 70 75 80

Asp Leu Gln Asp Val Leu Lys Arg Phe Ala Phe Asp Val Val Cys Lys 85 90 95

Val Ser Leu Gly Trp Asp Pro Asp Cys Leu Asp Leu Thr Arg Pro Val 100 105 110

Asn Pro Leu Val Glu Ala Phe Asp Thr Ala Ala Glu Ile Ser Ala Arg
115 120 125

Arg Ala Thr Glu Pro Ile Tyr Ala Val Trp Lys Thr Lys Arg Val Leu 130 135 140

Asn Val Gly Ser Glu Arg Thr Leu Arg Glu Ala Ile Arg Thr Val His 145 150 155 160

Val Leu Val Ser Glu Ile Val Arg Ala Lys Lys Lys Ser Leu Glu Ile

165
170
175
Clu Mba Clu Ala Clu Ala Lys Cla Asa Leu Ser Arg Phe Leu Xaa

Gly Thr Gly Ala Glu Ala Lys Gln Asp Leu Leu Ser Arg Phe Leu Xaa 180 185 190

Ala Gly His Asn Gly Glu Ala Val Arg Asp Met Val Ile Ser Phe Ile
195 200 205

Met Ala Gly Arg Asp Thr Thr Ser Ala Ala Met Thr Trp Leu Phe Trp

210 215 220 Leu Leu Thr Glu Asn Asp Asp Val Glu Arg Lys Ile Leu Glu Glu Val

```
225
                    230
                                         235
Asn Pro Leu Leu Ser Leu Gly Leu Glu Phe Glu Asp Leu Lys Glu Met
                                    250
                245
Thr Tyr Thr Lys Ala Cys Leu Cys Glu Ala Met Arg Leu Tyr Pro Pro
                                265
                                                     270
            260
Val Ser Trp Asp Ser Lys His Ala Ala Asn Asp Asp Val Leu Pro Asp
                            280
                                                 285
        275
Gly Thr His Val Lys Lys Gly Asp Lys Val Thr Tyr Phe Pro Tyr Gly
                                             300
                        295
Met Gly Arg Met Glu Thr Leu Trp Gly Ala Asp Ser Glu Glu Phe Lys
                                         315
                    310
Pro Asn Arg Trp Phe Asp Ser Glu Pro Gly Cys Thr Arg Pro Val Leu
                325
                                    330
Lys Pro Ile Ser Pro Tyr Lys Phe Ser Val Phe Gln Ala Gly Pro Arg
                                                     350
                                345
            340
Val Cys Val Gly Lys Glu Met Ala Phe Met Gln Met Lys Phe Val Val
                            360
                                                 365
Gly Ser Val Leu Ser Arg Phe Glu Ile Lys Pro
    370
                        375
```

- (2) INFORMATION FOR SEQ ID NO:764:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1368
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593641
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:764: atgccgataa aggtattgtc gtcgcttgat gtagctcgaa cacaatggta ccatttcaaa gcgatcatag tagcgggaat gggtctattc accgacgcat acgatctttt ctgcatagca 120 180 ccggtcatga aaatgattag tcatgtttat tacaacggta tcggtggtga ttacccgctc 240 teggetacea ttatgtegga gtttgetaat aagaggaeae gtggegegtt tategetgeg 300 gtgttttcga tgcaagggtt ggggattttg gttagctctg ccgtgaccat ggctgtttgc gtggcgttta agagaagtgg cggtggtttg gaggtggatg cggcggctcc gacggaagct 360 gacttggcct ggagacttat acttatgatc ggtgctcttc ctgctgcatt gacgttctat 420 tggcgaatgt tgatgcctga aaccgcaaga tacacagcac ttgtagaaaa caatatcgtc 480 caagcaqcaa aagacatgca aagagtcatg tcaagatctc atatctccga cgaagccacg 540 600 acqqatccac etectectec geogecacet tectacaaac tetteteceg etgettette 660 cgcctccatg gtcgcgacct cttcgcagcc tcctttaatt ggttcctagt agacattgtc 720 ttctacacaa gcaacctcct cctgtcccat atcttcagtc attactccaa gaaaccttcc 780 actgcagaaa acgtctacga cgcagccttt gaagtggcgg aattaggagc catcatcgct gettgeteca ceatteegg ttattggtte acagtttact teategacaa gataggtegt 840 900 gtcaaaatcc agattatggg gtttttcttc atggccgtta tttatttagt cgctggtatt ccgtacagtt ggtattggtc aaagcacgag cataataata aaggcttcat ggttctctac 960 ggtttggttt tcttcttttg caattttggt cccaacacta caacttttat tattcccgca 1020 gagcatttcc cggctaggtt taggtctact tgtcacggga tctctggtgc cgcgggtaag 1080 cttggggcta ttgtgggcac tgttgggttc ttgtgggcta ccaagaagat ggaaagcgat 1140 gataaaaacc agatttatcc cgaagtaaac cgtatgagaa ttgctttctt gattcttggt 1200 ggcgtttgca ttgctggaat cttggtgacg tatttcttca ccaaggaaac tatgggaaga 1260 tcgttagagg agaacgagca tgaccaagat aacaatgctg agtctgaaga tgagccacag 1320 attgttgact ggcaatcctc cgtgagcact ttgcttcaga cacgatga
- (2) INFORMATION FOR SEQ ID NO:765:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765: Met Pro Ile Lys Val Leu Ser Ser Leu Asp Val Ala Arg Thr Gln Trp 10 Tyr His Phe Lys Ala Ile Ile Val Ala Gly Met Gly Leu Phe Thr Asp 25 Ala Tyr Asp Leu Phe Cys Ile Ala Pro Val Met Lys Met Ile Ser His 40 Val Tyr Tyr Asn Gly Ile Gly Gly Asp Tyr Pro Leu Ser Ala Thr Ile 55 Met Ser Glu Phe Ala Asn Lys Arg Thr Arg Gly Ala Phe Ile Ala Ala 70 75 Val Phe Ser Met Gln Gly Leu Gly Ile Leu Val Ser Ser Ala Val Thr 90 Met Ala Val Cys Val Ala Phe Lys Arg Ser Gly Gly Gly Leu Glu Val 100 105 Asp Ala Ala Pro Thr Glu Ala Asp Leu Ala Trp Arg Leu Ile Leu 120 Met Ile Gly Ala Leu Pro Ala Ala Leu Thr Phe Tyr Trp Arg Met Leu 135 140 Met Pro Glu Thr Ala Arg Tyr Thr Ala Leu Val Glu Asn Asn Ile Val 150 155 Gln Ala Ala Lys Asp Met Gln Arg Val Met Ser Arg Ser His Ile Ser 170 165 Asp Glu Ala Thr Thr Asp Pro Pro Pro Pro Pro Pro Pro Pro Ser Tyr 180 185 Lys Leu Phe Ser Arg Cys Phe Phe Arg Leu His Gly Arg Asp Leu Phe 200 205 Ala Ala Ser Phe Asn Trp Phe Leu Val Asp Ile Val Phe Tyr Thr Ser 215 220 Asn Leu Leu Ser His Ile Phe Ser His Tyr Ser Lys Lys Pro Ser 230 235 Thr Ala Glu Asn Val Tyr Asp Ala Ala Phe Glu Val Ala Glu Leu Gly 245 250 Ala Ile Ile Ala Ala Cys Ser Thr Ile Pro Gly Tyr Trp Phe Thr Val 265 260 Tyr Phe Ile Asp Lys Ile Gly Arg Val Lys Ile Gln Ile Met Gly Phe 280 Phe Phe Met Ala Val Ile Tyr Leu Val Ala Gly Ile Pro Tyr Ser Trp 295 Tyr Trp Ser Lys His Glu His Asn Asn Lys Gly Phe Met Val Leu Tyr 310 315 Gly Leu Val Phe Phe Phe Cys Asn Phe Gly Pro Asn Thr Thr Thr Phe 325 330 Ile Ile Pro Ala Glu His Phe Pro Ala Arg Phe Arg Ser Thr Cys His 345 340 Gly Ile Ser Gly Ala Ala Gly Lys Leu Gly Ala Ile Val Gly Thr Val 360 Gly Phe Leu Trp Ala Thr Lys Lys Met Glu Ser Asp Asp Lys Asn Gln 380 375 Ile Tyr Pro Glu Val Asn Arg Met Arg Ile Ala Phe Leu Ile Leu Gly 395 390 Gly Val Cys Ile Ala Gly Ile Leu Val Thr Tyr Phe Phe Thr Lys Glu 410 405 Thr Met Gly Arg Ser Leu Glu Glu Asn Glu His Asp Gln Asp Asn Asn 430 425 Ala Glu Ser Glu Asp Glu Pro Gln Ile Val Asp Trp Gln Ser Ser Val

Ser Thr Leu Leu Gln Thr Arg 450 455

- (2) INFORMATION FOR SEQ ID NO:766:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..429
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593644
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:
- Met Gly Leu Phe Thr Asp Ala Tyr Asp Leu Phe Cys Ile Ala Pro Val 1 5 10 15
- Met Lys Met Ile Ser His Val Tyr Tyr Asn Gly Ile Gly Gly Asp Tyr 20 25 30
- Pro Leu Ser Ala Thr Ile Met Ser Glu Phe Ala Asn Lys Arg Thr Arg
- Gly Ala Phe Ile Ala Ala Val Phe Ser Met Gln Gly Leu Gly Ile Leu 50 55 60
- Val Ser Ser Ala Val Thr Met Ala Val Cys Val Ala Phe Lys Arg Ser 65 70 75 80
- Gly Gly Leu Glu Val Asp Ala Ala Ala Pro Thr Glu Ala Asp Leu
 85 90 95
- Ala Trp Arg Leu Ile Leu Met Ile Gly Ala Leu Pro Ala Ala Leu Thr $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$
- Phe Tyr Trp Arg Met Leu Met Pro Glu Thr Ala Arg Tyr Thr Ala Leu 115 120 125
- Val Glu Asn Asn Ile Val Gln Ala Ala Lys Asp Met Gln Arg Val Met 130 135 140
- Ser Arg Ser His Ile Ser Asp Glu Ala Thr Thr Asp Pro Pro Pro 145 150 155 160
- Pro Pro Pro Pro Ser Tyr Lys Leu Phe Ser Arg Cys Phe Phe Arg Leu
 165 170 175
- His Gly Arg Asp Leu Phe Ala Ala Ser Phe Asn Trp Phe Leu Val Asp
 180
 185
 190
- Ile Val Phe Tyr Thr Ser Asn Leu Leu Ser His Ile Phe Ser His 195 200 205
- Tyr Ser Lys Lys Pro Ser Thr Ala Glu Asn Val Tyr Asp Ala Ala Phe 210 215 220
- Glu Val Ala Glu Leu Gly Ala Ile Ile Ala Ala Cys Ser Thr Ile Pro
 225 230 235 240
- Gly Tyr Trp Phe Thr Val Tyr Phe Ile Asp Lys Ile Gly Arg Val Lys 245 250 255
- Ile Gln Ile Met Gly Phe Phe Phe Met Ala Val Ile Tyr Leu Val Ala 260 265 270
- Gly Ile Pro Tyr Ser Trp Tyr Trp Ser Lys His Glu His Asn Asn Lys 275 280 285
- Gly Phe Met Val Leu Tyr Gly Leu Val Phe Phe Phe Cys Asn Phe Gly 290 295 300
- Pro Asn Thr Thr Phe Ile Ile Pro Ala Glu His Phe Pro Ala Arg 305 310 315 320
- Phe Arg Ser Thr Cys His Gly Ile Ser Gly Ala Ala Gly Lys Leu Gly
 325 330 335
- Ala Ile Val Gly Thr Val Gly Phe Leu Trp Ala Thr Lys Lys Met Glu 340 345 350
- Ser Asp Asp Lys Asn Gln Ile Tyr Pro Glu Val Asn Arg Met Arg Ile 355 360 365

 Ala Phe Leu Ile Leu Gly Gly Val Cys Ile Ala Gly Ile Leu Val Thr

375 370 Tyr Phe Phe Thr Lys Glu Thr Met Gly Arg Ser Leu Glu Glu Asn Glu 395 390 His Asp Gln Asp Asn Asn Ala Glu Ser Glu Asp Glu Pro Gln Ile Val 405 410 Asp Trp Gln Ser Ser Val Ser Thr Leu Leu Gln Thr Arg 425 420 (2) INFORMATION FOR SEQ ID NO:767: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 501 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593649
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767: 60 atgccgataa aggtattgtc gtcgcttgat gtagctcgaa cacaatggta ccatttcaaa gcgatcatag tagcgggaat gggtctattc accgacgcat acgatctttt ctgcatagca 120 ccggtcatga aaatgattag tcatgtttat tacaacggta tcggtggtga ttacccgctc 180 teggetacea ttatgtegga gtttgetaat aagaggaeae gtggegegtt tategetgeg 240 gtgttttcga tgcaagggtt ggggattttg gttagctctg ccgtgaccat ggctgtttgc 300 gtggcgttta agagaagtgg cggtggtttg gaggtggatg cggcggctcc gacggaagct 360 gacttggcct ggagacttat acttatgatc ggtgctcttc ctgctgcatt gacgttctat 420 tggcgaatgt tgatgcctga aaccgcaagg tatcagatcc tatcagctcc agctaatcaa 480 ccaaatacac agcacttgta g
- (2) INFORMATION FOR SEQ ID NO:768:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593650
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

Met Pro Ile Lys Val Leu Ser Ser Leu Asp Val Ala Arg Thr Gln Trp 5 10 Tyr His Phe Lys Ala Ile Ile Val Ala Gly Met Gly Leu Phe Thr Asp 20 25

Ala Tyr Asp Leu Phe Cys Ile Ala Pro Val Met Lys Met Ile Ser His 40

Val Tyr Tyr Asn Gly Ile Gly Gly Asp Tyr Pro Leu Ser Ala Thr Ile 55

Met Ser Glu Phe Ala Asn Lys Arg Thr Arg Gly Ala Phe Ile Ala Ala 75 70

Val Phe Ser Met Gln Gly Leu Gly Ile Leu Val Ser Ser Ala Val Thr 90 85

Met Ala Val Cys Val Ala Phe Lys Arg Ser Gly Gly Leu Glu Val 105 100

Asp Ala Ala Aro Thr Glu Ala Asp Leu Ala Trp Arg Leu Ile Leu 120 125

Met Ile Gly Ala Leu Pro Ala Ala Leu Thr Phe Tyr Trp Arg Met Leu 140 135

Met Pro Glu Thr Ala Arg Tyr Gln Ile Leu Ser Ala Pro Ala Asn Gln 150 155 Pro Asn Thr Gln His Leu

- (2) INFORMATION FOR SEQ ID NO:769:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593652
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

Met Gly Leu Phe Thr Asp Ala Tyr Asp Leu Phe Cys Ile Ala Pro Val 1 5 10 15

Met Lys Met Ile Ser His Val Tyr Tyr As
n Gly Ile Gly Gly Asp Tyr 20 2530

Pro Leu Ser Ala Thr Ile Met Ser Glu Phe Ala Asn Lys Arg Thr Arg 35 40 45

Gly Ala Phe Ile Ala Ala Val Phe Ser Met Gln Gly Leu Gly Ile Leu 50 60

Val Ser Ser Ala Val Thr Met Ala Val Cys Val Ala Phe Lys Arg Ser 65 70 75 80

Gly Gly Leu Glu Val Asp Ala Ala Pro Thr Glu Ala Asp Leu 85 90 95

Ala Trp Arg Leu Ile Leu Met Ile Gly Ala Leu Pro Ala Ala Leu Thr $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Phe Tyr Trp Arg Met Leu Met Pro Glu Thr Ala Arg Tyr Gln Ile Leu 115 120 125

Ser Ala Pro Ala Asn Gln Pro Asn Thr Gln His Leu 130 135 140

- (2) INFORMATION FOR SEQ ID NO:770:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..462
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593663
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

tegtttggag ttggteetat tgatgegett tttggaggtg gaaacttace aggatttgtg
gteggageta ttgeagegge aattageagt gttgtggeat ttacegttet tacaatagaa 120
actttgeact atgtgatte agetggagte gtegeegetg tgaggaacat cataggatae 180
geatteagea acageaaaga agttttggae tatgtegeeg acetaactee tttgetetge
cteteettta teetegaegg etttacagea gttettaatg ggattgetag gggaagtget 300
cteagtegtg agttgaaegg aaaaggattg tggtgeggtg ttgtggttgg atetaetgtg 360
caageeacta tactggetat tgteaeaget teeataaatt ggaaggaaea ggetgagaag 420
geaaggaaga gaattgtee aactgaaaat agattggett aa

- (2) INFORMATION FOR SEQ ID NO:771:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153

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(D) OTHER INFORMATION: / Ceres Seq. ID 1593664
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:
Ser Phe Gly Val Gly Pro Ile Asp Ala Leu Phe Gly Gly Asn Leu
                                    10
Pro Gly Phe Val Val Gly Ala Ile Ala Ala Ile Ser Ser Val Val
                                25
            20
Ala Phe Thr Val Leu Thr Ile Glu Thr Leu His Tyr Val Ile Ser Ala
                            40
Gly Val Val Ala Ala Val Arg Asn Ile Ile Gly Tyr Ala Phe Ser Asn
                        55
                                            60
Ser Lys Glu Val Leu Asp Tyr Val Ala Asp Leu Thr Pro Leu Leu Cys
                                        75
                    70
Leu Ser Phe Ile Leu Asp Gly Phe Thr Ala Val Leu Asn Gly Ile Ala
                                    90
                85
Arg Gly Ser Ala Phe Ser Arg Glu Leu Asn Gly Lys Gly Leu Trp Cys
            100
                                105
Gly Val Val Val Gly Ser Thr Val Gln Ala Thr Ile Leu Ala Ile Val
                                                125
                            120
Thr Ala Ser Ile Asn Trp Lys Glu Gln Ala Glu Lys Ala Arg Lys Arg
                        135
                                            140
Ile Val Ser Thr Glu Asn Arg Leu Ala
                    150
(2) INFORMATION FOR SEQ ID NO:772:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1422 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..1422
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593707
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:
atggcggaaa actacaatta tggcggtagt ggcggttttt ttatcgagat tggatccgaa
                                                                        60
                                                                       120
tacqtcqcaq qagttgagca attcatgaca tttgctaata gtcagcctat agtacagagt
agtcaaagta aatttcattg tccttgtggt gtatgcaaga atgaaaaaca catcatctcg
                                                                       180
ggcagaagag ttagtagtca tttgtttagt gaggaattta tgcctgatta ttatgtttgg
                                                                       240
tataaqcatg gagaagaaat gaatattgat ataggaacga gttccatgga taggacgtat
                                                                       300
                                                                       360
tttagttcga atcatgaaga agtgggtaat gttgtagaag atccatatgt ggatatggtg
                                                                       420
aacqatqcat ttaattttaa cgtggggtat gatgataact atcatcatga tgatagttat
                                                                       480
cagaatgtgg aagaaccggt ctataaccat ttaaacaagt tctacgactt gttagaaggt
                                                                       540
qcaaataatc catcgtacga tgattgtcgt gaagagcagt cgcagttatc cttagcatct
cqactcatqc acaacaaqqc agagtataat atgagtgaaa agttggtgga ctccatttgc
                                                                       600
gaaatgttta cagatttttt accagaagga aaccaggeta caacttcaca ttaccagatc
                                                                       660
                                                                       720
qagaaqttga tgcgtaattt aggacttcca tatcatacga ttgatgtttg tcagaataat
tgtatgctat tttggaaaga agacgaaaaa gaagatcaat gtcgattttg tggcgcacaa
                                                                       780
agatggaagc ctgaggacga ccgtcgaaga accaaagtac catatagtcg tatgtggtat
                                                                       840
ctacctattg gagaccggtt gaagagaatg tatcagagcc ataagacagc tgcggtaatg
                                                                       900
cgatggcatg ttgagcacca atcaaaggag ggagaaatga ataatccttt agatgcagtg
                                                                       960
gagtggagat atttccaaga gttacatccc cggtttgccg aagaaccccg taacgtttat
                                                                      1020
ctcgggttgt gtactgatgg gttcaatcca tttggcatgt ctcgtaatca ttcgttgtgg
                                                                      1080
                                                                      1140
cctqtqatcc tqaatccata taatttaccc cctqtcctaa gcgaacatgc agaaaacaga
agcaataaca gaattactaa aatcactcga ccacaacagg ctgatgncag aagtaggatg
                                                                      1200
                                                                      1260
tggtcgagta acaggtcgag taatagacag gatacgaaac agctatactc gactgcacag
tctgttgcca gacactgggt gtggtcgaag tggtgcccta gcctattcga atggttaaca
                                                                      1320
                                                                      1380
agcgcaatca agctatccct agacaacagg ttcaacaaca gaccaattca ctcccgtgat
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- (2) INFORMATION FOR SEQ ID NO:773:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 amino acids

agaaatcctc aagcaaagct agcccagact aattcccatt aa

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593708 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:773: Met Ala Glu Asn Tyr Asn Tyr Gly Gly Ser Gly Gly Phe Phe Ile Glu 10 Ile Gly Ser Glu Tyr Val Ala Gly Val Glu Gln Phe Met Thr Phe Ala 25 Asn Ser Gln Pro Ile Val Gln Ser Ser Gln Ser Lys Phe His Cys Pro 40 Cys Gly Val Cys Lys Asn Glu Lys His Ile Ile Ser Gly Arg Arg Val 55 Ser Ser His Leu Phe Ser Glu Glu Phe Met Pro Asp Tyr Tyr Val Trp 70 75 Tyr Lys His Gly Glu Glu Met Asn Ile Asp Ile Gly Thr Ser Ser Met 90 85 Asp Arg Thr Tyr Phe Ser Ser Asn His Glu Glu Val Gly Asn Val Val 100 105 110 Glu Asp Pro Tyr Val Asp Met Val Asn Asp Ala Phe Asn Phe Asn Val 115 120 125 Gly Tyr Asp Asp Asn Tyr His His Asp Asp Ser Tyr Gln Asn Val Glu 135 140 Glu Pro Val Tyr Asn His Leu Asn Lys Phe Tyr Asp Leu Leu Glu Gly 155 150 Ala Asn Asn Pro Ser Tyr Asp Asp Cys Arg Glu Glu Gln Ser Gln Leu 165 170 Ser Leu Ala Ser Arg Leu Met His Asn Lys Ala Glu Tyr Asn Met Ser 185 190 180 Glu Lys Leu Val Asp Ser Ile Cys Glu Met Phe Thr Asp Phe Leu Pro 200 205 Glu Gly Asn Gln Ala Thr Thr Ser His Tyr Gln Ile Glu Lys Leu Met 220 215 Arg Asn Leu Gly Leu Pro Tyr His Thr Ile Asp Val Cys Gln Asn Asn 235 230 Cys Met Leu Phe Trp Lys Glu Asp Glu Lys Glu Asp Gln Cys Arg Phe 245 250 Cys Gly Ala Gln Arg Trp Lys Pro Glu Asp Asp Arg Arg Thr Lys 265 Val Pro Tyr Ser Arg Met Trp Tyr Leu Pro Ile Gly Asp Arg Leu Lys 280 285 Arg Met Tyr Gln Ser His Lys Thr Ala Ala Val Met Arg Trp His Val 295 300 Glu His Gln Ser Lys Glu Gly Glu Met Asn Asn Pro Leu Asp Ala Val 310 315 Glu Trp Arg Tyr Phe Gln Glu Leu His Pro Arg Phe Ala Glu Glu Pro 330 335 Arg Asn Val Tyr Leu Gly Leu Cys Thr Asp Gly Phe Asn Pro Phe Gly 345 Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu Asn Pro Tyr Asn 360 365 Leu Pro Pro Val Leu Ser Glu His Ala Glu Asn Arg Ser Asn Asn Arg 375 380 Ile Thr Lys Ile Thr Arg Pro Gln Gln Ala Asp Xaa Arg Ser Arg Met 390 395 Trp Ser Ser Asn Arg Ser Ser Asn Arg Gln Asp Thr Lys Gln Leu Tyr

Ser Thr Ala Gln Ser Val Ala Arg His Trp Val Trp Ser Lys Trp Cys 420 425 430

Pro Ser Leu Phe Glu Trp Leu Thr Ser Ala Ile Lys Leu Ser Leu Asp 435 440 445

Asn Arg Phe Asn Asn Arg Pro Ile His Ser Arg Asp Arg Asn Pro Gln 450 455 460

Ala Lys Leu Ala Gln Thr Asn Ser His

- 165 470
- (2) INFORMATION FOR SEQ ID NO:774:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 445 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..445
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593710
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:
- Met Thr Phe Ala Asn Ser Gln Pro Ile Val Gln Ser Ser Gln Ser Lys
 1 5 10 15

Phe His Cys Pro Cys Gly Val Cys Lys Asn Glu Lys His Ile Ile Ser 20 25 30

Gly Arg Arg Val Ser Ser His Leu Phe Ser Glu Glu Phe Met Pro Asp 35 40 45

Tyr Tyr Val Trp Tyr Lys His Gly Glu Glu Met Asn Ile Asp Ile Gly 50 60

Thr Ser Ser Met Asp Arg Thr Tyr Phe Ser Ser Asn His Glu Glu Val 65 70 75 80

Gly Asn Val Val Glu Asp Pro Tyr Val Asp Met Val Asn Asp Ala Phe 85 90 95

Asn Phe Asn Val Gly Tyr Asp Asp Asn Tyr His His Asp Asp Ser Tyr 100 105 110

Gln Asn Val Glu Glu Pro Val Tyr Asn His Leu Asn Lys Phe Tyr Asp 115 120 125

Leu Leu Glu Gly Ala Asn Asn Pro Ser Tyr Asp Asp Cys Arg Glu Glu
130 135 140

Gln Ser Gln Leu Ser Leu Ala Ser Arg Leu Met His Asn Lys Ala Glu 145 150 155 160

Tyr Asn Met Ser Glu Lys Leu Val Asp Ser Ile Cys Glu Met Phe Thr
165 170 175

Asp Phe Leu Pro Glu Gly Asn Gln Ala Thr Thr Ser His Tyr Gln Ile 180 185 190

Glu Lys Leu Met Arg Asn Leu Gly Leu Pro Tyr His Thr Ile Asp Val 195 200 205

Cys Gln Asn Asn Cys Met Leu Phe Trp Lys Glu Asp Glu Lys Glu Asp 210 215 220

Gln Cys Arg Phe Cys Gly Ala Gln Arg Trp Lys Pro Glu Asp Asp Arg 225 230 235 240

Arg Arg Thr Lys Val Pro Tyr Ser Arg Met Trp Tyr Leu Pro Ile Gly 245 250 255

Asp Arg Leu Lys Arg Met Tyr Gln Ser His Lys Thr Ala Ala Val Met 260 265 270

Arg Trp His Val Glu His Gln Ser Lys Glu Gly Glu Met Asn Asn Pro

Leu Asp Ala Val Glu Trp Arg Tyr Phe Gln Glu Leu His Pro Arg Phe 290 295 300

Ala Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys Thr Asp Gly Phe 305 310 315 320
Asn Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu

```
330
                325
Asn Pro Tyr Asn Leu Pro Pro Val Leu Ser Glu His Ala Glu Asn Arg
                                                    350
                                345
            340
Ser Asn Asn Arg Ile Thr Lys Ile Thr Arg Pro Gln Gln Ala Asp Xaa
                            360
                                                365
Arg Ser Arg Met Trp Ser Ser Asn Arg Ser Ser Asn Arg Gln Asp Thr
                                            380
    370
                        375
Lys Gln Leu Tyr Ser Thr Ala Gln Ser Val Ala Arg His Trp Val Trp
                                        395
                    390
Ser Lys Trp Cys Pro Ser Leu Phe Glu Trp Leu Thr Ser Ala Ile Lys
               405
                                    410
                                                        415
Leu Ser Leu Asp Asn Arg Phe Asn Asn Arg Pro Ile His Ser Arg Asp
           420
                               425
Arg Asn Pro Gln Ala Lys Leu Ala Gln Thr Asn Ser His
                           440
        435
```

- (2) INFORMATION FOR SEQ ID NO:775:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..753
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593711
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775: gacttatata tggttgattc aattgtatcg ttcggtgttg aaaagctttg gaaactcctg 60 agccaagaat atgagcgatt ccagggagtt gaagagcaaa ttactgagct aagagatgat 120 180 ctgaagatgt taatggcctt tctatctgat gcagatgcaa agaaacaaac ccgtgccctt gcaagaaatt gcctcgaaga gataaaggaa atcacttatg atgctgagga tataatcgaa 240 acctttcttc taaaaggcag tggcaacaag agtcacatga gaagccttgc ttgctttcca 300 360 agtggtcgta gggagattgc cttgcaaatc acaagcatca gtaagaggat ctccaaggtt atccaactta tgcagacttt aggcataaaa tcagacatta tggacggtgt ggatttgcaa 420 gctcaactgg aaaggagaag ggagtcgcgt catacatttt ctagtgaatc tgagagcaat 480 540 cttgttggtt tggagaaaaa tgttgagaaa ttggttgaag aattggtggg aaacgatagc 600 agtcatgggg tatctattac tggtttgggt ggtcttggca aaaccaccct tgcacggcaa gtttttgatc atgataagat aaaaactcat tttgatggac ttgcgtgggt gtgtgtatca 660 caagagttta cacggaagga tgtgtggcag accattttgg ggcatcttag tcctgcagat 720 aaaqattcaa aattgccgga agacgatatt cag
- (2) INFORMATION FOR SEQ ID NO:776:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..251
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593712
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:
- Asp Leu Tyr Met Val Asp Ser Ile Val Ser Phe Gly Val Glu Lys Leu 1 5 10 15
- Trp Lys Leu Leu Ser Gln Glu Tyr Glu Arg Phe Gln Gly Val Glu Glu 20 25 30
- Gln Ile Thr Glu Leu Arg Asp Asp Leu Lys Met Leu Met Ala Phe Leu 35 40 45
- Ser Asp Ala Asp Ala Lys Lys Gln Thr Arg Ala Leu Ala Arg Asn Cys 50 55 60

 Leu Glu Glu Ile Lys Glu Ile Thr Tyr Asp Ala Glu Asp Ile Ile Glu

70 75 Thr Phe Leu Leu Lys Gly Ser Gly Asn Lys Ser His Met Arg Ser Leu 85 90 95 Ala Cys Phe Pro Ser Gly Arg Arg Glu Ile Ala Leu Gln Ile Thr Ser 100 105 110 Ile Ser Lys Arg Ile Ser Lys Val Ile Gln Leu Met Gln Thr Leu Gly 115 120 125 Ile Lys Ser Asp Ile Met Asp Gly Val Asp Leu Gln Ala Gln Leu Glu 130 135 140 Arg Arg Arg Glu Ser Arg His Thr Phe Ser Ser Glu Ser Glu Ser Asn 150 155 160 Leu Val Gly Leu Glu Lys Asn Val Glu Lys Leu Val Glu Glu Leu Val 170 175 165 Gly Asn Asp Ser Ser His Gly Val Ser Ile Thr Gly Leu Gly Gly Leu 190 180 185 Gly Lys Thr Thr Leu Ala Arg Gln Val Phe Asp His Asp Lys Ile Lys 200 205 Thr His Phe Asp Gly Leu Ala Trp Val Cys Val Ser Gln Glu Phe Thr 220 215 Arg Lys Asp Val Trp Gln Thr Ile Leu Gly His Leu Ser Pro Ala Asp 235 225 230 Lys Asp Ser Lys Leu Pro Glu Asp Asp Ile Gln 245

- (2) INFORMATION FOR SEQ ID NO:777:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..248
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593713
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:
- Met Val Asp Ser Ile Val Ser Phe Gly Val Glu Lys Leu Trp Lys Leu 1 5 10 15
- Leu Ser Gln Glu Tyr Glu Arg Phe Gln Gly Val Glu Glu Gln Ile Thr 20 25 30
- Glu Leu Arg Asp Asp Leu Lys Met Leu Met Ala Phe Leu Ser Asp Ala 35 40 45
- Asp Ala Lys Lys Gln Thr Arg Ala Leu Ala Arg Asn Cys Leu Glu Glu 50 55 60
- Ile Lys Glu Ile Thr Tyr Asp Ala Glu Asp Ile Ile Glu Thr Phe Leu 65 70 75 80
- Leu Lys Gly Ser Gly Asn Lys Ser His Met Arg Ser Leu Ala Cys Phe 85 90 95
- Pro Ser Gly Arg Arg Glu Ile Ala Leu Gln Ile Thr Ser Ile Ser Lys 100 105 110
- Arg Ile Ser Lys Val Ile Gln Leu Met Gln Thr Leu Gly Ile Lys Ser 115 120 125
- Asp Ile Met Asp Gly Val Asp Leu Gln Ala Gln Leu Glu Arg Arg Arg 130 135 140
- Glu Ser Arg His Thr Phe Ser Ser Glu Ser Glu Ser Asn Leu Val Gly 145 150 155 160
- Leu Glu Lys Asn Val Glu Lys Leu Val Glu Glu Leu Val Gly Asn Asp 165 170 175
- Ser Ser His Gly Val Ser Ile Thr Gly Leu Gly Gly Leu Gly Lys Thr
- Thr Leu Ala Arg Gln Val Phe Asp His Asp Lys Ile Lys Thr His Phe 195 200 205

120

Val Trp Gln Thr Ile Leu Gly His Leu Ser Pro Ala Asp Lys Asp Ser 225 230 235 240

Lys Leu Pro Glu Asp Asp Ile Gln

245

- (2) INFORMATION FOR SEQ ID NO:778:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..209
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593714
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met Leu Met Ala Phe Leu Ser Asp Ala Asp Ala Lys Lys Gln Thr Arg
1 10 15

Ala Leu Ala Arg Asn Cys Leu Glu Glu Ile Lys Glu Ile Thr Tyr Asp 20 25 30

Ala Glu Asp Ile Ile Glu Thr Phe Leu Leu Lys Gly Ser Gly Asn Lys
35 40 45

Ser His Met Arg Ser Leu Ala Cys Phe Pro Ser Gly Arg Arg Glu Ile
50 55 60

Ala Leu Gln Ile Thr Ser Ile Ser Lys Arg Ile Ser Lys Val Ile Gln 65 70 75 80

Leu Met Gln Thr Leu Gly Ile Lys Ser Asp Ile Met Asp Gly Val Asp 85 90 95

Leu Gln Ala Gln Leu Glu Arg Arg Glu Ser Arg His Thr Phe Ser 100 105 110

Ser Glu Ser Glu Ser Asn Leu Val Gly Leu Glu Lys Asn Val Glu Lys

115
120
125
Leu Val Gly Cly Leu Val Gly Asn Asn Ser Ser His Gly Val Ser Ile

Leu Val Glu Glu Leu Val Gly Asn Asp Ser Ser His Gly Val Ser Ile 130 135 140

Thr Gly Leu Gly Gly Leu Gly Lys Thr Thr Leu Ala Arg Gln Val Phe 145 150 155 160

Asp His Asp Lys Ile Lys Thr His Phe Asp Gly Leu Ala Trp Val Cys 165 170 175

Val Ser Gln Glu Phe Thr Arg Lys Asp Val Trp Gln Thr Ile Leu Gly
180 185 190

His Leu Ser Pro Ala Asp Lys Asp Ser Lys Leu Pro Glu Asp Asp Ile 195 200 205

Gln

- (2) INFORMATION FOR SEQ ID NO:779:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..210
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593751
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779: accgagcace tetecectaa acgeategat tteateatgg gagggtetea getetgeaac gaeteaatea attegateaa aacteateag aggaaggeag attettaeac aaaaggeaag ageeegatga tgggaeetga ceaceagate acattetggg aaagegaaac cacegaeete

```
gataaacctc acgatgacgc tcccgtataa
(2) INFORMATION FOR SEQ ID NO:780:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..69
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593752
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:
Thr Glu His Leu Ser Pro Lys Arg Ile Asp Phe Ile Met Gly Gly Ser
              5
                                   10
Gln Leu Cys Asn Asp Ser Ile Asn Ser Ile Lys Thr His Gln Arg Lys
                               25
           2.0
Ala Asp Phe Tyr Thr Lys Gly Lys Ser Pro Met Met Gly Pro Asp His
                           40
Gln Ile Thr Phe Trp Glu Ser Glu Thr Thr Asp Leu Asp Lys Pro His
                        55
    50
Asp Asp Ala Pro Val
65
(2) INFORMATION FOR SEQ ID NO:781:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 42 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..42
          (D) OTHER INFORMATION: / Ceres Seq. ID 1593753
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:
Pro Ser Thr Ser Pro Leu Asn Ala Ser Ile Ser Ser Trp Glu Gly Leu
                                   10
              5
Ser Ser Ala Thr Thr Gln Ser Ile Arg Ser Lys Leu Ile Arg Gly Arg
                               25
           20
Gln Ile Phe Thr Gln Lys Ala Arg Ala Arg
                           40
(2) INFORMATION FOR SEQ ID NO:782:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 57 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..57
           (D) OTHER INFORMATION: / Ceres Seq. ID 1593754
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:
Met Gly Gly Ser Gln Leu Cys Asn Asp Ser Ile Asn Ser Ile Lys Thr
                                    10
His Gln Arg Lys Ala Asp Phe Tyr Thr Lys Gly Lys Ser Pro Met Met
                                25
Gly Pro Asp His Gln Ile Thr Phe Trp Glu Ser Glu Thr Thr Asp Leu
                            40
Asp Lys Pro His Asp Asp Ala Pro Val
```

180

240

300 360

- (2) INFORMATION FOR SEQ ID NO:783:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..366
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593769
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783: gaagagaagt tgggaagacc ggtccatctt ggtgaggtgt tcatccaaac acacactaag tcggatggct catttattga tcagaaggcg gagaagattg ctcaagctta tgagcagaat gtgagagata ggctgtcagc actagaggcg gctgcttctg ctgtctttga tggctcttca cgacctccgg agctcacact agatgattat atagccatct ttctcgagtc cacagaaagg

gattcaagag gcaatcctta tggacttgta tgtctaaaag acactctagg cagtgccaac cgccaacact ccggttcctc atcatccttt caagccctag aaaaatggct gcaggaagct

caaagg

- (2) INFORMATION FOR SEQ ID NO:784:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:
- Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Thr His Thr Lys Ser Asp Gly Ser Phe Ile Asp Gln Lys Ala Glu Lys 20 25 30

Ile Ala Gln Ala Tyr Glu Gln Asn Val Arg Asp Arg Leu Ser Ala Leu 35 40 45

Glu Ala Ala Ser Ala Val Phe Asp Gly Ser Ser Arg Pro Pro Glu
50 55 60

Leu Thr Leu Asp Asp Tyr Ile Ala Ile Phe Leu Glu Ser Thr Glu Arg 65 70 75 80
Asp Ser Arg Gly Asn Pro Tyr Gly Leu Val Cys Leu Lys Asp Thr Leu

sp Ser Arg Gly Asn Pro Tyr Gly Leu val Cys Leu Lys Asp III Leu
85 90 95

Gly Ser Ala Asn Arg Gln His Ser Gly Ser Ser Ser Ser Phe Gln Ala 100 105 110

Leu Glu Lys Trp Leu Gln Glu Ala Gln Arg 115 120

- (2) INFORMATION FOR SEQ ID NO:785:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 748 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..748
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593773
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

atacgcttct tcgtcgtggt gtcttgacga attggcggag attatgaagt gcaaggaaga ttttggtcaa acagtgatgg ccattttcta cgaagtggat ccaactgatg tagagaagca

gaccggaggt tttggggaag tcttcacaga aacttgtaaa ggtaaaacag ctgaggacat 240 tgagaaatgg agtcaagctc ttgcaaaagt ggcaactgtc attagttacc tttcaagcag 300 ctgggatact gaaacagaaa tgatcgaaga aattgccact gatgtttcga atatgttgac taagtcaacg caatcaaggg atttcgtcgg cttaattgga atgggatctc atatggagaa 360 420 gatgaaaccg ttgctatgcc tagagtcaga ggaagtgagg atatttgctg caggagatat ttgtcaagta ctgagtgatg atacagcagg tagcagcact gttataggaa tagatctcac 480 attacctgag aaggccgacg aggacgaaga attttatata agtgaaagag catttgaaaa 540 600 tatgactaac ctccaattct taaaaattag tggtgattgc agtagattgt actttccgcc acgtctgaac tccatatctc gaaaacttat attactatct tggggtcagt ttccgatgac 660 acttttgcct tctaatttta atccacagtc cctggtcaat ctaaccatga ggagaagcaa 720 gcttgagaag ttgtgggacg gaaataaa

- (2) INFORMATION FOR SEQ ID NO:786:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..249
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593774
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Tyr Ala Ser Ser Trp Cys Leu Asp Glu Leu Ala Glu Ile Met Lys 1 10 15

Cys Lys Glu Asp Phe Gly Gln Thr Val Met Ala Ile Phe Tyr Glu Val 20 25 30

Asp Pro Thr Asp Val Glu Lys Gln Thr Gly Gly Phe Gly Glu Val Phe 35 40 45

Thr Glu Thr Cys Lys Gly Lys Thr Ala Glu Asp Ile Glu Lys Trp Ser 50 55 60

Gln Ala Leu Ala Lys Val Ala Thr Val Ile Ser Tyr Leu Ser Ser Ser 65 70 75 80

Trp Asp Thr Glu Thr Glu Met Ile Glu Glu Ile Ala Thr Asp Val Ser 85 90 95

Asn Met Leu Thr Lys Ser Thr Gln Ser Arg Asp Phe Val Gly Leu Ile 100 105 110

Gly Met Gly Ser His Met Glu Lys Met Lys Pro Leu Cys Leu Glu
115 120 125

Ser Glu Glu Val Arg Ile Phe Ala Ala Gly Asp Ile Cys Gln Val Leu 130 135 140

Ser Asp Asp Thr Ala Gly Ser Ser Thr Val Ile Gly Ile Asp Leu Thr 145 150 155 160

Leu Pro Glu Lys Ala Asp Glu Asp Glu Glu Phe Tyr Ile Ser Glu Arg 165 170 175

Ala Phe Glu Asn Met Thr Asn Leu Gln Phe Leu Lys Ile Ser Gly Asp 180 185 190

Cys Ser Arg Leu Tyr Phe Pro Pro Arg Leu Asn Ser Ile Ser Arg Lys 195 200 205

Leu Ile Leu Leu Ser Trp Gly Gln Phe Pro Met Thr Leu Leu Pro Ser 210 215 220

Asn Phe Asn Pro Gln Ser Leu Val Asn Leu Thr Met Arg Arg Ser Lys 225 230 235 240

Leu Glu Lys Leu Trp Asp Gly Asn Lys 245

- (2) INFORMATION FOR SEQ ID NO:787:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..235
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593775
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:
- Met Lys Cys Lys Glu Asp Phe Gly Gln Thr Val Met Ala Ile Phe Tyr 1 5 10 15
- Glu Val Asp Pro Thr Asp Val Glu Lys Gln Thr Gly Gly Phe Gly Glu 20 25 30
- Val Phe Thr Glu Thr Cys Lys Gly Lys Thr Ala Glu Asp Ile Glu Lys
 35 40 45
- Trp Ser Gln Ala Leu Ala Lys Val Ala Thr Val Ile Ser Tyr Leu Ser 50 55 60
- Ser Ser Trp Asp Thr Glu Thr Glu Met Ile Glu Glu Ile Ala Thr Asp 65 70 75 80
- Val Ser Asn Met Leu Thr Lys Ser Thr Gln Ser Arg Asp Phe Val Gly
 85 90 95
- 85 90 95

 Leu Ile Gly Met Gly Ser His Met Glu Lys Met Lys Pro Leu Cys
- 100 105 110 Leu Glu Ser Glu Glu Val Arg Ile Phe Ala Ala Gly Asp Ile Cys Gln
- 115 120 125 Val Leu Ser Asp Asp Thr Ala Gly Ser Ser Thr Val Ile Gly Ile Asp
- Val Leu Ser Asp Asp Thr Ala Gly Ser Ser Thr Val Tie Gly Tie Asp 130 135 140
- Leu Thr Leu Pro Glu Lys Ala Asp Glu Asp Glu Glu Phe Tyr Ile Ser 145 150 150 155 160
- Glu Arg Ala Phe Glu Asn Met Thr Asn Leu Gln Phe Leu Lys Ile Ser 165 170 175 Gly Asp Cys Ser Arg Leu Tyr Phe Pro Pro Arg Leu Asn Ser Ile Ser
- 180 185 190
 Arg Lys Leu Ile Leu Leu Ser Trp Gly Gln Phe Pro Met Thr Leu Leu
- 195 200 205 Pro Ser Asn Phe Asn Pro Gln Ser Leu Val Asn Leu Thr Met Arg Arg
- 210 215 220 Ser Lys Leu Glu Lys Leu Trp Asp Gly Asn Lys 225 230 235
- (2) INFORMATION FOR SEQ ID NO:788:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..224
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593776
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:
- Met Ala Ile Phe Tyr Glu Val Asp Pro Thr Asp Val Glu Lys Gln Thr

 1 5 10 15
- Gly Gly Phe Gly Glu Val Phe Thr Glu Thr Cys Lys Gly Lys Thr Ala
- Glu Asp Ile Glu Lys Trp Ser Gln Ala Leu Ala Lys Val Ala Thr Val
- Ile Ser Tyr Leu Ser Ser Ser Trp Asp Thr Glu Thr Glu Met Ile Glu
 50 55 60
- Glu Ile Ala Thr Asp Val Ser Asn Met Leu Thr Lys Ser Thr Gln Ser 65 70 75 80
- Arg Asp Phe Val Gly Leu Ile Gly Met Gly Ser His Met Glu Lys Met 85 90 95
- Lys Pro Leu Cys Leu Glu Ser Glu Glu Val Arg Ile Phe Ala Ala

			100					105					110		
Gly	Asp	Ile 115	Cys	Gln	Val	Leu	Ser 120	Asp	Asp	Thr	Ala	Gly 125	Ser	Ser	Thr
Val	Ile 130	Gly	Ile	Asp	Leu	Thr 135	Leu	Pro	Glu	Lys	Ala 140	Asp	Glu	Asp	Glu
Glu 145	Phe	Tyr	Ile	Ser	Glu 150	Arg	Ala	Phe	Glu	Asn 155	Met	Thr	Asn	Leu	Gln 160
Phe	Leu	Lys	Ile	Ser 165	Gly	Asp	Cys	Ser	Arg 170	Leu	Tyr	Phe	Pro	Pro 175	Arg
Leu	Asn	Ser	Ile 180	Ser	Arg	Lys	Leu	Ile 185	Leu	Leu	Ser	Trp	Gly 190	Gln	Phe
Pro	Met	Thr 195	Leu	Leu	Pro	Ser	Asn 200	Phe	Asn	Pro	Gln	Ser 205	Leu	Val	Asn
Leu	Thr 210	Met	Arg	Arg		Lys 215	Leu	Glu	Lys	Leu	Trp 220	Asp	Gly	Asn	Lys

- (2) INFORMATION FOR SEQ ID NO:789:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..795
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593781
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789: tcaccaccac caccaaagaa acattacgta tacaagtctc ctcctccc ggttaagcac 60 120 tactctcccc ctccggttta ccactcacca ccaccaccaa aaaaacatta cgtttacaag 180 tctcctcctc ctccggttaa gcactactct ccccctccgg tttaccattc cccacccca 240 cctaaaaagc attacgtcta caaatctcca ccaccaccgg tgaagcacta ctcacctcct 300 coggtttacc attocccacc acccccaaag aaacactacg tgtacaaatc tcctcctcct 360 ccggttaagc actactctcc tcctccggtt taccattccc caccaccacc aaagaaacac 420 tacqtqtaca aatctcctcc tcctccagtt aagcactact ctcctcctcc ggtttaccat 480 tccccaccc caccaaagaa acactacgtg tacaaatctc caccaccacc ggtgaagcac 540 tactctcccc ctccagttta ccattcccca ccaccaccaa agaaacatta cgtatacaag 600 tecectecte etecggttaa geactaetet eccectecag tetaetatte eccaceacea ccaaaqaaac attacgtata caagtcccct cctcctccgg ttaagcacta ctctcctcct 660 720 coggtttacc actotccacc ancaccaaaa gaaaagtacg tgtacaaatc acctcctcct 780 cctccagtac accactacte tecaccacae cateettace tetacaaate tecteetet ccataccact attag
- (2) INFORMATION FOR SEQ ID NO:790:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..264
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593782
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Ser Pro Pro Pro Lys Lys His Tyr Val Tyr Lys Ser Pro Pro Pro 1 5 10 15

Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro Pro 20 25 30

Pro Lys Lys His Tyr Val Tyr Lys Ser Pro Pro Pro Pro Val Lys His 35 40 45

```
Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro Pro Pro Lys Lys His
                      55
Tyr Val Tyr Lys Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro
                                    75
                  70
Pro Val Tyr His Ser Pro Pro Pro Lys Lys His Tyr Val Tyr Lys
              85
                                 90
Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His
                                               110
                             105
          100
Ser Pro Pro Pro Pro Lys Lys His Tyr Val Tyr Lys Ser Pro Pro
                        120
                                            125
      115
Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro
                     135
                                        140
Pro Lys Lys His Tyr Val Tyr Lys Ser Pro Pro Pro Pro Val Lys His
                      155
                 150
Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro Pro Pro Lys Lys His
                                170
              165
Tyr Val Tyr Lys Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro
                            185
                                               190
          180
Pro Val Tyr Tyr Ser Pro Pro Pro Lys Lys His Tyr Val Tyr Lys
                                            205
                        200
Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His
                                        220
                     215
Ser Pro Pro Xaa Pro Lys Glu Lys Tyr Val Tyr Lys Ser Pro Pro
                                    235
                 230
Pro Pro Val His His Tyr Ser Pro Pro His His Pro Tyr Leu Tyr Lys
                                 250
              245
Ser Pro Pro Pro Pro Tyr His Tyr
           260
```

- (2) INFORMATION FOR SEQ ID NO:791:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 701 base pairs
 - (B) TYPE: nucleic acid
 - (b) TIPE. NUCLEIC acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..701
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

tcgttgaata tctcggagct attggtagac gttcccgaat cagccacggt tggctcactg 60 aaactagcgg tattggaggc ggtaacgaga ttctcaagga tggattaaac attggagtgc 120 tetttcaagg taaaaccate gttgatgact ccaaaacget tettcagatt gggateccat 180 acgatgatga cgatgacgaa aacctcggtt ctttgggatt catgctagaa ccgcaaaaat 240 cagaaacaac aacaataaca acgttaacca ctgtttcccc gagaacacga cttagacaaa 300 atcaggtcct agggtccgtg gatagcactg aggcagtagc agctaaatcc gtggttccag 360 tacgtatgaa accggcctgg cagccagaga tggttcaacg gagaataaga cggccattca 420 480 ctgtctcaga agtagaagct ttggttcagg ccgtagagag gctcggcacc ggaaggtggc 540 gcgacgtgaa gtctcatgca tttaaccatg taaatcatcg tacctacgtt gacctcaaga acagaaatga tctagttttc aaagggagag aattcacagc cccgcaagtg atccttaagg 600 caacagagga catggatgca tggaataatc gtaaggaacc acaaccccaa gtgacaagct 660 ctacacgtga tcggtgtgta aaatggcnac ccccttctca c

- (2) INFORMATION FOR SEQ ID NO:792:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1593810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Val Glu Tyr Leu Gly Ala Ile Gly Arg Arg Ser Arg Ile Ser His Gly

1 5 10 15

Trp Leu Thr Glu Thr Ser Gly Ile Gly Gly Gly Asn Glu Ile Leu Lys
20 25 30

Asp Gly Leu Asn Ile Gly Val Leu Phe Gln Gly Lys Thr Ile Val Asp

35 40 45
Asp Ser Lys Thr Leu Leu Gln Ile Gly Ile Pro Tyr Asp Asp Asp Asp

Asp Ser Lys Thr Leu Leu Gin lie Gly lie Pro lyr Asp Asp Asp 50

50

60

7 The Gly Rep Leu Cly Ser Leu Cly Pho Met Leu Gly Pro Gly Lys Ser

Asp Glu Asn Leu Gly Ser Leu Gly Phe Met Leu Glu Pro Gln Lys Ser

70

75

80

Glu Thr Thr Thr Ile Thr Thr Leu Thr Thr Val Ser Pro Arg Thr Arg 85 90 95 Leu Arg Gln Asn Gln Val Leu Gly Ser Val Asp Ser Thr Glu Ala Val

100 105 110 Pro Mrt Luc Pro Ala Tran Cla Pro

Ala Ala Lys Ser Val Val Pro Val Arg Met Lys Pro Ala Trp Gln Pro 115 120 125

Glu Met Val Gln Arg Arg Ile Arg Arg Pro Phe Thr Val Ser Glu Val 130 135 140

Glu Ala Leu Val Gln Ala Val Glu Arg Leu Gly Thr Gly Arg Trp Arg 145 150 155 160

Asp Val Lys Ser His Ala Phe Asn His Val Asn His Arg Thr Tyr Val 165 170 175

Asp Leu Lys Asn Arg Asn Asp Leu Val Phe Lys Gly Arg Glu Phe Thr 180 185 190

Ala Pro Gln Val Ile Leu Lys Ala Thr Glu Asp Met Asp Ala Trp Asn 195 200 205

Asn Arg Lys Glu Pro Gln Pro Gln Val Thr Ser Ser Thr Arg Asp Arg 210 215 220

Cys Val Lys Trp Xaa Pro Pro Ser His 225 230

- (2) INFORMATION FOR SEQ ID NO:793:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Met Leu Glu Pro Gln Lys Ser Glu Thr Thr Thr Ile Thr Thr Leu Thr 1 5 10

Thr Val Ser Pro Arg Thr Arg Leu Arg Gln Asn Gln Val Leu Gly Ser 20 25 30

Val Asp Ser Thr Glu Ala Val Ala Ala Lys Ser Val Val Pro Val Arg 35 40 45

Met Lys Pro Ala Trp Gln Pro Glu Met Val Gln Arg Arg Ile Arg Arg
50 60

Pro Phe Thr Val Ser Glu Val Glu Ala Leu Val Gln Ala Val Glu Arg 65 70 75 80

Leu Gly Thr Gly Arg Trp Arg Asp Val Lys Ser His Ala Phe Asn His 85 90 95

Val Asn His Arg Thr Tyr Val Asp Leu Lys Asn Arg Asn Asp Leu Val 100 105 110

Phe Lys Gly Arg Glu Phe Thr Ala Pro Gln Val Ile Leu Lys Ala Thr 115 120 125

Glu Asp Met Asp Ala Trp Asn Asn Arg Lys Glu Pro Gln Pro Gln Val 130 135 140 Thr Ser Ser Thr Arg Asp Arg Cys Val Lys Trp Xaa Pro Pro Ser His 145 150 155 160

- (2) INFORMATION FOR SEQ ID NO:794:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..675
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593815
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794: 60 qcttcaqqat tqttctatct ccatgaggaa tgggancaag ttgtgattca ccgtgacgtg 120 aaagctagca atgttctgtt agatgctgat ttcaatggta gactcggtga ttttgggttg 180 gctcggttgt atgatcacgg ctcggatcct cagaccactc acgttgttgg aacattgggt tacttagcac ctgaacattc ccggactgga cgtgccacta ccgcgactga tgtctatqcq 240 tttggtgcgt ttcttttaga agttgtttcc ggtagacgac ccatcgagtt ccatagtgca 300 360 agcgatgata cgttcttgct tgtggaatgg gttttcagtt tgtggctcag aggtaacata 420 atggaagcga aagatccgaa gctcggttct tcaggttatg atcttgaaga ggttgaaatg gtattgaaac tcggtctgtt gtgttcgcat tcagaccctc gggctagacc aagtatgagg 480 caggicttac aatatctaag aggagacatg gcactgcctg aattaacgcc citggatitg 540 tcggcgggga gcgtgatgaa tctgggaggc cgggacggct ttagcggtat tgcaatgact 600 gatttttcca ctgtgtttaa agggtttacc ggaggatctt ccattgctga ctctctactc 660
- (2) INFORMATION FOR SEQ ID NO:795:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

tccqqtqqqa qqtqa

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593816
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:
- Ala Ser Gly Leu Phe Tyr Leu His Glu Glu Trp Xaa Gln Val Val Ile 1 5 10 15 His Arg Asp Val Lys Ala Ser Asn Val Leu Leu Asp Ala Asp Phe Asn
- 20 25 30 Gly Arg Leu Gly Asp Phe Gly Leu Ala Arg Leu Tyr Asp His Gly Ser
- Asp Pro Gln Thr Thr His Val Val Gly Thr Leu Gly Tyr Leu Ala Pro 50 55 60
- Glu His Ser Arg Thr Gly Arg Ala Thr Thr Ala Thr Asp Val Tyr Ala 65 70 75 80
- Phe Gly Ala Phe Leu Leu Glu Val Val Ser Gly Arg Arg Pro Ile Glu
 85 90 95
- Phe His Ser Ala Ser Asp Asp Thr Phe Leu Leu Val Glu Trp Val Phe
 100 105 110
- Ser Leu Trp Leu Arg Gly Asn Ile Met Glu Ala Lys Asp Pro Lys Leu 115 120 125
- Gly Ser Ser Gly Tyr Asp Leu Glu Glu Val Glu Met Val Leu Lys Leu 130 135 140
- Gly Leu Leu Cys Ser His Ser Asp Pro Arg Ala Arg Pro Ser Met Arg

150 155 145 Gln Val Leu Gln Tyr Leu Arg Gly Asp Met Ala Leu Pro Glu Leu Thr 165 170 Pro Leu Asp Leu Ser Ala Gly Ser Val Met Asn Leu Gly Gly Arg Asp 190 185 180 Gly Phe Ser Gly Ile Ala Met Thr Asp Phe Ser Thr Val Phe Lys Gly 200 205 195 Phe Thr Gly Gly Ser Ser Ile Ala Asp Ser Leu Leu Ser Gly Gly Arg 220 215

(2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 739 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..739
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593817
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

tgatcttgag tgggtcaggc tggtgctgac ggctgatcca ggtcttagaa tggaaagtat 60 tactgatccg aaaaccccac gtcgaaagga acatcgtcgt gtttcaagta tagttgccta 120 180 cgaggaagta agggctgctg cagcgaaggg agaggcacct ccaggtcttc ctctcaaagg 240 ggctggtcag gattcatcag atgcacaacc aatggccaat ggtggcatgc tgaaagcagg 300 tgatgcctta tctggtgaat tttgggaggg gaagcgacta agaattcgta aagattcaat atatqqcaac ctaccaggtt gggacttgcg ctctatcatt gtgaagagcg gtgatgactg 360 tcqqcaqqaa catcttqcqq ttcaacttat atctcatttt tttqatatat tccaqqaaqc 420 480 agggettece etetggttae gteettatga agtettggtg acatetteat acaetgeeet 540 tatagaaaca attccagata cggcttctat tcattctatt aaaagtagat accctaacat 600 cacaagcctg cgtgattttt ttgatgccaa gtttaaagag aactctccaa gttttaagct tgctcaggta cattttatgg ttttatggct caagtccaca agcaagttgg ctgttttctt 660 tcaqaaactt tctgttaaac atgatgttgt tctaatgaga gctgtggaat atatgttaaa 720 ttttctctcc caaaaattc

- (2) INFORMATION FOR SEQ ID NO:797:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..246
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593818
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

Asp Leu Glu Trp Val Arg Leu Val Leu Thr Ala Asp Pro Gly Leu Arg

1 10 15

Met Clu Ser Ile Thr Asp Pro Lys Thr Pro Arg Arg Lys Glu His Arg

Met Glu Ser Ile Thr Asp Pro Lys Thr Pro Arg Arg Lys Glu His Arg 20 25 30

Arg Val Ser Ser Ile Val Ala Tyr Glu Glu Val Arg Ala Ala Ala 35 40 45

Lys Gly Glu Ala Pro Pro Gly Leu Pro Leu Lys Gly Ala Gly Gln Asp 50 55 60

Ser Ser Asp Ala Gln Pro Met Ala Asn Gly Gly Met Leu Lys Ala Gly 65 70 75 80

Asp Ala Leu Ser Gly Glu Phe Trp Glu Gly Lys Arg Leu Arg Ile Arg 85 90 95

Lys Asp Ser Ile Tyr Gly Asn Leu Pro Gly Trp Asp Leu Arg Ser Ile

100 105 Ile Val Lys Ser Gly Asp Asp Cys Arg Gln Glu His Leu Ala Val Gln 115 120 125 Leu Ile Ser His Phe Phe Asp Ile Phe Gln Glu Ala Gly Leu Pro Leu 130 135 140 Trp Leu Arg Pro Tyr Glu Val Leu Val Thr Ser Ser Tyr Thr Ala Leu 150 155 160 Ile Glu Thr Ile Pro Asp Thr Ala Ser Ile His Ser Ile Lys Ser Arg 165 170 Tyr Pro Asn Ile Thr Ser Leu Arg Asp Phe Phe Asp Ala Lys Phe Lys 180 185 190 Glu Asn Ser Pro Ser Phe Lys Leu Ala Gln Val His Phe Met Val Leu 195 200 205 Trp Leu Lys Ser Thr Ser Lys Leu Ala Val Phe Phe Gln Lys Leu Ser 210 215 220 Val Lys His Asp Val Val Leu Met Arg Ala Val Glu Tyr Met Leu Asn 230 235 Phe Leu Ser Gln Lys Phe 245

(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..230
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Met Glu Ser Ile Thr Asp Pro Lys Thr Pro Arg Arg Lys Glu His Arg 1 5 10 15 Arg Val Ser Ser Ile Val Ala Tyr Glu Glu Val Arg Ala Ala Ala Ala

Arg Val Ser Ser lie Val Ala Tyr Giu Giu Val Arg Ala Ala Ala Ala 20 25 30

Lys Gly Glu Ala Pro Pro Gly Leu Pro Leu Lys Gly Ala Gly Gln Asp

35 40 45 Ser Ser Asp Ala Gln Pro Met Ala Asn Gly Gly Met Leu Lys Ala Gly

50 55 60
Asp Ala Leu Ser Gly Glu Phe Trp Glu Gly Lys Arg Leu Arg Ile Arg

Lys Asp Ser Ile Tyr Gly Asn Leu Pro Gly Trp Asp Leu Arg Ser Ile

85

90

95

Ile Val Lys Ser Gly Asp Asp Cys Arg Gln Glu His Leu Ala Val Gln
100 105 110

Leu Ile Ser His Phe Phe Asp Ile Phe Gln Glu Ala Gly Leu Pro Leu 115 120 125

Trp Leu Arg Pro Tyr Glu Val Leu Val Thr Ser Ser Tyr Thr Ala Leu 130 135 140

Ile Glu Thr Ile Pro Asp Thr Ala Ser Ile His Ser Ile Lys Ser Arg 145 150 155 160

Tyr Pro Asn Ile Thr Ser Leu Arg Asp Phe Phe Asp Ala Lys Phe Lys
165 170 175

Glu Asn Ser Pro Ser Phe Lys Leu Ala Gln Val His Phe Met Val Leu
180 185 190

Trp Leu Lys Ser Thr Ser Lys Leu Ala Val Phe Phe Gln Lys Leu Ser

Val Lys His Asp Val Val Leu Met Arg Ala Val Glu Tyr Met Leu Asn 210 215 220

Phe Leu Ser Gln Lys Phe

25

- (2) INFORMATION FOR SEQ ID NO:799:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..176
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593820
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

Met Ala Asn Gly Gly Met Leu Lys Ala Gly Asp Ala Leu Ser Gly Glu
1 5 10 15

Phe Trp Glu Gly Lys Arg Leu Arg Ile Arg Lys Asp Ser Ile Tyr Gly 20 25 30

Asn Leu Pro Gly Trp Asp Leu Arg Ser Ile Ile Val Lys Ser Gly Asp 35 40 45

Asp Cys Arg Gln Glu His Leu Ala Val Gln Leu Ile Ser His Phe Phe 50 55 60

Asp Ile Phe Gln Glu Ala Gly Leu Pro Leu Trp Leu Arg Pro Tyr Glu 65 70 75 80

Val Leu Val Thr Ser Ser Tyr Thr Ala Leu Ile Glu Thr Ile Pro Asp 85 90 95

Thr Ala Ser Ile His Ser Ile Lys Ser Arg Tyr Pro Asn Ile Thr Ser 100 105 110

Leu Arg Asp Phe Phe Asp Ala Lys Phe Lys Glu Asn Ser Pro Ser Phe 115 120 125

Lys Leu Ala Gln Val His Phe Met Val Leu Trp Leu Lys Ser Thr Ser 130 135 140

Lys Leu Ala Val Phe Phe Gln Lys Leu Ser Val Lys His Asp Val Val
145 150 155 160

Leu Met Arg Ala Val Glu Tyr Met Leu Asn Phe Leu Ser Gln Lys Phe
165 170 175

- (2) INFORMATION FOR SEQ ID NO:800:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..813
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593869
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

ataacaatca	taaccattac	cgctctcttt	cacacacact.	tecetettet	cctccatcac	60
acygogacca	cygoogecyo	Lastastast		*********	tattatata	120
		tcctacttct				
gatggactca	gtactcgatt	atgctcgatt	ctccgttatt	catcgtctga	cggcgtcaac	180
ggcggaagta	gcggtggcga	tttcggtaac	gataacgatt	ccgttagtgt	tgtttcggat	240
gttcagagtc	ctaattactt	aaaattcacc	gatgaagaat	tgatgaagca	atgtagatta	300
gagacattta	gagtttcagg	acctggagga	caacaccgga	acaagcgtga	ctccgccgtg	360
cgtctgaaac	atctccccac	cggaatcgta	gctcaagccg	tcgaagatcg	ttcacagcac	420
aagaaccgtg	cttctgctct	aaaccgtctt	cgtacgctcc	tcgccattaa	agtgagaaac	480
aaagtggaca	ttgaagctta	tgctcctcct	ccagagcttc	ttcagattct	acctcctaag	540
tctaccatta	gaacttcttc	tggttcacag	attggtccca	acaatcctaa	atttgtacct	600
ggaatgcaag	ctttgcttga	tgttatttct	gcttctgacg	gttctatcgc	tgattctgcc	660
		tggtggctta				720
cgtatggctg	tcaatagcat	gagagcagcc	aaggtactgt	ttgttgatta	ccaatccaaa	780

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Client Docket No. 80146.003
tactttqtta tcaaqattat qccaataagg tag
(2) INFORMATION FOR SEQ ID NO:801:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 270 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..270
        (D) OTHER INFORMATION: / Ceres Seq. ID 1593870
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:
Met Ala Ile Met Ala Val Ala Ala Leu Phe His Ala Arg Phe Pro Leu
                     10
        5
Leu Leu Arg Arg Ser Ile Pro Leu Leu Ser Ala Pro Thr Ser Val Ile
     20 25
Tyr Asn His Arg Thr Leu Leu Ser Asp Gly Leu Ser Thr Arg Leu Cys
                       40
Ser Ile Leu Arg Tyr Ser Ser Ser Asp Gly Val Asn Gly Gly Ser Ser
                   55
Gly Gly Asp Phe Gly Asn Asp Asn Asp Ser Val Ser Val Ser Asp
                70 75
Val Gln Ser Pro Asn Tyr Leu Lys Phe Thr Asp Glu Glu Leu Met Lys
             85 90
Gln Cys Arg Leu Glu Thr Phe Arg Val Ser Gly Pro Gly Gly Gln His
                          105 110
Arg Asn Lys Arg Asp Ser Ala Val Arg Leu Lys His Leu Pro Thr Gly
                       120
Ile Val Ala Gln Ala Val Glu Asp Arg Ser Gln His Lys Asn Arg Ala
                   135 140
Ser Ala Leu Asn Arg Leu Arg Thr Leu Leu Ala Ile Lys Val Arg Asn
                150
                                 155
Lys Val Asp Ile Glu Ala Tyr Ala Pro Pro Pro Glu Leu Leu Gln Ile
                              170
             165
Leu Pro Pro Lys Ser Thr Ile Arg Thr Ser Ser Gly Ser Gln Ile Gly
         180 185 190
Pro Asn Asn Pro Lys Phe Val Pro Gly Met Gln Ala Leu Leu Asp Val
                       200
Ile Ser Ala Ser Asp Gly Ser Ile Ala Asp Ser Ala Lys Leu Leu Gly
                    215
                                     220
Leu Ser Thr Gly Gly Leu Ser Arg Leu Ile Leu Ser His Asp Gly Leu
                 230
                                  235
Arg Met Ala Val Asn Ser Met Arg Ala Ala Lys Val Leu Phe Val Asp
                              250
             245
Tyr Gln Ser Lys Tyr Phe Val Ile Lys Ile Met Pro Ile Arg
          260
                           265
(2) INFORMATION FOR SEQ ID NO:802:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 267 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
```

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593872
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

Met Ala Val Ala Ala Leu Phe His Ala Arg Phe Pro Leu Leu Arg 10 5

```
Arg Ser Ile Pro Leu Leu Ser Ala Pro Thr Ser Val Ile Tyr Asn His
                         25
Arg Thr Leu Leu Ser Asp Gly Leu Ser Thr Arg Leu Cys Ser Ile Leu
                      40
Arg Tyr Ser Ser Ser Asp Gly Val Asn Gly Gly Ser Ser Gly Gly Asp
                  55
Phe Gly Asn Asp Asn Asp Ser Val Ser Val Val Ser Asp Val Gln Ser
             70
                               75
Pro Asn Tyr Leu Lys Phe Thr Asp Glu Glu Leu Met Lys Gln Cys Arg
                            90
           85
Leu Glu Thr Phe Arg Val Ser Gly Pro Gly Gly Gln His Arg Asn Lys
        100 105
                                        110
Arg Asp Ser Ala Val Arg Leu Lys His Leu Pro Thr Gly Ile Val Ala
     115 120 125
Gln Ala Val Glu Asp Arg Ser Gln His Lys Asn Arg Ala Ser Ala Leu
  130 135 140
Asn Arg Leu Arg Thr Leu Leu Ala Ile Lys Val Arg Asn Lys Val Asp
                          155
             150
Ile Glu Ala Tyr Ala Pro Pro Pro Glu Leu Leu Gln Ile Leu Pro Pro
            165 170 175
Lys Ser Thr Ile Arg Thr Ser Ser Gly Ser Gln Ile Gly Pro Asn Asn
        180 185 190
Pro Lys Phe Val Pro Gly Met Gln Ala Leu Leu Asp Val Ile Ser Ala
     195 200 205
Ser Asp Gly Ser Ile Ala Asp Ser Ala Lys Leu Leu Gly Leu Ser Thr
   210 215 220
Gly Gly Leu Ser Arg Leu Ile Leu Ser His Asp Gly Leu Arg Met Ala
             230 235
Val Asn Ser Met Arg Ala Ala Lys Val Leu Phe Val Asp Tyr Gln Ser
                            250
Lys Tyr Phe Val Ile Lys Ile Met Pro Ile Arg
```

(2) INFORMATION FOR SEQ ID NO:803:

260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..408
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

atgagtaacg tgggtgtgac agtacgagat cgagagcggc ttattcgtac ggttcattgc agacttccct caccgccgtt gatggagaga atgaacatga gcgaagagga ggagcaatgc aaaagaaacc aagaggcatt caagagattc ttcgagcaaa tccccaggac tgcggtgata ggcatgcttt ccttctcct ccacggccag atgagtaagt tcgagaaagc tccaagcaag cctctttcca atgctttcgc cttcgcctcc gtgggctacg ttgtgttgca ggtcgcacac ggctttgctc gagctaatcg tccttcatct ttcgctttcg acttcctct tgttctctgt 360 ggacttgcat ccgttgccat tctcttcact gccatcttca acgactga

- (2) INFORMATION FOR SEQ ID NO:804:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135

60

120

180

(D) OTHER INFORMATION: / Ceres Seq. ID 1593877 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804: Met Ser Asn Val Gly Val Thr Val Arg Asp Arg Glu Arg Leu Ile Arg 10 Thr Val His Cys Arg Leu Pro Ser Pro Pro Leu Met Glu Arg Met Asn 20 25 Met Ser Glu Glu Glu Glu Cys Lys Arg Asn Gln Glu Ala Phe Lys 40 Arg Phe Phe Glu Gln Ile Pro Arg Thr Ala Val Ile Gly Met Leu Ser 55 Phe Phe Leu His Gly Gln Met Ser Lys Phe Glu Lys Ala Pro Ser Lys 70 75 Pro Leu Ser Asn Ala Phe Ala Phe Ala Ser Val Gly Tyr Val Val Leu 90 85 Gln Val Ala His Gly Phe Ala Arg Ala Asn Arg Pro Ser Ser Phe Ala 105 110 100 Phe Asp Phe Leu Ser Val Leu Cys Gly Leu Ala Ser Val Ala Ile Leu 120 125 115 Phe Thr Ala Ile Phe Asn Asp 135 130 (2) INFORMATION FOR SEQ ID NO:805: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..108 (D) OTHER INFORMATION: / Ceres Seq. ID 1593879 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:805: Met Glu Arg Met Asn Met Ser Glu Glu Glu Glu Gln Cys Lys Arg Asn 5 10 Gln Glu Ala Phe Lys Arg Phe Phe Glu Gln Ile Pro Arg Thr Ala Val 25 Ile Gly Met Leu Ser Phe Phe Leu His Gly Gln Met Ser Lys Phe Glu 4.0 4.5 Lys Ala Pro Ser Lys Pro Leu Ser Asn Ala Phe Ala Phe Ala Ser Val 55 60 Gly Tyr Val Val Leu Gln Val Ala His Gly Phe Ala Arg Ala Asn Arg 70 75 Pro Ser Ser Phe Ala Phe Asp Phe Leu Ser Val Leu Cys Gly Leu Ala 90 Ser Val Ala Ile Leu Phe Thr Ala Ile Phe Asn Asp 100 (2) INFORMATION FOR SEQ ID NO:806: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 240 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..240 (D) OTHER INFORMATION: / Ceres Seq. ID 1593888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806: atgagtaacg tgggtgtgac agtacgagat cgagagcggc ttattcgtac ggttcattgc agacttccct caccgccgtt gatggagaga atgaacatga gcgaagagga ggagcaatgc aaaagaaacc aagaggcatt caagagattc ttcgagcaaa tccccaggac tgcggtqata

ggcatgcttt ccttcttcct ccacggccag atgagtcgca cacggctttg ctcgagctaa 240

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(2) INFORMATION FOR SEQ ID NO:807:(i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593889
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

Met Ser Asn Val Gly Val Thr Val Arg Asp Arg Glu Arg Leu Ile Arg 1 5 10 15

Thr Val His Cys Arg Leu Pro Ser Pro Pro Leu Met Glu Arg Met Asn 20 25 30

Met Ser Glu Glu Glu Glu Gln Cys Lys Arg Asn Gln Glu Ala Phe Lys 35 40 45

Arg Phe Phe Glu Gln Ile Pro Arg Thr Ala Val Ile Gly Met Leu Ser 50 55 60

Phe Phe Leu His Gly Gln Met Ser Arg Thr Arg Leu Cys Ser Ser 65 70 75

- (2) INFORMATION FOR SEQ ID NO:808:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..52
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1593891
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

Met Glu Arg Met Asn Met Ser Glu Glu Glu Glu Gln Cys Lys Arg Asn 1 5 10 15

Gln Glu Ala Phe Lys Arg Phe Phe Glu Gln Ile Pro Arg Thr Ala Val 20 25 30

Ile Gly Met Leu Ser Phe Phe Leu His Gly Gln Met Ser Arg Thr Arg 35 40 45

Leu Cys Ser Ser 50

(2) INFORMATION FOR SEQ ID NO:809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594065
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

atgatgtett tgeteecaaa teeegaceeg attaetgtae eeetggteet eaagetttge 60 teettteete egeeaeggag getettetet eteaggetea ggegetteae eegaaagtea 120 teatetette tteegttggt egetgtteg teteteteeg etaetgnege aaaacetaee 180 agatggagag agaageegga attggeggaa agegaeteaa ttteeeteet eaaegagagg 240 atteggegtg aceteggeaa gagagagaet getagaeegg eeatggaete tgaggaggee 300

360 gagaagtaca ttcacatggt caaggaacaa caagagaggg gtctgcagaa gctcaaagga 420 attaggcaag gtacaaaggc tgctggtgac ggtgctttta gttacaaggt tgacccttac 480 agtctccttt ccqqtqatta tqtqqtqcac aagaaagtag gcattgggcg ttttgttggg atcaagtttg atgtccccaa ggactcctct gagcccctcg aatatgtctt tatagagtat 540 600 qctqatqqta tqqccaagct tcccctcaaa caggcctcgc gtttgctcta ccgatacaat 660 cttccaaatg agactaaacg gcctcggact ttgagtcggc tgagtgacac tagtgtttgg gaaagaagaa agaccaaagg aaaagtagca attcagaaaa tggtcgttga cttgatggag 720 780 ctatatette ataggettag acagaagaga tatecatate egaagaacee cateatgget gattttgcgg ctcaatttcc ttataacgcc actcctgacc agaagcaggc tttcctggat 840 gttgaaaagg atttgactga gagagaaaca cctatggacc gattgatctg tggagatgtt 900 ggctttggta aaacagaggt tgctctacga gccatctttt gtgtggtctc aactggaaaa 960 caagctatgg ttttagcacc gacaattgta ttggcgaana acattacgat agatttgggg 1020 tcaagcagaa agaaaagatt gcatctttca aaacatccgt ggatgtgctt acattgtccg 1080 caacacccat accaaggaca ct

- (2) INFORMATION FOR SEQ ID NO:810:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..367
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594066
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:810: Met Met Ser Leu Leu Pro Asn Pro Asp Pro Ile Thr Val Pro Leu Val 5 10 Leu Lys Leu Cys Ser Phe Pro Pro Pro Arg Arg Leu Phe Ser Leu Arg 30 20 25 Leu Arg Arg Phe Thr Arg Lys Ser Ser Ser Leu Leu Pro Leu Val Ala 45 40 Val Ser Ser Leu Ser Ala Thr Xaa Ala Lys Pro Thr Arg Trp Arg Glu 55 60 Lys Pro Glu Leu Ala Glu Ser Asp Ser Ile Ser Leu Leu Asn Glu Arg 70 75 65 Ile Arg Arg Asp Leu Gly Lys Arg Glu Thr Ala Arg Pro Ala Met Asp 90 Ser Glu Glu Ala Glu Lys Tyr Ile His Met Val Lys Glu Gln Glu 105 100 Arg Gly Leu Gln Lys Leu Lys Gly Ile Arg Gln Gly Thr Lys Ala Ala 120 125 Gly Asp Gly Ala Phe Ser Tyr Lys Val Asp Pro Tyr Ser Leu Leu Ser 130 135 Gly Asp Tyr Val Val His Lys Lys Val Gly Ile Gly Arg Phe Val Gly 155 150 145 Ile Lys Phe Asp Val Pro Lys Asp Ser Ser Glu Pro Leu Glu Tyr Val 170 165 Phe Ile Glu Tyr Ala Asp Gly Met Ala Lys Leu Pro Leu Lys Gln Ala 185 180 Ser Arg Leu Leu Tyr Arg Tyr Asn Leu Pro Asn Glu Thr Lys Arg Pro 200 195 Arg Thr Leu Ser Arg Leu Ser Asp Thr Ser Val Trp Glu Arg Arg Lys 215 220 Thr Lys Gly Lys Val Ala Ile Gln Lys Met Val Val Asp Leu Met Glu 230 235 Leu Tyr Leu His Arg Leu Arg Gln Lys Arg Tyr Pro Tyr Pro Lys Asn 250 245 Pro Ile Met Ala Asp Phe Ala Ala Gln Phe Pro Tyr Asn Ala Thr Pro 265 Asp Gln Lys Gln Ala Phe Leu Asp Val Glu Lys Asp Leu Thr Glu Arg

280 275 Glu Thr Pro Met Asp Arg Leu Ile Cys Gly Asp Val Gly Phe Gly Lys 290 295 300 Thr Glu Val Ala Leu Arg Ala Ile Phe Cys Val Val Ser Thr Gly Lys 310 315 Gln Ala Met Val Leu Ala Pro Thr Ile Val Leu Ala Xaa Asn Ile Thr 325 330 335 Ile Asp Leu Gly Ser Ser Arg Lys Lys Arg Leu His Leu Ser Lys His 340 345

- Pro Trp Met Cys Leu His Cys Pro Gln His Pro Tyr Gln Gly His 355 360 365
- (2) INFORMATION FOR SEQ ID NO:811:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..366
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594068 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:811: Met Ser Leu Leu Pro Asn Pro Asp Pro Ile Thr Val Pro Leu Val Leu 5 10 Lys Leu Cys Ser Phe Pro Pro Pro Arg Arg Leu Phe Ser Leu Arg Leu 25 20 Arg Arg Phe Thr Arg Lys Ser Ser Ser Leu Leu Pro Leu Val Ala Val 40 Ser Ser Leu Ser Ala Thr Xaa Ala Lys Pro Thr Arg Trp Arg Glu Lys 55 Pro Glu Leu Ala Glu Ser Asp Ser Ile Ser Leu Leu Asn Glu Arg Ile 75 70 Arg Arg Asp Leu Gly Lys Arg Glu Thr Ala Arg Pro Ala Met Asp Ser 90 95 8.5 Glu Glu Ala Glu Lys Tyr Ile His Met Val Lys Glu Gln Gln Glu Arg 100 105 Gly Leu Gln Lys Leu Lys Gly Ile Arg Gln Gly Thr Lys Ala Ala Gly 120 Asp Gly Ala Phe Ser Tyr Lys Val Asp Pro Tyr Ser Leu Leu Ser Gly 135 140 Asp Tyr Val Val His Lys Lys Val Gly Ile Gly Arg Phe Val Gly Ile 150 155 Lys Phe Asp Val Pro Lys Asp Ser Ser Glu Pro Leu Glu Tyr Val Phe 170 165 Ile Glu Tyr Ala Asp Gly Met Ala Lys Leu Pro Leu Lys Gln Ala Ser 185 180 Arg Leu Leu Tyr Arg Tyr Asn Leu Pro Asn Glu Thr Lys Arg Pro Arg 200 Thr Leu Ser Arg Leu Ser Asp Thr Ser Val Trp Glu Arg Arg Lys Thr 220 215 Lys Gly Lys Val Ala Ile Gln Lys Met Val Val Asp Leu Met Glu Leu 235 230 Tyr Leu His Arg Leu Arg Gln Lys Arg Tyr Pro Tyr Pro Lys Asn Pro 250 245 Ile Met Ala Asp Phe Ala Ala Gln Phe Pro Tyr Asn Ala Thr Pro Asp 265 Gln Lys Gln Ala Phe Leu Asp Val Glu Lys Asp Leu Thr Glu Arg Glu

280 Thr Pro Met Asp Arg Leu Ile Cys Gly Asp Val Gly Phe Gly Lys Thr

295

285

Glu Val Ala Leu Arg Ala Ile Phe Cys Val Val Ser Thr Gly Lys Gln 305 310 315 320

Ala Met Val Leu Ala Pro Thr Ile Val Leu Ala Xaa Asn Ile Thr Ile 325 330 335

Asp Leu Gly Ser Ser Arg Lys Lys Arg Leu His Leu Ser Lys His Pro 340 345 350

Trp Met Cys Leu His Cys Pro Gln His Pro Tyr Gln Gly His 355 360 365

- (2) INFORMATION FOR SEQ ID NO:812:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..100
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:812: gttctgcatc aacatgtctc ttgccgattt ctactcttct cgtccccaat tcggacaagg cttgtcatta atgtcggcga ctccagagat gatgttgtag
- (2) INFORMATION FOR SEQ ID NO:813:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..33
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594108
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

Val Leu His Gln His Val Ser Cys Arg Phe Leu Leu Phe Ser Ser Pro 1 5 5 10 5 15 15 11e Arg Thr Arg Leu Val Ile Asn Val Gly Asp Ser Arg Asp Val 20 25 30

Val

- (2) INFORMATION FOR SEQ ID NO:814:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..32
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594109

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

Phe Cys Ile Asn Met Ser Leu Ala Asp Phe Tyr Ser Ser Arg Pro Gln 1 5 10 15 Phe Gly Gln Gly Leu Ser Leu Met Ser Ala Thr Pro Glu Met Met Leu

(2) INFORMATION FOR SEQ ID NO:815:

2.0

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2366 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2366
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594130
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815: atgaaaagca aggaagagat aagagtttct gggtcgctta gagggttcac tttatgcgcc 60 aagtttgaga aacaaaagga gatctcttca gctctctctc atgacatcac tttgtcgagt 120 tcqtacaaqc aacaaqaqca gacaacaaqa atggtttctt caatcaagcc gcctaagaga 180 ttgcagcaat tcaggcccgt aattgcagct ggagcacctg acttgtgtaa ggttcaagca 240 300 cgagcqtqtc gggtagctct agatccttct ctttgtctct ttaaaggagt tggttgtgtt 360 qtqttqcttt qtaaqtttgg tatcagagct tccaggttac tacctaggag cgagaagatc tgctcaagat gtcttcgggc agagcagagg tggagaagtt cgacggagat ggggattaca 420 tcctqtqqaa aqaaaaqtta ctqqctcata tqqaqatqtt qgqacttttq gagggtctcg 480 gggaagaaga ggaagcagtg gttgaagatt ctaccactga gattagtgat ggaggaaacc 540 600 aagacccaga aactgcaact tctaaactgg aagacaagat cctcaaagaa aaaaagagga aaagccagat ctaccatcat cttgagcctg ggaaacaatg ttctgagaaa ggtcatcaaa 660 720 caaaagacag cagcaggtat gataaaggtc ctggatcagt tatttatggc aaaatctctt 780 ccaaatcgca tttacttgaa gcagaggctg tatggctaca agatgagtga gaatatgacg atggaggaga atgttaatga tttcttcaag ttaatatcgg acttggaaaa cgtaaaggtt 840 900 gtagtcccag atgaagatca agccatagtc ttgctcatgt ctttaccaag acagtttgat caactgaagg agacactgaa gtactgcaag actacacttc atctcgaaga aatcacaagt 960 1020 gccataaggt ctaagatctt ggagttggga gctagtgagg cagatcaaaa accaggggga 1080 aatgaccgaa caagaacaag agcagatcta agtcaaaggg agcaggaaaa acgtgttgga tctgtggcaa ggagggagag gaacaagcaa ggttccacat ctgaaagagg agaggcttct 1140 1200 actqtaactq ctcaaqtcac tgatgcagct gcactagtag tttcaagagc tttacttggc 1260 tttqctqaaq tcaccccaqa tacatqqatt ctaqacacaq ggtgttcctt ccatatgacc 1320 tqcaqaaaqq attqqatcat aqacttcaaq qaqactqcaa qcgggaaagt aaggatgggc 1380 aatqatactt attctqaaqt qaaaggaatt ggggatgtca gaatcaagaa tgaggatgga 1440 tctactatct tgctcactga tgtcaggctt ggtcacattg gtgcaaaaag gctgcaggtt 1500 ttqqtcaqta aaqqtcatct qqataaqaac atgattaaag agttqcagtt ttqtgaagat 1560 tqqttaqctt tqqaqctqca aaqcatqtca caaaagataa actcgactat gtgcattctg 1620 atctatgggg atcaccgaat gtaccattct ccattgattg aaaaccaaca ggacaagaag 1680 ctcaagattc tcaaaacaga taatgggctg gagttctgta accaggagtt tgattcattc 1740 tqcaqaaaaq aaqqaqttat aaqqcacatg acatgtgctt acacaccaca gcagaatggt 1800 qttgctgaaa ggatgaacag gaccatcatg aacaaggtca gatgcatgtt aagtgaatca qqqttqqqqa aacaqttctq qqcaqaaqca gcgtctactg ccgtgttcct catcaacaaa 1860 agcccaagct cttcaataga gtttgatatt cctgaagaga agtggactgg tcatccacca 1920 1980 gattacaaga tactcaagaa gtttggatca gtcgcttata ttcattcaga tcaaggaaag ctgaatccta gagcaaagaa ggggattttt ctcggatatc cagatggtgt aaagggattc 2040 aaaqtqtqqc tqctaqaaqa caqqaaatqt gtaqtctctc qaqacattqt ttttcaaqaa 2100 aatcaqatqt acaaqqaact gcagaagaat gatatgtctg aggaagaaaa acagctcact 2160 gaagtagaaa ggactctcat agagctaaag aatttgtctg cagatgatga aaatcagagt 2220 gaaggaggag ataagtcaaa ccaagaacaa gcttcaacaa caagatctgc aagtaaagac 2280 aaacaagtag aggaaactga ttctgatgat gattgtctag agaactatct actggccagg 2340 gatagaattc gaagacagat cagaga
- (2) INFORMATION FOR SEQ ID NO:816:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 788 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..788
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594131
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

Met Lys Ser Lys Glu Glu Ile Arg Val Ser Gly Ser Leu Arg Gly Phe 10 Thr Leu Cys Ala Lys Phe Glu Lys Gln Lys Glu Ile Ser Ser Ala Leu 2.0 25 Ser His Asp Ile Thr Leu Ser Ser Ser Tyr Lys Gln Gln Glu Gln Thr 4.0 Thr Arg Met Val Ser Ser Ile Lys Pro Pro Lys Arg Leu Gln Gln Phe 55 Arg Pro Val Ile Ala Ala Gly Ala Pro Asp Leu Cys Lys Val Gln Ala 75 70 Arg Ala Cys Arg Val Ala Leu Asp Pro Ser Leu Cys Leu Phe Lys Gly 90 85 Val Gly Cys Val Val Leu Leu Cys Lys Phe Gly Ile Arg Ala Ser Arg 105 Leu Leu Pro Arg Ser Glu Lys Ile Cys Ser Arg Cys Leu Arg Ala Glu 125 120 Gln Arg Trp Arg Ser Ser Thr Glu Met Gly Ile Thr Ser Cys Gly Lys 140 135 Lys Ser Tyr Trp Leu Ile Trp Arg Cys Trp Asp Phe Trp Arg Val Ser 155 150 Gly Lys Lys Arg Lys Gln Trp Leu Lys Ile Leu Pro Leu Arg Leu Val 170 165 Met Glu Glu Thr Lys Thr Gln Lys Leu Gln Leu Leu Asn Trp Lys Thr 185 190 180 Arg Ser Ser Lys Lys Lys Arg Gly Lys Ala Arg Ser Thr Ile Ile Leu 200 205 Ser Leu Gly Asn Asn Val Leu Arg Lys Val Ile Lys Gln Lys Thr Ala 215 220 Ala Gly Met Ile Lys Val Leu Asp Gln Leu Phe Met Ala Lys Ser Leu 235 240 230 Pro Asn Arg Ile Tyr Leu Lys Gln Arg Leu Tyr Gly Tyr Lys Met Ser 245 250 Glu Asn Met Thr Met Glu Glu Asn Val Asn Asp Phe Phe Lys Leu Ile 265 260 Ser Asp Leu Glu Asn Val Lys Val Val Val Pro Asp Glu Asp Gln Ala 275 280 Ile Val Leu Leu Met Ser Leu Pro Arg Gln Phe Asp Gln Leu Lys Glu 295 Thr Leu Lys Tyr Cys Lys Thr Thr Leu His Leu Glu Glu Ile Thr Ser 315 310 Ala Ile Arg Ser Lys Ile Leu Glu Leu Gly Ala Ser Glu Ala Asp Gln 325 330 335 Lys Pro Gly Gly Asn Asp Arg Thr Arg Thr Arg Ala Asp Leu Ser Gln 340 345 Arg Glu Gln Glu Lys Arg Val Gly Ser Val Ala Arg Arg Glu Arg Asn 360 Lys Gln Gly Ser Thr Ser Glu Arg Gly Glu Ala Ser Thr Val Thr Ala 375 Gln Val Thr Asp Ala Ala Ala Leu Val Val Ser Arg Ala Leu Leu Gly 395 390 Phe Ala Glu Val Thr Pro Asp Thr Trp Ile Leu Asp Thr Gly Cys Ser 410 Phe His Met Thr Cys Arg Lys Asp Trp Ile Ile Asp Phe Lys Glu Thr 425 420 Ala Ser Gly Lys Val Arg Met Gly Asn Asp Thr Tyr Ser Glu Val Lys 440 Gly Ile Gly Asp Val Arg Ile Lys Asn Glu Asp Gly Ser Thr Ile Leu 455 Leu Thr Asp Val Arg Leu Gly His Ile Gly Ala Lys Arg Leu Gln Val 475 470 Leu Val Ser Lys Gly His Leu Asp Lys Asn Met Ile Lys Glu Leu Gln

485 490 Phe Cys Glu Asp Trp Leu Ala Leu Glu Leu Gln Ser Met Ser Gln Lys 505 510 500 Ile Asn Ser Thr Met Cys Ile Leu Ile Tyr Gly Asp His Arg Met Tyr 520 His Ser Pro Leu Ile Glu Asn Gln Gln Asp Lys Lys Leu Lys Ile Leu 540 530 535 Lys Thr Asp Asn Gly Leu Glu Phe Cys Asn Gln Glu Phe Asp Ser Phe 550 555 Cys Arg Lys Glu Gly Val Ile Arg His Met Thr Cys Ala Tyr Thr Pro 565 570 Gln Gln Asn Gly Val Ala Glu Arg Met Asn Arg Thr Ile Met Asn Lys 580 585 Val Arg Cys Met Leu Ser Glu Ser Gly Leu Gly Lys Gln Phe Trp Ala 595 600 Glu Ala Ala Ser Thr Ala Val Phe Leu Ile Asn Lys Ser Pro Ser Ser 620 610 615 Ser Ile Glu Phe Asp Ile Pro Glu Glu Lys Trp Thr Gly His Pro Pro 635 630 Asp Tyr Lys Ile Leu Lys Lys Phe Gly Ser Val Ala Tyr Ile His Ser 650 655 645 Asp Gln Gly Lys Leu Asn Pro Arg Ala Lys Lys Gly Ile Phe Leu Gly 660 665 670 Tyr Pro Asp Gly Val Lys Gly Phe Lys Val Trp Leu Leu Glu Asp Arg 685 680 Lys Cys Val Val Ser Arg Asp Ile Val Phe Gln Glu Asn Gln Met Tyr 690 695 700 Lys Glu Leu Gln Lys Asn Asp Met Ser Glu Glu Glu Lys Gln Leu Thr 705 710 715 720 Glu Val Glu Arg Thr Leu Ile Glu Leu Lys Asn Leu Ser Ala Asp Asp 725 730 735 Glu Asn Gln Ser Glu Gly Gly Asp Lys Ser Asn Gln Glu Gln Ala Ser 740 745 750 Thr Thr Arg Ser Ala Ser Lys Asp Lys Gln Val Glu Glu Thr Asp Ser 755 760 765 Asp Asp Asp Cys Leu Glu Asn Tyr Leu Leu Ala Arg Asp Arg Ile Arg 780 775 Arg Gln Ile Arg 785 (2) INFORMATION FOR SEQ ID NO:817: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 738 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..738 (D) OTHER INFORMATION: / Ceres Seq. ID 1594133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817: Met Val Ser Ser Ile Lys Pro Pro Lys Arg Leu Gln Gln Phe Arg Pro

 (xi)
 SEQUENCE DESCRIPTION: SEQ ID NO:817:

 Met Val
 Ser Ser Ile Lys Pro Pro Lys Arg Leu Gln Gln Phe Arg Pro 1

 1
 5

 10
 15

 Val
 Ile Ala Ala Gly Ala Pro Asp Leu Cys Lys Val Gln Ala Arg Ala 20

 20
 25

 30

 Cys Arg Val Ala Leu Asp Pro Ser Leu Cys Leu Phe Lys Gly Val Gly 35

 Cys Val Val Leu Leu Cys Lys Phe Gly Ile Arg Ala Ser Arg Leu Leu 50

 Pro Arg Ser Glu Lys Ile Cys Ser Arg Cys Leu Arg Ala Glu Gln Arg 70

Trp Arg Ser Ser Thr Glu Met Gly Ile Thr Ser Cys Gly Lys Lys Ser 90 Tyr Trp Leu Ile Trp Arg Cys Trp Asp Phe Trp Arg Val Ser Gly Lys 105 100 Lys Arg Lys Gln Trp Leu Lys Ile Leu Pro Leu Arg Leu Val Met Glu 120 Glu Thr Lys Thr Gln Lys Leu Gln Leu Leu Asn Trp Lys Thr Arg Ser 135 140 Ser Lys Lys Arg Gly Lys Ala Arg Ser Thr Ile Ile Leu Ser Leu 150 155 Gly Asn Asn Val Leu Arg Lys Val Ile Lys Gln Lys Thr Ala Ala Gly 165 170 Met Ile Lys Val Leu Asp Gln Leu Phe Met Ala Lys Ser Leu Pro Asn 185 180 Arg Ile Tyr Leu Lys Gln Arg Leu Tyr Gly Tyr Lys Met Ser Glu Asn 200 205 Met Thr Met Glu Glu Asn Val Asn Asp Phe Phe Lys Leu Ile Ser Asp 210 215 220 Leu Glu Asn Val Lys Val Val Pro Asp Glu Asp Gln Ala Ile Val 230 235 Leu Leu Met Ser Leu Pro Arg Gln Phe Asp Gln Leu Lys Glu Thr Leu 250 245 Lys Tyr Cys Lys Thr Thr Leu His Leu Glu Glu Ile Thr Ser Ala Ile 260 265 Arg Ser Lys Ile Leu Glu Leu Gly Ala Ser Glu Ala Asp Gln Lys Pro 275 280 Gly Gly Asn Asp Arg Thr Arg Thr Arg Ala Asp Leu Ser Gln Arg Glu 300 295 Gln Glu Lys Arg Val Gly Ser Val Ala Arg Arg Glu Arg Asn Lys Gln 315 310 Gly Ser Thr Ser Glu Arg Gly Glu Ala Ser Thr Val Thr Ala Gln Val 330 325 Thr Asp Ala Ala Ala Leu Val Val Ser Arg Ala Leu Leu Gly Phe Ala 345 Glu Val Thr Pro Asp Thr Trp Ile Leu Asp Thr Gly Cys Ser Phe His 360 365 Met Thr Cys Arg Lys Asp Trp Ile Ile Asp Phe Lys Glu Thr Ala Ser 375 380 Gly Lys Val Arg Met Gly Asn Asp Thr Tyr Ser Glu Val Lys Gly Ile 395 390 Gly Asp Val Arg Ile Lys Asn Glu Asp Gly Ser Thr Ile Leu Leu Thr 410 415 405 Asp Val Arg Leu Gly His Ile Gly Ala Lys Arg Leu Gln Val Leu Val 420 425 Ser Lys Gly His Leu Asp Lys Asn Met Ile Lys Glu Leu Gln Phe Cys 440435 Glu Asp Trp Leu Ala Leu Glu Leu Gln Ser Met Ser Gln Lys Ile Asn 455 Ser Thr Met Cys Ile Leu Ile Tyr Gly Asp His Arg Met Tyr His Ser 475 470 Pro Leu Ile Glu Asn Gln Gln Asp Lys Lys Leu Lys Ile Leu Lys Thr 490 485 Asp Asn Gly Leu Glu Phe Cys Asn Gln Glu Phe Asp Ser Phe Cys Arg 505 500 Lys Glu Gly Val Ile Arg His Met Thr Cys Ala Tyr Thr Pro Gln Gln 520 515 Asn Gly Val Ala Glu Arg Met Asn Arg Thr Ile Met Asn Lys Val Arg 535 Cys Met Leu Ser Glu Ser Gly Leu Gly Lys Gln Phe Trp Ala Glu Ala 555 550 Ala Ser Thr Ala Val Phe Leu Ile Asn Lys Ser Pro Ser Ser Ser Ile

				565					570					575	
Glu	Phe	Asp	Ile 580	Pro	Glu	Glu	Lys	Trp 585	Thr	Gly	His	Pro	Pro 590	Asp	Tyr
Lys	Ile	Leu 595	Lys	Lys	Phe	Gly	Ser 600	Val	Ala	Tyr	Ile	His 605	Ser	Asp	Gln
Gly	Lys 610	Leu	Asn	Pro	Arg	Ala 615	Lys	Lys	Gly	Ile	Phe 620	Leu	Gly	Tyr	Pro
Asp 625	Gly	Val	Lys	Gly	Phe 630	Lys	Val	Trp	Leu	Leu 635	Glu	Asp	Arg	Lys	Cys 640
Val	Val	Ser	Arg	Asp 645	Ile	Val	Phe	Gln	Glu 650	Asn	Gln	Met	Tyr	Lys 655	Glu
Leu	Gln	Lys	Asn 660	Asp	Met	Ser	Glu	Glu 665	Glu	Lys	Gln	Leu	Thr 670	Glu	Val
Glu	Arg	Thr 675	Leu	Ile	Glu	Leu	Lys 680	Asn	Leu	Ser	Ala	Asp 685	Asp	Glu	Asn
Gln	Ser 690	Glu	Gly	Gly	Asp	Lys 695	Ser	Asn	Gln	Glu	Gln 700	Ala	Ser	Thr	Thr
Arg 705	Ser	Ala	Ser	Lys	Asp 710	Lys	Gln	Val	Glu	Glu 715	Thr	Asp	Ser	Asp	Asp 720
Asp	Cys	Leu	Glu	Asn 725	Tyr	Leu	Leu	Ala	Arg 730	Asp	Arg	Ile	Arg	Arg 735	Gln
Ile	Arg														

(2) INFORMATION FOR SEQ ID NO:818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -

tcctcatcaa caaaaqccca agctcttcaa tag

- (B) LOCATION: 1..1533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818: atgaaaagca aggaagagat aagagtttct gggtcgctta gagggttcac tttatgcgcc 60 aagtttgaga aacaaaagga gatctcttca gctctctctc atgacatcac tttgtcgagt 120 tcgtacaagc aacaagagca gacaacaaga atggtttctt caatcaagcc gcctaagaga 180 ttgcagcaat tcaggcccgt aattgcagct ggagcacctg acttgtgtaa ggttcaagca 240 300 cgagcgtgtc gggtagctct agatccttct ctttgtctct ttaaaggagt tggttgtt 360 gtgttgcttt gtaagtttgg tatcagagct tccaggttac tacctaggag cgagaagatc 420 tgctcaagat gtcttcgggc agagcagagg tggagaagtt cgacggagat ggggattaca 480 tcctgtggaa agaaaagtta ctggctcata tggagatgtt gggacttttg gagggtctcg gggaagaaga ggaagcagtg gttgaagatt ctaccactga gattagtgat ggaggaaacc 540 aagacccaga aactgcaact tctaaactgg aagacaagat cctcaaagaa aaaaagagga aaagccagat ctaccatcat cttgagcctg ggaaacaatg ttctgagaaa ggtcatcaaa 660 720 caaaagacag cagcagaggc agatcaaaaa ccagggggaa atgaccgaac aagaacaaga 780 gcagatctaa gtcaaaggga gcaggaaaaa cgtgttggat ctgtggcaag gagggagagg aacaagcaag gttccacatc tgaaagagga gaggcttcta ctgtaactgc tcaagtcact 840 gatgcagctg cactagtagt ttcaagagct ttacttggct ttgctgaagt caccccagat 900 acatggattc tagacacagg gtgttccttc catatgacct gcagaaagga ttggatcata 960 gacttcaagg agactgcaag cgggaaagta aggatgggca atgatactta ttctgaagtg 1020 aaaggaattg gggatgtcag aatcaagaat gaggatggat ctactatctt gctcactgat 1080 1140 gtcaggcttg gtcacattgg tgcaaaaagg ctgcaggttt tggtcagtaa aggtcatctg gataagaaca tgattaaaga gttgcagttt tgtgaagatt ggttagcttt ggagctgcaa 1200 agcatgtcac aaaagataaa ctcgactatg tgcattctga tctatgggga tcaccgaatg 1260 taccattctc cattgattga aaaccaacag gacaagaagc tcaagattct caaaacagat 1320 aatgggctgg agttctgtaa ccaggagttt gattcattct gcagaaaaga aggagttata 1380 1440 aggcacatga catgtgctta cacaccacag cagaatggtg ttgctgaaag gatgaacagg 1500 accatcatga acaagggttg gggaaacagt tctgggcaga agcagcgtct actgccgtgt

- (2) INFORMATION FOR SEQ ID NO:819:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819: Met Lys Ser Lys Glu Glu Ile Arg Val Ser Gly Ser Leu Arg Gly Phe 10 Thr Leu Cys Ala Lys Phe Glu Lys Gln Lys Glu Ile Ser Ser Ala Leu 20 25 Ser His Asp Ile Thr Leu Ser Ser Ser Tyr Lys Gln Gln Glu Gln Thr 40 Thr Arg Met Val Ser Ser Ile Lys Pro Pro Lys Arg Leu Gln Gln Phe 55 Arg Pro Val Ile Ala Ala Gly Ala Pro Asp Leu Cys Lys Val Gln Ala 75 7.0 Arg Ala Cys Arg Val Ala Leu Asp Pro Ser Leu Cys Leu Phe Lys Gly 90 85 Val Gly Cys Val Val Leu Leu Cys Lys Phe Gly Ile Arg Ala Ser Arg 100 105 Leu Leu Pro Arg Ser Glu Lys Ile Cys Ser Arg Cys Leu Arg Ala Glu 115 120 Gln Arg Trp Arg Ser Ser Thr Glu Met Gly Ile Thr Ser Cys Gly Lys 140 130 135 Lys Ser Tyr Trp Leu Ile Trp Arg Cys Trp Asp Phe Trp Arg Val Ser 150 155 Gly Lys Lys Arg Lys Gln Trp Leu Lys Ile Leu Pro Leu Arg Leu Val 165 170 175 Met Glu Glu Thr Lys Thr Gln Lys Leu Gln Leu Leu Asn Trp Lys Thr 185 190 Arg Ser Ser Lys Lys Lys Arg Gly Lys Ala Arg Ser Thr Ile Ile Leu 205 200 Ser Leu Gly Asn Asn Val Leu Arg Lys Val Ile Lys Gln Lys Thr Ala 220 215 Ala Glu Ala Asp Gln Lys Pro Gly Gly Asn Asp Arg Thr Arg Thr Arg 235 240 230 Ala Asp Leu Ser Gln Arg Glu Gln Glu Lys Arg Val Gly Ser Val Ala 250 Arg Arg Glu Arg Asn Lys Gln Gly Ser Thr Ser Glu Arg Gly Glu Ala 265 260 Ser Thr Val Thr Ala Gln Val Thr Asp Ala Ala Leu Val Val Ser 280 285 Arg Ala Leu Leu Gly Phe Ala Glu Val Thr Pro Asp Thr Trp Ile Leu 300 295 Asp Thr Gly Cys Ser Phe His Met Thr Cys Arg Lys Asp Trp Ile Ile 315 310 Asp Phe Lys Glu Thr Ala Ser Gly Lys Val Arg Met Gly Asn Asp Thr 330 Tyr Ser Glu Val Lys Gly Ile Gly Asp Val Arg Ile Lys Asn Glu Asp 345 Gly Ser Thr Ile Leu Leu Thr Asp Val Arg Leu Gly His Ile Gly Ala 360

Lys Arg Leu Gln Val Leu Val Ser Lys Gly His Leu Asp Lys Asn Met

Ile Lys Glu Leu Gln Phe Cys Glu Asp Trp Leu Ala Leu Glu Leu Gln

375

380

390 395 385 Ser Met Ser Gln Lys Ile Asn Ser Thr Met Cys Ile Leu Ile Tyr Gly 405 410 Asp His Arg Met Tyr His Ser Pro Leu Ile Glu Asn Gln Gln Asp Lys 420 425 Lys Leu Lys Ile Leu Lys Thr Asp Asn Gly Leu Glu Phe Cys Asn Gln 445 435 440 Glu Phe Asp Ser Phe Cys Arg Lys Glu Gly Val Ile Arg His Met Thr 450 455 Cys Ala Tyr Thr Pro Gln Gln Asn Gly Val Ala Glu Arg Met Asn Arg 470 475 480 Thr Ile Met Asn Lys Gly Trp Gly Asn Ser Ser Gly Gln Lys Gln Arg 485 490 495 Leu Leu Pro Cys Ser Ser Ser Thr Lys Ala Gln Ala Leu Gln 500 505 (2) INFORMATION FOR SEQ ID NO:820:

- - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 460 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..460
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594137
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:
- Met Val Ser Ser Ile Lys Pro Pro Lys Arg Leu Gln Gln Phe Arg Pro 10
- Val Ile Ala Ala Gly Ala Pro Asp Leu Cys Lys Val Gln Ala Arg Ala 25
- Cys Arg Val Ala Leu Asp Pro Ser Leu Cys Leu Phe Lys Gly Val Gly 40 45
- Cys Val Val Leu Leu Cys Lys Phe Gly Ile Arg Ala Ser Arg Leu Leu 60 55
- Pro Arg Ser Glu Lys Ile Cys Ser Arg Cys Leu Arg Ala Glu Gln Arg 70 75
- Trp Arg Ser Ser Thr Glu Met Gly Ile Thr Ser Cys Gly Lys Lys Ser 90 85
- Tyr Trp Leu Ile Trp Arg Cys Trp Asp Phe Trp Arg Val Ser Gly Lys 105 100
- Lys Arg Lys Gln Trp Leu Lys Ile Leu Pro Leu Arg Leu Val Met Glu 120 115 125
- Glu Thr Lys Thr Gln Lys Leu Gln Leu Leu Asn Trp Lys Thr Arg Ser 135
- Ser Lys Lys Lys Arg Gly Lys Ala Arg Ser Thr Ile Ile Leu Ser Leu 150 155 160
- Gly Asn Asn Val Leu Arg Lys Val Ile Lys Gln Lys Thr Ala Ala Glu 170 165
- Ala Asp Gln Lys Pro Gly Gly Asn Asp Arg Thr Arg Thr Arg Ala Asp 185 180
- Leu Ser Gln Arg Glu Gln Glu Lys Arg Val Gly Ser Val Ala Arg Arg 200
- Glu Arg Asn Lys Gln Gly Ser Thr Ser Glu Arg Gly Glu Ala Ser Thr 215 220
- Val Thr Ala Gln Val Thr Asp Ala Ala Ala Leu Val Val Ser Arg Ala 235 230
- Leu Leu Gly Phe Ala Glu Val Thr Pro Asp Thr Trp Ile Leu Asp Thr 250 245
- Gly Cys Ser Phe His Met Thr Cys Arg Lys Asp Trp Ile Ile Asp Phe 265

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Lys Glu Thr Ala Ser Gly Lys Val Arg Met Gly Asn Asp Thr Tyr Ser
                           280
                                                285
Glu Val Lys Gly Ile Gly Asp Val Arg Ile Lys Asn Glu Asp Gly Ser
                                            300
                       295
Thr Ile Leu Leu Thr Asp Val Arg Leu Gly His Ile Gly Ala Lys Arg
                                      315
                    310
Leu Gln Val Leu Val Ser Lys Gly His Leu Asp Lys Asn Met Ile Lys
                                    330
                325
Glu Leu Gln Phe Cys Glu Asp Trp Leu Ala Leu Glu Leu Gln Ser Met
                                                    350
                                345
            340
Ser Gln Lys Ile Asn Ser Thr Met Cys Ile Leu Ile Tyr Gly Asp His
                                                365
                            360
Arg Met Tyr His Ser Pro Leu Ile Glu Asn Gln Gln Asp Lys Lys Leu
                        375
                                            380
Lys Ile Leu Lys Thr Asp Asn Gly Leu Glu Phe Cys Asn Gln Glu Phe
                    390
                                       395
Asp Ser Phe Cys Arg Lys Glu Gly Val Ile Arg His Met Thr Cys Ala
                                                       415
                                    410
Tyr Thr Pro Gln Gln Asn Gly Val Ala Glu Arg Met Asn Arg Thr Ile
                                                   430
                                425
Met Asn Lys Gly Trp Gly Asn Ser Ser Gly Gln Lys Gln Arg Leu Leu
                            440
Pro Cys Ser Ser Ser Thr Lys Ala Gln Ala Leu Gln
                                            460
                        455
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- (2) INFORMATION FOR SEQ ID NO:821:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1371
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594182
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

atggaagete taaactetat ettaacegge tacgeegtgg cageeetate agtetaeget 60 ctttggttct acttcctgtc ccgaagacta accggtccca aagtcttacc gttcgtagga 120 agcttaccgt atctaatcgc taaccggagc cgaattcacg attggatcgc tgataatctc 180 cgagcaactg gtggtacgta tcaaacatgc accatggtga tacctttcgt agccaaggcg 240 caagggtttt acactgtgac gtgtcaccca aaaaacgtcg agcatatcct taagacacgg 300 ttcgacaact atccgaaagg tccgatgtgg cgcgctgctt tccacgacct gttaggacaa 360 ggaatettea acagegaegg tgaeaegtgg eteatgeaae gtaagaetge agegettgag 420 ttcacaacta gaactcttag acaagccatg gctcggtggg ttaacgggac tatcaagaac 480 cggttatggc ttatattaga ccgtgcggtt caaaacaaca aaccggttga tcttcaagat 540 tigtttttga ggttaacttt tgacaacatt tgtggtctga cttttggtaa agacccggag 600 acgctctctc tggatctacc ggataatccc ttctctgtcg cttttgacac cgcgacagag 660 gctactctaa agagacttct ctacaccggt ttcttgtgga ggattcagaa agctatgggg 720 attggatcag aagataagct caagaagagt cttgaagtcg ttgagactta catgaacgat 780 gcaatcgacg ctcggaaaaa ctctccctcc gatgatcttt tgtcacgttt cttgaagaaa 840 cgtgacgtta acggtaacgt tcttccaaca gatgttcttc agcgtatcgc gcttaacttt 900 gttctcgcgg gccgtgacac ttcttcggtg gccttgagct ggttcttctg gctcgtcatg 960 aataaccggg aggtggaaac gaagatcgtt aacgagttgt cgatggttct gaaggagaca 1020 cgtggcaatg atcaggagaa atggacggag gagccgttag agttcgacga ggcagatagg 1080 ctcgtttacc tcaaggctgc tttggctgaa acgctgcgtt tataccettc tgtgcctcag 1140 natgacgttt tgccggacgg gactttcgtg ncaagaggnt cgacggtgac ctactcgatt 1200 tactcgatcg gacgtatgaa aacaatttgg ggcgaagatt gtctcgagtt ccgtccggaa cggtggctga cagncgacgg tgaacggttt gagactnccc aaagatggtt acaagttcgt agcgttcnac gccggnccaa ggacttgctt gggaaaggac ttggcttata a

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822: Met Glu Ala Leu Asn Ser Ile Leu Thr Gly Tyr Ala Val Ala Ala Leu 10 5 Ser Val Tyr Ala Leu Trp Phe Tyr Phe Leu Ser Arg Arg Leu Thr Gly 25 Pro Lys Val Leu Pro Phe Val Gly Ser Leu Pro Tyr Leu Ile Ala Asn 40 Arg Ser Arg Ile His Asp Trp Ile Ala Asp Asn Leu Arg Ala Thr Gly 55 Gly Thr Tyr Gln Thr Cys Thr Met Val Ile Pro Phe Val Ala Lys Ala 75 70 Gln Gly Phe Tyr Thr Val Thr Cys His Pro Lys Asn Val Glu His Ile 90 Leu Lys Thr Arg Phe Asp Asn Tyr Pro Lys Gly Pro Met Trp Arg Ala 100 105 110 Ala Phe His Asp Leu Leu Gly Gln Gly Ile Phe Asn Ser Asp Gly Asp 115 120 125 Thr Trp Leu Met Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg 130 135 140 Thr Leu Arg Gln Ala Met Ala Arg Trp Val Asn Gly Thr Ile Lys Asn 145 150 155 Arg Leu Trp Leu Ile Leu Asp Arg Ala Val Gln Asn Asn Lys Pro Val 170 175 165 Asp Leu Gln Asp Leu Phe Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly 180 185 190 Leu Thr Phe Gly Lys Asp Pro Glu Thr Leu Ser Leu Asp Leu Pro Asp 200 205 195 Asn Pro Phe Ser Val Ala Phe Asp Thr Ala Thr Glu Ala Thr Leu Lys 220 215 Arg Leu Leu Tyr Thr Gly Phe Leu Trp Arg Ile Gln Lys Ala Met Gly 230 235 240 Ile Gly Ser Glu Asp Lys Leu Lys Lys Ser Leu Glu Val Val Glu Thr 250 255 245 Tyr Met Asn Asp Ala Ile Asp Ala Arg Lys Asn Ser Pro Ser Asp Asp 265 260 Leu Leu Ser Arg Phe Leu Lys Lys Arg Asp Val Asn Gly Asn Val Leu 280 Pro Thr Asp Val Leu Gln Arg Ile Ala Leu Asn Phe Val Leu Ala Gly 295 Arg Asp Thr Ser Ser Val Ala Leu Ser Trp Phe Phe Trp Leu Val Met 315 310 Asn Asn Arg Glu Val Glu Thr Lys Ile Val Asn Glu Leu Ser Met Val 330 Leu Lys Glu Thr Arg Gly Asn Asp Gln Glu Lys Trp Thr Glu Glu Pro 345 Leu Glu Phe Asp Glu Ala Asp Arg Leu Val Tyr Leu Lys Ala Ala Leu 360 Ala Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Gln Xaa Asp Val Leu 375 380 Pro Asp Gly Thr Phe Val Xaa Arg Xaa Ser Thr Val Thr Tyr Ser Ile 395 390 Tyr Ser Ile Gly Arg Met Lys Thr Ile Trp Gly Glu Asp Cys Leu Glu

410 405 Phe Arg Pro Glu Arg Trp Leu Thr Xaa Asp Gly Glu Arg Phe Glu Thr 420 425 430 Xaa Gln Arg Trp Leu Gln Val Arg Ser Val Xaa Arg Arg Xaa Lys Asp 435 440 445 Leu Leu Gly Lys Gly Leu Gly Leu 455 (2) INFORMATION FOR SEQ ID NO:823: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..385 (D) OTHER INFORMATION: / Ceres Seq. ID 1594185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823: Met Val Ile Pro Phe Val Ala Lys Ala Gln Gly Phe Tyr Thr Val Thr 10 Cys His Pro Lys Asn Val Glu His Ile Leu Lys Thr Arg Phe Asp Asn 25 20 Tyr Pro Lys Gly Pro Met Trp Arg Ala Ala Phe His Asp Leu Leu Gly 40 Gln Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu Met Gln Arg Lys 55 Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg Gln Ala Met Ala 75 70 Arg Trp Val Asn Gly Thr Ile Lys Asn Arg Leu Trp Leu Ile Leu Asp 85 90 Arg Ala Val Gln Asn Asn Lys Pro Val Asp Leu Gln Asp Leu Phe Leu 105 Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Thr Phe Gly Lys Asp Pro 120 125 Glu Thr Leu Ser Leu Asp Leu Pro Asp Asn Pro Phe Ser Val Ala Phe 135 140 Asp Thr Ala Thr Glu Ala Thr Leu Lys Arg Leu Leu Tyr Thr Gly Phe 150 155 Leu Trp Arg Ile Gln Lys Ala Met Gly Ile Gly Ser Glu Asp Lys Leu 170 175 165 Lys Lys Ser Leu Glu Val Val Glu Thr Tyr Met Asn Asp Ala Ile Asp 180 185 190 Ala Arg Lys Asn Ser Pro Ser Asp Asp Leu Leu Ser Arg Phe Leu Lys 195 200 205 Lys Arg Asp Val Asn Gly Asn Val Leu Pro Thr Asp Val Leu Gln Arg 220 215 Ile Ala Leu Asn Phe Val Leu Ala Gly Arg Asp Thr Ser Ser Val Ala 235 230 Leu Ser Trp Phe Phe Trp Leu Val Met Asn Asn Arg Glu Val Glu Thr 250 245 Lys Ile Val Asn Glu Leu Ser Met Val Leu Lys Glu Thr Arg Gly Asn 265 260 Asp Gln Glu Lys Trp Thr Glu Glu Pro Leu Glu Phe Asp Glu Ala Asp 280 Arg Leu Val Tyr Leu Lys Ala Ala Leu Ala Glu Thr Leu Arg Leu Tyr 295 Pro Ser Val Pro Gln Xaa Asp Val Leu Pro Asp Gly Thr Phe Val Xaa

310

325

Arg Xaa Ser Thr Val Thr Tyr Ser Ile Tyr Ser Ile Gly Arg Met Lys

315

330

(2) INFORMATION FOR SEQ ID NO:827: (i) SEQUENCE CHARACTERISTICS:

Thr Ile Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu Arg Trp Leu 340 345 Thr Xaa Asp Gly Glu Arg Phe Glu Thr Xaa Gln Arg Trp Leu Gln Val 360 365 Arg Ser Val Xaa Arg Arg Xaa Lys Asp Leu Leu Gly Lys Gly Leu Gly 375 380 Leu 385 (2) INFORMATION FOR SEQ ID NO:824: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..129 (D) OTHER INFORMATION: / Ceres Seq. ID 1594192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824: ctgctcgcca agtgtttcaa gactatcaag tttctaacag ataagttgag ttgttcctcc 60 tccaccactg ctattccaca aggacaacct cctatggaga tgccatcgag gagatttgat gagccttag (2) INFORMATION FOR SEQ ID NO:825: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..42 (D) OTHER INFORMATION: / Ceres Seq. ID 1594193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825: Leu Leu Ala Lys Cys Phe Lys Thr Ile Lys Phe Leu Thr Asp Lys Leu 5 10 Ser Cys Ser Ser Ser Thr Thr Ala Ile Pro Gln Gly Gln Pro Pro Met 25 30 20 Glu Met Pro Ser Arg Arg Phe Asp Glu Pro (2) INFORMATION FOR SEQ ID NO:826: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..336 (D) OTHER INFORMATION: / Ceres Seq. ID 1594249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826: atggcatatc ctctctctac aaactctcgt tggatcatcg acgaaaaagg gcaaagagtg 60 aagctggcgt gtgtgaattg gccatcacat ttgcagcctg tggtggcgga agggctgagc 120 aagcagagtg tagatgactt ggccaagaag ataatggcaa tgggtttcaa ctgtgttagg 180 tttacttggc cacttgatct agctacaaat gagacgttgg ctaataatgt tactgtgaga 240 caatcttttc aaagtcttgg tcttaatgat gatatttctg gtttcgaaac aaagaaccca 300 tccatgattg atcttcccct cattgaagct tacaag

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594250
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

Met Ala Tyr Pro Leu Ser Thr Asn Ser Arg Trp Ile Ile Asp Glu Lys 5 10

Gly Gln Arg Val Lys Leu Ala Cys Val Asn Trp Pro Ser His Leu Gln 25

Pro Val Val Ala Glu Gly Leu Ser Lys Gln Ser Val Asp Asp Leu Ala 4.5 4.0

Lys Lys Ile Met Ala Met Gly Phe Asn Cys Val Arg Phe Thr Trp Pro 55 60

Leu Asp Leu Ala Thr Asn Glu Thr Leu Ala Asn Asn Val Thr Val Arg 70 75

Gln Ser Phe Gln Ser Leu Gly Leu Asn Asp Asp Ile Ser Gly Phe Glu 90

Thr Lys Asn Pro Ser Met Ile Asp Leu Pro Leu Ile Glu Ala Tyr Lys 105

- (2) INFORMATION FOR SEQ ID NO:828:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..61
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594252
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

Met Ala Met Gly Phe Asn Cys Val Arg Phe Thr Trp Pro Leu Asp Leu 5 1.0

Ala Thr Asn Glu Thr Leu Ala Asn Asn Val Thr Val Arg Gln Ser Phe 25

Gln Ser Leu Gly Leu Asn Asp Asp Ile Ser Gly Phe Glu Thr Lys Asn 40

Pro Ser Met Ile Asp Leu Pro Leu Ile Glu Ala Tyr Lys 55

- (2) INFORMATION FOR SEQ ID NO:829:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..447
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

atgtatataa aatacctact tgcatggtta aaatatctgc aagactacaa ctctctcgct tttnctaaag cgaaacaaag tggtttgcct ccactggtgt gggacgtaaa gatcgcaagc tatgcaacat ggtgggctaa ccagaggaga tacgactgct ccttaaccca ctcgaccggc

ccatacggtg agaacttgtt ctggggaagt ggctcagact ttacatcgac tttcgcagtg 240 gagtcatgga ctgtggaggc taagtcctac aaccacatga ccaacacgtg tgaaggagat 300 ggtatgtgtg gtcactacac tcagatcgtg tggcgtgaaa ccaggcgcct aggttgcgct 360 agagttgtct gcgagaacgg cgcaggagtt ttcatcactt gcaactacga ccctccgggt 420 aactacgttg gggagaagcc ttactaa

- (2) INFORMATION FOR SEQ ID NO:830:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594283
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met Tyr Ile Lys Tyr Leu Leu Ala Trp Leu Lys Tyr Leu Gln Asp Tyr 1 10 15

Asn Ser Leu Ala Phe Xaa Lys Ala Lys Gln Ser Gly Leu Pro Pro Leu 20 25 30

Val Trp Asp Val Lys Ile Ala Ser Tyr Ala Thr Trp Trp Ala Asn Gln 35 40 45

Arg Arg Tyr Asp Cys Ser Leu Thr His Ser Thr Gly Pro Tyr Gly Glu
50 60

Asn Leu Phe Trp Gly Ser Gly Ser Asp Phe Thr Ser Thr Phe Ala Val 65 70 75 80

Glu Ser Trp Thr Val Glu Ala Lys Ser Tyr Asn His Met Thr Asn Thr 85 90 95

Cys Glu Gly Asp Gly Met Cys Gly His Tyr Thr Gln Ile Val Trp Arg $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Glu Thr Arg Arg Leu Gly Cys Ala Arg Val Val Cys Glu Asn Gly Ala 115 120 125

Gly Val Phe Ile Thr Cys Asn Tyr Asp Pro Pro Gly Asn Tyr Val Gly 130 135 140

Glu Lys Pro Tyr

145

- (2) INFORMATION FOR SEQ ID NO:831:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..573
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594285
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

atgageteat ectatttaeg agtaatatta etettaggtg ecettaatgt egeegtttet 60 ttatcaataa ccaactcatt aataaccaaa tccgcaacac ttggtcaggt gttccgaatc 120 tgtaagaatt tgtgtccggg atgtgaccac gactccttgc agttcttgtt ccgacacaac 180 ctggtccgtg ccgcaagatt cgaacctcct ttgatatggg accgcagact ccagaactac 240 gcccaagggt gggctaatca aagaagggga gattgtgctt tgagacactc tgtctcaaac 300 ggagagttta atctcggcga gaacatctac tggggatacg gcgccaactg gtctccggcc 360 gacgcggtgg ttgcatgggc cagcgagaag aggttttatc attacggctc caacacgtgc 420 gacgctggtc agatgtgtgg tcattacaca cagattgtgt ggaagagcac taggagggtc 480 ggatgtgcac gtgtggtgtg cgacaatggt gggatcttca tgacttgtaa ctatgatcct 540 cccggtaact acatcggcca gaaaccctat taa

- (2) INFORMATION FOR SEQ ID NO:832:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..190
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594286
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

Met Ser Ser Ser Tyr Leu Arg Val Ile Leu Leu Leu Gly Ala Leu Asn 1 5 10 15

Val Ala Val Ser Leu Ser Ile Thr Asn Ser Leu Ile Thr Lys Ser Ala 20 25 30

Thr Leu Gly Gln Val Phe Arg Ile Cys Lys Asn Leu Cys Pro Gly Cys 35 40 45

Asp His Asp Ser Leu Gln Phe Leu Phe Arg His Asn Leu Val Arg Ala 50 55 60

Ala Arg Phe Glu Pro Pro Leu Ile Trp Asp Arg Arg Leu Gln Asn Tyr 65 70 75 80

Ala Gln Gly Trp Ala Asn Gln Arg Arg Gly Asp Cys Ala Leu Arg His 85 90 95

Ser Val Ser Asn Gly Glu Phe Asn Leu Gly Glu Asn Ile Tyr Trp Gly
100 105 110

Tyr Gly Ala Asn Trp Ser Pro Ala Asp Ala Val Val Ala Trp Ala Ser 115 120 125

Glu Lys Arg Phe Tyr His Tyr Gly Ser Asn Thr Cys Asp Ala Gly Gln 130 135 140

Met Cys Gly His Tyr Thr Gln Ile Val Trp Lys Ser Thr Arg Arg Val 145 150 155 160

Gly Cys Ala Arg Val Val Cys Asp Asn Gly Gly Ile Phe Met Thr Cys 165 170 175

Asn Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Lys Pro Tyr 180 185 190

- (2) INFORMATION FOR SEQ ID NO:833:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594332
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

(222) 02202102				_			
	atggtagatc	aaaataaagc	atttggttgg	gcggccaacg	acgaatcggg	cgtcctctct	60
	ccatttcatt	tctctagaag	agaaaatggt	gagaacgatg	taacggtgaa	gatcttgttc	120
	tataatattt	gtcactctga	tcttcatacc	atcaagaacc	attggggatt	ctctcgttac	180
	cccattattc	ccaaqcatga	aatcgttgga	atagcaacaa	aagttgggaa	gaatgtgaca	240
	aagtttaaag	aaggagaccg	agtaggagta	ggcgtaataa	tcggttcatg	ccaatcatgt	300
	gaatcatgta	accaagactt	agaaaactat	tgtcctaaag	tcgttttcac	atacaactct	360
	catteeteta	acqqaaccaq	cagaaaccaa	ggtggttatt	ccgacgtaat	tgttgtcgat	420
	caccacttta	tcctaagcat	tcccgatggt	ttaccaagcg	attcaggcgc	gccgctgctc	480
	tatactage	tcactatata	cagtcccatg	aagtattatg	gcatgactaa	agaatcaggg	540
	aaaggtttag	atataaataa	acttggtgga	cttaatcata	togotottaa	gattggtaaa	600
	adacytttay	gigigaatgg	tgtgattagt	aggtgatga	adaaadadad	agaaggaatt	660
	gcctttggtt	taagagttac	Lylyallagi	aggicalcaa	agaaagagag	agaageaace	720
	gatcggcttg	gtgctgattc	gtttcttgtt	acaacggatt	ctcaaaagat	gaaggaagcg	
	gttggaacta	tggatttcat	tatcgatacg	gtatcagcag	aacatgctct	attaccgttg	780
	tttagtttgc	ttaaagtgaa	tggaaagctt	gtggctttag	gcttaccgga	gaagccactc	840
	gacctgccaa	ttttctctct	agttctcgga	aggaaaatgg	tgggaggaag	tcagattgga	900
			-				

gggatgaagg ggacacaaga gatgcttgag ttctgtgcca agcataaaat cgtttcggat attgagetea taaagatgag tgatateaac tetgegatgg acegtttgge taaatetgat 1020 gtcaggtacc ggttcgtgat cgatgtggcc aactctttac tccctgaatc gtcagctgag 1080 attttaacgg agcaggtgga ccatggagtc tcgatcacgt ctagattctg a

- (2) INFORMATION FOR SEQ ID NO:834:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..376
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594333
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Met Val Asp Gln Asn Lys Ala Phe Gly Trp Ala Ala Asn Asp Glu Ser 10 5

Gly Val Leu Ser Pro Phe His Phe Ser Arg Arg Glu Asn Gly Glu Asn 25 20

Asp Val Thr Val Lys Ile Leu Phe Cys Gly Val Cys His Ser Asp Leu 4.5 40

His Thr Ile Lys Asn His Trp Gly Phe Ser Arg Tyr Pro Ile Ile Pro 60 55

Gly His Glu Ile Val Gly Ile Ala Thr Lys Val Gly Lys Asn Val Thr 75 7.0

Lys Phe Lys Glu Gly Asp Arg Val Gly Val Gly Val Ile Ile Gly Ser 90 85

Cys Gln Ser Cys Glu Ser Cys Asn Gln Asp Leu Glu Asn Tyr Cys Pro 105 110

Lys Val Val Phe Thr Tyr Asn Ser Arg Ser Ser Asp Gly Thr Ser Arg 125 120

Asn Gln Gly Gly Tyr Ser Asp Val Ile Val Val Asp His Arg Phe Val 140 135

Leu Ser Ile Pro Asp Gly Leu Pro Ser Asp Ser Gly Ala Pro Leu Leu 155 150

Cys Ala Gly Ile Thr Val Tyr Ser Pro Met Lys Tyr Tyr Gly Met Thr 175 170 165

Lys Glu Ser Gly Lys Arg Leu Gly Val Asn Gly Leu Gly Gly Leu Gly 185 190 180

His Ile Ala Val Lys Ile Gly Lys Ala Phe Gly Leu Arg Val Thr Val 200 205

Ile Ser Arg Ser Ser Lys Lys Glu Arg Glu Ala Ile Asp Arg Leu Gly 215

Ala Asp Ser Phe Leu Val Thr Thr Asp Ser Gln Lys Met Lys Glu Ala 235 230

Val Gly Thr Met Asp Phe Ile Ile Asp Thr Val Ser Ala Glu His Ala 250 245

Leu Leu Pro Leu Phe Ser Leu Leu Lys Val Asn Gly Lys Leu Val Ala 265 260

Leu Gly Leu Pro Glu Lys Pro Leu Asp Leu Pro Ile Phe Ser Leu Val 285 280

Leu Gly Arg Lys Met Val Gly Gly Ser Gln Ile Gly Gly Met Lys Gly 295 300 290

Thr Gln Glu Met Leu Glu Phe Cys Ala Lys His Lys Ile Val Ser Asp 310

Ile Glu Leu Ile Lys Met Ser Asp Ile Asn Ser Ala Met Asp Arg Leu 330 325

Ala Lys Ser Asp Val Arg Tyr Arg Phe Val Ile Asp Val Ala Asn Ser 345 340

Leu Leu Pro Glu Ser Ser Ala Glu Ile Leu Thr Glu Gln Val Asp His

365 360 Gly Val Ser Ile Thr Ser Arg Phe 370 375 (2) INFORMATION FOR SEQ ID NO:835: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..207 (D) OTHER INFORMATION: / Ceres Seq. ID 1594335 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835: Met Lys Tyr Tyr Gly Met Thr Lys Glu Ser Gly Lys Arg Leu Gly Val 10 5 Asn Gly Leu Gly Gly Leu Gly His Ile Ala Val Lys Ile Gly Lys Ala 25 20 Phe Gly Leu Arg Val Thr Val Ile Ser Arg Ser Ser Lys Lys Glu Arg 40 Glu Ala Ile Asp Arg Leu Gly Ala Asp Ser Phe Leu Val Thr Thr Asp 60 55 Ser Gln Lys Met Lys Glu Ala Val Gly Thr Met Asp Phe Ile Ile Asp 75 70 Thr Val Ser Ala Glu His Ala Leu Leu Pro Leu Phe Ser Leu Leu Lys 85 90 Val Asn Gly Lys Leu Val Ala Leu Gly Leu Pro Glu Lys Pro Leu Asp 105 110 Leu Pro Ile Phe Ser Leu Val Leu Gly Arg Lys Met Val Gly Gly Ser 120 125 Gln Ile Gly Gly Met Lys Gly Thr Gln Glu Met Leu Glu Phe Cys Ala 140 135 Lys His Lys Ile Val Ser Asp Ile Glu Leu Ile Lys Met Ser Asp Ile 155 150 Asn Ser Ala Met Asp Arg Leu Ala Lys Ser Asp Val Arg Tyr Arg Phe 170 165 Val Ile Asp Val Ala Asn Ser Leu Leu Pro Glu Ser Ser Ala Glu Ile 185 180 Leu Thr Glu Gln Val Asp His Gly Val Ser Ile Thr Ser Arg Phe (2) INFORMATION FOR SEQ ID NO:836: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2619 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..2619 (D) OTHER INFORMATION: / Ceres Seq. ID 1594437 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:836: atgccattag ttagaaagaa tggcgtcgtt atgaggattg gatctccaat gcttcacgaa 60 tcagagaatt tggtgggaga tggagttgaa gcaccmccgc gaggagaaag agatgaaatt 120 ggagaagaag ttgggggtga aacgaatgtg gtatctgagt cttgtggcgg agaagacgga 180 gcacaagatg cagctaaacc aacgccggaa agagaagcag atcgaattgg agaagaagct 240 cgaggtcaag cgaatgtagt atcaaatgtt gatgtggcag acgtggccga agttcgttct 300 ccacttaggc gaagtaaacg aaggcaaatc agattggaag aagaagctca cgatgcagtt 360 420 quaccaatgc cqqaaqqaqa agcaaatcaa attggagaag aagctcgagg tcagtccgtt gatgtggcag atgcaaccgc agtttgttct ccacttaggc gaagtaaacg aaggcaaaat 480

540 agattggaag aggaagctga tgttgcagtt gaagaatcaa ctcgtcgtga aattggacaa 600 gaggaagagg aagctttagg tgaaacgtct tgtggcggag aagaggaagc tcacgatgaa gctcaagaat caggcgttga tgtgacagat gcagtcgaag ttcgtgctcc acttagacga 660 720 agtaaacgaa ggagaatcag agatgaagaa gaggaggatt tagaggctga agttcctgct 780 cttgatgaak wmgatgactg tgcagtccaa ggagatgaag actgcgatga ggttgatgat gcagtagata ctaatagaga agaagatgat actgctggat taggtgtcga agaagatggt 840 900 aacttagaca tggaaagaga ttttccagag gctaatggag aagaagaagc tagtgacaat gacagggtag atgatatatg ggatgaagac aagattccag atcetttgte etetgacgat 960 gaagatgatg atagagtaga ggcagctcga aatgatcttg gtgatcctga gattttacta 1020 gcattggaga agacttataa ctctcctgaa gatttcaagc ttgctctttt gatgtattcc 1080 ctaaagacaa ggtatgacat taaactttat aaatctgaag ctatggttgt tgctgctaag 1140 tgtgtgtatg ttagtgatga gggtgttgaa tgtccgtgga gagtccgttg ctcttatgag 1200 aagagaaaac ataagatgca aatacgaact tattacaatg agcatacttg tgtgaggtca 1260 ggacattcga agatgttaaa ggtgtcatct attgggtttt tgtttgaaga aaggttgaga 1320 gtgaatccaa aactcactaa acatgagatg gttgctgaga tcttaagaga atacaagttg 1380 gaagtgactc cagaccaatg tgctaaggca aagacaaaag ttttgagagc tagacgtgct 1440 agtcatgatt ctcattttgc taggatatgg gattatcaag cagaggtgtt attgcggaat 1500 ccggggacag agttcaacat agagacagtt gcaggagcag tgattggaag caagcagaga 1560 ttttaccggt tatatatttg ttttcaagct caaagggagt catggaaaca aacttgcaga 1620 cctataatag ggatagatgg agcttttctg aaatgggaca taaaaggaca tctattagcc 1680 acagttggaa gagatggtga caatcgaatt gtccgtattg cttggtctgt agtcgagata 1740 gaaaatgatg acaattggga ctggttcttg agacagctct ctacaagctt ggggctatgc 1800 gaaatgactg atctagcaat catttcagat aaacaatctg gtttagtcaa ggctatccat 1860 accattette egcaagetga geategacaa tgtteaaaae acateatgga taattggaaa 1920 agggacaacc aggacattga gctacaacgg aaaaaaaaga aggttgaaag ctatgtgaac 1980 gactactaca caagaaatag gtggcgagaa acatatttcc gtggctgcct gtcttgccac 2040 caccatggga gaagaggcaa taccggaagg ccaagcaatt atgcaagaag gaaaggaaga 2100 aatgaagttg cctcttcctc aaatccgaac aaaatgtcaa gggaaaagag gatcatgaca 2160 tgctctaact gcttgcaaga agggcacaac aagaaatcat gcaaaaatgc tactgtttta 2220 2280 agtocaccaa agagaccaag aggtogacca aggataaatg agccacaagg gcatgtagaa 2340 ggatcagatg gacatgataa tggctcacaa gggcagggta atgtgttaca agggcaggaa 2400 aatatgttac aaggacagaa taatgtgtca caagggcagg ataatggctc acaagggcag 2460 aacaatggct cacaagggca gaacaatggc tcacaaacac aaagccaaag aggaagaggt cgtggaacac aaagacaaag gggaacaact cgtggagcac aaagacagag gggaagaggt 2520 2580 cgtggaacat cacaagtgtc tgaacaacca caaggagaag cacaaccgca aggacttgct ggacttgcac catggtttga atgttctcgt ggaacatga

- (2) INFORMATION FOR SEQ ID NO:837:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..872
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594438
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

Met Leu His Glu Ser Glu Asn Leu Val Gly Asp Gly Val Glu Ala Xaa 20 25 30

Pro Arg Gly Glu Arg Asp Glu Ile Gly Glu Glu Val Gly Gly Glu Thr 35 40 45

Asn Val Val Ser Glu Ser Cys Gly Glu Asp Gly Ala Gln Asp Ala
50 55 60

Ala Lys Pro Thr Pro Glu Arg Glu Ala Asp Arg Ile Gly Glu Glu Ala 65 70 75 80
Arg Gly Gln Ala Asn Val Val Ser Asn Val Asp Val Ala Asp Val Ala

85 90 95
Glu Val Arg Ser Pro Leu Arg Arg Ser Lys Arg Gln Ile Arg Leu

105 100 Glu Glu Glu Ala His Asp Ala Val Glu Pro Met Pro Glu Gly Glu Ala 120 Asn Gln Ile Gly Glu Glu Ala Arg Gly Gln Ser Val Asp Val Ala Asp 140 135 Ala Thr Ala Val Cys Ser Pro Leu Arg Arg Ser Lys Arg Arg Gln Asn 150 155 Arg Leu Glu Glu Glu Ala Asp Val Ala Val Glu Glu Ser Thr Arg Arg 165 170 Glu Ile Gly Gln Glu Glu Glu Ala Leu Gly Glu Thr Ser Cys Gly 185 180 Gly Glu Glu Glu Ala His Asp Glu Ala Gln Glu Ser Gly Val Asp Val 200 Thr Asp Ala Val Glu Val Arg Ala Pro Leu Arg Arg Ser Lys Arg Arg 220 215 Arg Ile Arg Asp Glu Glu Glu Asp Leu Glu Ala Glu Val Pro Ala 235 230 Leu Asp Glu Xaa Asp Asp Cys Ala Val Gln Gly Asp Glu Asp Cys Asp 250 245 Glu Val Asp Asp Ala Val Asp Thr Asn Arg Glu Glu Asp Asp Thr Ala 265 Gly Leu Gly Val Glu Glu Asp Gly Asn Leu Asp Met Glu Arg Asp Phe 280 Pro Glu Ala Asn Gly Glu Glu Glu Ala Ser Asp Asn Asp Arg Val Asp 300 295 Asp Ile Trp Asp Glu Asp Lys Ile Pro Asp Pro Leu Ser Ser Asp Asp 315 310 Glu Asp Asp Asp Arg Val Glu Ala Ala Arg Asn Asp Leu Gly Asp Pro 330 Glu Ile Leu Leu Ala Leu Glu Lys Thr Tyr Asn Ser Pro Glu Asp Phe 340 345 Lys Leu Ala Leu Leu Met Tyr Ser Leu Lys Thr Arg Tyr Asp Ile Lys 360 Leu Tyr Lys Ser Glu Ala Met Val Val Ala Ala Lys Cys Val Tyr Val 380 375 370 Ser Asp Glu Gly Val Glu Cys Pro Trp Arg Val Arg Cys Ser Tyr Glu 390 395 Lys Arg Lys His Lys Met Gln Ile Arg Thr Tyr Tyr Asn Glu His Thr 410 415 405 Cys Val Arg Ser Gly His Ser Lys Met Leu Lys Val Ser Ser Ile Gly 425 420 Phe Leu Phe Glu Glu Arg Leu Arg Val Asn Pro Lys Leu Thr Lys His 445 440 Glu Met Val Ala Glu Ile Leu Arg Glu Tyr Lys Leu Glu Val Thr Pro 460 455 Asp Gln Cys Ala Lys Ala Lys Thr Lys Val Leu Arg Ala Arg Arg Ala 475 470 Ser His Asp Ser His Phe Ala Arg Ile Trp Asp Tyr Gln Ala Glu Val 490 485 Leu Leu Arg Asn Pro Gly Thr Glu Phe Asn Ile Glu Thr Val Ala Gly 505 Ala Val Ile Gly Ser Lys Gln Arg Phe Tyr Arg Leu Tyr Ile Cys Phe 520 525 Gln Ala Gln Arg Glu Ser Trp Lys Gln Thr Cys Arg Pro Ile Ile Gly 540 535 Ile Asp Gly Ala Phe Leu Lys Trp Asp Ile Lys Gly His Leu Leu Ala 555 550 Thr Val Gly Arg Asp Gly Asp Asn Arg Ile Val Arg Ile Ala Trp Ser 570 565 Val Val Glu Ile Glu Asn Asp Asp Asn Trp Asp Trp Phe Leu Arg Gln 585

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Leu Ser Thr Ser Leu Gly Leu Cys Glu Met Thr Asp Leu Ala Ile Ile
                      600
      595
Ser Asp Lys Gln Ser Gly Leu Val Lys Ala Ile His Thr Ile Leu Pro
         615
                                   620
Gln Ala Glu His Arg Gln Cys Ser Lys His Ile Met Asp Asn Trp Lys
    630
                                635
Arg Asp Asn Gln Asp Ile Glu Leu Gln Arg Lys Lys Lys Val Glu
                 650
       645
Ser Tyr Val Asn Asp Tyr Tyr Thr Arg Asn Arg Trp Arg Glu Thr Tyr
              665
         660
Phe Arg Gly Cys Leu Ser Cys His His His Gly Arg Arg Gly Asn Thr
      675 680
Gly Arg Pro Ser Asn Tyr Ala Arg Arg Lys Gly Arg Asn Glu Val Ala
                        700
       695
Ser Ser Ser Asn Pro Asn Lys Met Ser Arg Glu Lys Arg Ile Met Thr
                                715
705 710
Cys Ser Asn Cys Leu Gln Glu Gly His Asn Lys Lys Ser Cys Lys Asn
                    730
            725
Ala Thr Val Leu Ser Pro Pro Lys Arg Pro Arg Gly Arg Pro Arg Ile
         740 745
Asn Glu Pro Gln Gly His Val Glu Gly Ser Asp Gly His Asp Asn Gly
                                       765
            760
Ser Gln Gly Gln Gly Asn Val Leu Gln Gly Gln Glu Asn Met Leu Gln
                                   780
                   775
Gly Gln Asn Asn Val Ser Gln Gly Gln Asp Asn Gly Ser Gln Gly Gln
                    795
                790
Asn Asn Gly Ser Gln Gly Gln Asn Asn Gly Ser Gln Thr Gln Ser Gln
                             810 815
             805
Arg Gly Arg Gly Arg Gly Thr Gln Arg Gln Arg Gly Thr Thr Arg Gly
                          825
         820
Ala Gln Arg Gln Arg Gly Arg Gly Arg Gly Thr Ser Gln Val Ser Glu
                      840 845
Gln Pro Gln Gly Glu Ala Gln Pro Gln Gly Leu Ala Gly Leu Ala Pro
                    855
Trp Phe Glu Cys Ser Arg Gly Thr
                870
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- (2) INFORMATION FOR SEQ ID NO:838:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 862 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..862
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594440
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:
- Met Arg Ile Gly Ser Pro Met Leu His Glu Ser Glu Asn Leu Val Gly 10 5
- Asp Gly Val Glu Ala Xaa Pro Arg Gly Glu Arg Asp Glu Ile Gly Glu 25
- Glu Val Gly Gly Glu Thr Asn Val Val Ser Glu Ser Cys Gly Gly 40 4.5
- Asp Gly Ala Gln Asp Ala Ala Lys Pro Thr Pro Glu Arg Glu Ala Asp
- Arg Ile Gly Glu Glu Ala Arg Gly Gln Ala Asn Val Val Ser Asn Val 75 70
- Asp Val Ala Asp Val Ala Glu Val Arg Ser Pro Leu Arg Arg Ser Lys 90
- Arg Arg Gln Ile Arg Leu Glu Glu Glu Ala His Asp Ala Val Glu Pro

Met Pro Glu Gly Glu Ala Asn Gln Ile Gly Glu Glu Ala Arg Gly Gln Ser Val Asp Val Ala Asp Ala Thr Ala Val Cys Ser Pro Leu Arg Arg Ser Lys Arg Arg Gln Asn Arg Leu Glu Glu Glu Ala Asp Val Ala Val Glu Glu Ser Thr Arg Arg Glu Ile Gly Gln Glu Glu Glu Ala Leu Gly Glu Thr Ser Cys Gly Gly Glu Glu Glu Ala His Asp Glu Ala Gln Glu Ser Gly Val Asp Val Thr Asp Ala Val Glu Val Arg Ala Pro Leu Arg Arg Ser Lys Arg Arg Ile Arg Asp Glu Glu Glu Asp Leu Glu Ala Glu Val Pro Ala Leu Asp Glu Xaa Asp Asp Cys Ala Val Gln Gly Asp Glu Asp Cys Asp Glu Val Asp Asp Ala Val Asp Thr Asn Arg Glu Glu Asp Asp Thr Ala Gly Leu Gly Val Glu Glu Asp Gly Asn Leu Asp Met Glu Arg Asp Phe Pro Glu Ala Asn Gly Glu Glu Glu Ala Ser Asp Asn Asp Arg Val Asp Asp Ile Trp Asp Glu Asp Lys Ile Pro Asp Pro Leu Ser Ser Asp Asp Glu Asp Asp Asp Arg Val Glu Ala Ala Arg Asn Asp Leu Gly Asp Pro Glu Ile Leu Leu Ala Leu Glu Lys Thr Tyr Asn Ser Pro Glu Asp Phe Lys Leu Ala Leu Leu Met Tyr Ser Leu Lys Thr Arg Tyr Asp Ile Lys Leu Tyr Lys Ser Glu Ala Met Val Val Ala Ala Lys Cys Val Tyr Val Ser Asp Glu Gly Val Glu Cys Pro Trp Arg Val Arg Cys Ser Tyr Glu Lys Arg Lys His Lys Met Gln Ile Arg Thr Tyr Tyr Asn Glu His Thr Cys Val Arg Ser Gly His Ser Lys Met Leu Lys Val Ser Ser Ile Gly Phe Leu Phe Glu Glu Arg Leu Arg Val Asn Pro Lys Leu Thr Lys His Glu Met Val Ala Glu Ile Leu Arg Glu Tyr Lys Leu Glu Val Thr Pro Asp Gln Cys Ala Lys Ala Lys Thr Lys Val 455 460 Leu Arg Ala Arg Ala Ser His Asp Ser His Phe Ala Arg Ile Trp Asp Tyr Gln Ala Glu Val Leu Leu Arg Asn Pro Gly Thr Glu Phe Asn Ile Glu Thr Val Ala Gly Ala Val Ile Gly Ser Lys Gln Arg Phe Tyr Arg Leu Tyr Ile Cys Phe Gln Ala Gln Arg Glu Ser Trp Lys Gln Thr Cys Arg Pro Ile Ile Gly Ile Asp Gly Ala Phe Leu Lys Trp Asp Ile Lys Gly His Leu Leu Ala Thr Val Gly Arg Asp Gly Asp Asn Arg Ile Val Arg Ile Ala Trp Ser Val Val Glu Ile Glu Asn Asp Asp Asn Trp 570 575 Asp Trp Phe Leu Arg Gln Leu Ser Thr Ser Leu Gly Leu Cys Glu Met

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Thr Asp Leu Ala Ile Ile Ser Asp Lys Gln Ser Gly Leu Val Lys Ala
                       600
Ile His Thr Ile Leu Pro Gln Ala Glu His Arg Gln Cys Ser Lys His
                                     620
 610 615
Ile Met Asp Asn Trp Lys Arg Asp Asn Gln Asp Ile Glu Leu Gln Arg
                630
                               635
Lys Lys Lys Lys Val Glu Ser Tyr Val Asn Asp Tyr Tyr Thr Arg Asn
                            650
             645
Arg Trp Arg Glu Thr Tyr Phe Arg Gly Cys Leu Ser Cys His His His
                          665
Gly Arg Arg Gly Asn Thr Gly Arg Pro Ser Asn Tyr Ala Arg Arg Lys
      675 680
Gly Arg Asn Glu Val Ala Ser Ser Ser Asn Pro Asn Lys Met Ser Arg
   690 695
                                     700
Glu Lys Arg Ile Met Thr Cys Ser Asn Cys Leu Gln Glu Gly His Asn
    710 715
Lys Lys Ser Cys Lys Asn Ala Thr Val Leu Ser Pro Pro Lys Arg Pro
                           730
             725
Arg Gly Arg Pro Arg Ile Asn Glu Pro Gln Gly His Val Glu Gly Ser
                          745
          740
Asp Gly His Asp Asn Gly Ser Gln Gly Gln Gly Asn Val Leu Gln Gly
                       760
                                        765
Gln Glu Asn Met Leu Gln Gly Gln Asn Asn Val Ser Gln Gly Gln Asp
                    775
                                     780
Asn Gly Ser Gln Gly Gln Asn Asn Gly Ser Gln Gly Gln Asn Asn Gly
                 790
                                  795
Ser Gln Thr Gln Ser Gln Arg Gly Arg Gly Arg Gly Thr Gln Arg Gln
                              810
             805
Arg Gly Thr Thr Arg Gly Ala Gln Arg Gln Arg Gly Arg Gly Arg Gly
                          825
                                            830
Thr Ser Gln Val Ser Glu Gln Pro Gln Gly Glu Ala Gln Pro Gln Gly
                                        845
                       840
Leu Ala Gly Leu Ala Pro Trp Phe Glu Cys Ser Arg Gly Thr
                   855
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- (2) INFORMATION FOR SEQ ID NO:839:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..260
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

ctttaacgat gttcattggg ataatgatac cgttctttgg gggccttctc gntttctttq 60 gaggatttgc gtttgctcca acatcgtatt ttcttccttg cataatgtgg ctgctaatct 120 ataaaccaaa gaggtttagc ctgtcgtggt ggacgaattg ggtatgtata gtgcttggag 180 ttgttttgat gatcttatca tcaataggag ggttaaggca aatcattatt cagtccaaag 240 attacagttt cttctcttga

- (2) INFORMATION FOR SEQ ID NO:840:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 (D) OTHER INFORMATION: / Ceres Seq. ID 1594466 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840: Leu Thr Met Phe Ile Gly Ile Met Ile Pro Phe Phe Gly Gly Leu Leu 10 5 Xaa Phe Phe Gly Gly Phe Ala Phe Ala Pro Thr Ser Tyr Phe Leu Pro 25 20 Cys Ile Met Trp Leu Leu Ile Tyr Lys Pro Lys Arg Phe Ser Leu Ser 45 4.0 Trp Trp Thr Asn Trp Val Cys Ile Val Leu Gly Val Val Leu Met Ile 60 55 Leu Ser Ser Ile Gly Gly Leu Arg Gln Ile Ile Ile Gln Ser Lys Asp 75 Tyr Ser Phe Phe Ser (2) INFORMATION FOR SEQ ID NO:841: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..83 (D) OTHER INFORMATION: / Ceres Seq. ID 1594467 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:841: Met Phe Ile Gly Ile Met Ile Pro Phe Phe Gly Gly Leu Leu Xaa Phe 10 5 Phe Gly Gly Phe Ala Phe Ala Pro Thr Ser Tyr Phe Leu Pro Cys Ile 25 Met Trp Leu Leu Ile Tyr Lys Pro Lys Arg Phe Ser Leu Ser Trp Trp 40 35 Thr Asn Trp Val Cys Ile Val Leu Gly Val Val Leu Met Ile Leu Ser 55 Ser Ile Gly Gly Leu Arg Gln Ile Ile Ile Gln Ser Lys Asp Tyr Ser 70 65 Phe Phe Ser

- (2) INFORMATION FOR SEQ ID NO:842:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594468
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met Ile Pro Phe Phe Gly Gly Leu Leu Xaa Phe Phe Gly Gly Phe Ala 10 5

Phe Ala Pro Thr Ser Tyr Phe Leu Pro Cys Ile Met Trp Leu Leu Ile 25

Tyr Lys Pro Lys Arg Phe Ser Leu Ser Trp Trp Thr Asn Trp Val Cys 40

Ile Val Leu Gly Val Val Leu Met Ile Leu Ser Ser Ile Gly Gly Leu 55

Arg Gln Ile Ile Ile Gln Ser Lys Asp Tyr Ser Phe Phe Ser 7.0

(2) INFORMATION FOR SEQ ID NO:843:

(ix) FEATURE:

(A) NAME/KEY: -

Client Docket No. 80146.003 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..165 (D) OTHER INFORMATION: / Ceres Seq. ID 1594479 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843: 60 qqqqtttqqn qaatatqqaa agatataqqa qaaqqqaqca qcaqtaaqqt qqtqatqcat aggtegttga catgeeggeg gagtgageee tggaacteea acgaeteeaa ceaeteegae 120 gacgccacgt tgtacagcgg tgactcaagg agtcagcacc gttag (2) INFORMATION FOR SEQ ID NO:844: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..54 (D) OTHER INFORMATION: / Ceres Seq. ID 1594480 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:844: Gly Val Trp Xaa Ile Trp Lys Asp Ile Gly Glu Gly Ser Ser Ser Lys 10 5 1 Val Val Met His Arg Ser Leu Thr Cys Arg Arg Ser Glu Pro Trp Asn 25 30 Ser Asn Asp Ser Asn His Ser Asp Asp Ala Thr Leu Tyr Ser Gly Asp 35 40 45 Ser Arg Ser Gln His Arg 50 (2) INFORMATION FOR SEQ ID NO:845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..36 (D) OTHER INFORMATION: / Ceres Seq. ID 1594481 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:845: Met His Arg Ser Leu Thr Cys Arg Arg Ser Glu Pro Trp Asn Ser Asn 10 5 Asp Ser Asn His Ser Asp Asp Ala Thr Leu Tyr Ser Gly Asp Ser Arg 25 20 Ser Gln His Arg 35 (2) INFORMATION FOR SEQ ID NO:846: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1800 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

(B) LOCATION: 1..1800

(D) OTHER INFORMATION: / Ceres Seq. ID 1594517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846: atgcctaacg ccggtcgtgg aggatctcga aagaggaaga ccacaccaaa cgtgactcaa 60 agagtcggag gttcaacgcc tgctggaaga ccctcttcgc taccgcagca gtacgctttc 120 accccggcgg cagcgacggt tcaagttcct gcattgattc cgcctctagg agccggtgcc 180 ggcgcctcat cctctgcccc ccactactgt aactacccac caccgcagca actcttccaa 240 300 cactccacca atcaaccaca gcgtgtagat ccgttgccac cacaagagac tgctcagcaa 360 gaccctcctc tttcgccaga tccagaaact gcatctcaca gtcatccctc gttgctaggc aacaacttcg aagagggcat tcctgcagtg ttgtcggagc tccaagaaga ctccgtggtt 420 480 gctctgaatg acattctctc tgtgcctggc agagaagcgt ggtgttgtgt gttgtcttcc attccctggc cgaaaaccga atkgtttact cgagacagag gatctcgctt ggttaggaag 540 600 atcactagaa ttttttaca aaaattcgat gctcccttct ataactggtc atgtgtgcta 660 qytqataaaa qaqaaagatt atttttagag tttgcgaaaa ctcaccagtg ggatccctta 720 ataacaqqqa caqtccaqta ttacttcaat gagatcgtca agaggcgctt gaaggacatg 780 gttagcaccg caaggacaac tcgagagcag cctccatgga ttggagaaac gatgtgggga 840 acaatgtgtg cttactggga cacagaagca gcacataaaa ggagtcagac ctattccaaa geteatetet etgacegtaa eggtateagt ceteaegtee actaetetgg gecaaaatet 900 960 tttcaagaaa tcccagatga attggaagag aagttgggaa gaccggtcca tcttggtgag 1020 gtgttcatcc aaacacacac taagtcggat ggctcatttg ttgatcagaa gtcggagaag 1080 attgctcaag cttatcagca gaatgaagag aagttgggaa gaccggtcca tcttggtgag 1140 gtgttcatcc aaacacacac taagtcggat ggctcatttg ttgatcagaa gtcggagaag attgctcaag cttatcagca gaatgaagag aagttgggaa gaccggtcca tcttggtgag 1200 gtgttcatcc aaacacacac taagtcggat ggctcatttg ttgatcagaa gtcggagaag 1260 attgctcaag cttatcagca gaatgaagag aagttgggaa gaccggtcca tcttggtgag 1320 gtgttcatcc aaacacacac taagtcggat ggctcatttg ttgatcagaa gtcggagaag 1380 attgctcaag cttatcagca gaatgtgaga tataggctgt cagcactaga ggcggatgct 1440 tetgetatet etgatggete tteaegacet ceagagetea caetagatga ttataeagee 1500 atctttctcg agtccacaga aagggattca agaggcaatc cttatggact tggatgtcta 1560 aaagacactc taagcagtgc caaccgccat cactccggtt cctcatcatc ctttcaagcc 1620 ctagaagaac ggctgcagga agctcaaagg aaaatagaag agcaggctgc atataatgag 1680 aagagagatg ctgagattgc tgcccgagaa gctgagtcat cccgagtcac aactgagcaa 1740 aaggacaaga tcgagcaatt gtctttaggc gagaagtatc tccgccaaac cgatccgtag 1800

(2) INFORMATION FOR SEQ ID NO:847:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 599 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..599
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594518
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met Pro Asn Ala Gly Arg Gly Gly Ser Arg Lys Arg Lys Thr Thr Pro

1 10 15

15 10 15

Asn Val Thr Gln Arg Val Gly Gly Ser Thr Pro Ala Gly Arg Pro Ser 20 25 30

Ser Leu Pro Gln Gln Tyr Ala Phe Thr Pro Ala Ala Ala Thr Val Gln 35 40 45

Val Pro Ala Leu Ile Pro Pro Leu Gly Ala Gly Ala Gly Ala Ser Ser 50 55 60

Ser Ala Pro His Tyr Cys Asn Tyr Pro Pro Gln Gln Leu Phe Gln 65 70 75 80

His Ser Thr Asn Gln Pro Gln Arg Val Asp Pro Leu Pro Pro Gln Glu 85 90 95

Thr Ala Gln Gln Asp Pro Pro Leu Ser Pro Asp Pro Glu Thr Ala Ser 100 105 110 His Ser His Pro Ser Leu Leu Gly Asn Asn Phe Glu Glu Gly Ile Pro

Ala Val Leu Ser Glu Leu Gln Glu Asp Ser Val Val Ala Leu Asn Asp Ile Leu Ser Val Pro Gly Arg Glu Ala Trp Cys Cys Val Leu Ser Ser Ile Pro Trp Pro Lys Thr Glu Xaa Phe Thr Arg Asp Arg Gly Ser Arg Leu Val Arg Lys Ile Thr Arg Ile Phe Leu Gln Lys Phe Asp Ala Pro Phe Tyr Asn Trp Ser Cys Val Leu Xaa Asp Lys Arg Glu Arg Leu Phe Leu Glu Phe Ala Lys Thr His Gln Trp Asp Pro Leu Ile Thr Gly Thr 210 215 Val Gln Tyr Tyr Phe Asn Glu Ile Val Lys Arg Arg Leu Lys Asp Met Val Ser Thr Ala Arg Thr Thr Arg Glu Gln Pro Pro Trp Ile Gly Glu Thr Met Trp Gly Thr Met Cys Ala Tyr Trp Asp Thr Glu Ala Ala His Lys Arg Ser Gln Thr Tyr Ser Lys Ala His Leu Ser Asp Arg Asn Gly Ile Ser Pro His Val His Tyr Ser Gly Pro Lys Ser Phe Gln Glu Ile Pro Asp Glu Leu Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp Gln 410 415 Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Val Arg Tyr Arg Leu Ser Ala Leu Glu Ala Asp Ala Ser Ala Ile Ser Asp Gly Ser Ser Arg Pro Pro Glu Leu Thr Leu Asp Asp Tyr Thr Ala Ile Phe Leu Glu Ser Thr Glu Arg Asp Ser Arg Gly Asn Pro Tyr Gly Leu Gly Cys Leu Lys Asp Thr Leu Ser Ser Ala Asn Arg His His Ser Gly Ser Ser Ser Phe Gln Ala Leu Glu Glu Arg Leu Gln Glu Ala Gln Arg Lys Ile Glu Glu Gln Ala Ala Tyr Asn Glu Lys Arg Asp Ala Glu Ile Ala Ala Arg Glu Ala Glu Ser Ser Arg Val Thr Thr Glu Gln Lys Asp Lys Ile Glu Gln Leu Ser Leu Gly Glu Lys Tyr Leu Arg Gln Thr Asp Pro

- (2) INFORMATION FOR SEQ ID NO:848:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..360
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594520
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:
- Met Val Ser Thr Ala Arg Thr Thr Arg Glu Gln Pro Pro Trp Ile Gly
 1 5 10 15
- Glu Thr Met Trp Gly Thr Met Cys Ala Tyr Trp Asp Thr Glu Ala Ala 20 25 30
- His Lys Arg Ser Gln Thr Tyr Ser Lys Ala His Leu Ser Asp Arg Asn 35 40 45
- Gly Ile Ser Pro His Val His Tyr Ser Gly Pro Lys Ser Phe Gln Glu
 50 60
- Ile Pro Asp Glu Leu Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly 65 70 75 80
- Glu Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp
- 65 90 95
 Gln Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys
 100 105 110
- Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr 115 120 125
- Lys Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln
 130 135 140
- Ala Tyr Gln Gln Asn Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly 145 150 155 160
- Glu Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp 165 170 175
- Gln Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys 180 185 190
- Leu Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr 195 200 205
- Lys Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln 210 215 220
- Ala Tyr Gln Gln Asn Val Arg Tyr Arg Leu Ser Ala Leu Glu Ala Asp 225 230 235 240
- Ala Ser Ala Ile Ser Asp Gly Ser Ser Arg Pro Pro Glu Leu Thr Leu 245 250 255
- Asp Asp Tyr Thr Ala Ile Phe Leu Glu Ser Thr Glu Arg Asp Ser Arg 260 265 270
- Gly Asn Pro Tyr Gly Leu Gly Cys Leu Lys Asp Thr Leu Ser Ser Ala 275 280 285
- Asn Arg His His Ser Gly Ser Ser Ser Ser Phe Gln Ala Leu Glu Glu 290 295 300
- Arg Leu Gln Glu Ala Gln Arg Lys Ile Glu Glu Gln Ala Ala Tyr Asn 305 310 315 320
- Glu Lys Arg Asp Ala Glu Ile Ala Ala Arg Glu Ala Glu Ser Ser Arg 325 330 335
- Val Thr Thr Glu Gln Lys Asp Lys Ile Glu Gln Leu Ser Leu Gly Glu 340 345 350
- Lys Tyr Leu Arg Gln Thr Asp Pro 355 360
- (2) INFORMATION FOR SEQ ID NO:849:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 823 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..823
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594543
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849: atggttgacg caattgtatc gttcggtgtt gaaaagcttt gggagctcgt gagcaaaaat 60 tatqaccqat ttcagggagt tgaagagcaa attactgttc tagaaagtga tctgaagatg 120 ttaatgtcct ttctgagtga tgcggatgca aggcaacaaa caactgaact tgctagaaac 180 tgtgtggacg acgtaaagga aatcacttac gatgctgagg atataattga aacatatctt 240 ctgaagcgag aacggagtga aagcagtggc atcaagaatc acatgagaag tettgettge 300 attcaaagtg gtcgtaggaa gactgcctta gaaatcacaa gcattagtaa gagaatctcc 360 aaagtgatcc aggttatgca gactttaggc atacaatcga acattattga aggtggatat 420 ttgcaggctc tacaagatag gaaaagagag atgcgtcata catttcctat tgagactgaa 480 agcaatcttg ttggtttgga gacaaatgtt gagaaattgg ttgaagcttt ggtgggaaat 540 600 gatageagte atggggtate cataactgge ttgggtggte ttggcaaaac caccettgca cggcaggttt ttaatcatac taaggttaaa gatcattttg atgcacttgc gtgggtgtgc 660 gtatcacaag agtttacacg gaagcatgtg tgggagacca tcttgaagaa acttagtcat 720 ggagattacg ttgctgacat gaatgaaggc gaacttcaag agaaactcat tcagttgttg 780 qaaacaaaaa aggctttgat cgtctttgat gacgtatgga aaa
- (2) INFORMATION FOR SEQ ID NO:850:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..274
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:
- Met Val Asp Ala Ile Val Ser Phe Gly Val Glu Lys Leu Trp Glu Leu

 1 15 15
- Val Ser Lys Asn Tyr Asp Arg Phe Gln Gly Val Glu Glu Gln Ile Thr 20 25 30
- Val Leu Glu Ser Asp Leu Lys Met Leu Met Ser Phe Leu Ser Asp Ala 35 40 45
- Asp Ala Arg Gln Gln Thr Thr Glu Leu Ala Arg Asn Cys Val Asp Asp 50 55 60
- Val Lys Glu Ile Thr Tyr Asp Ala Glu Asp Ile Ile Glu Thr Tyr Leu 65 70 75 80
- Leu Lys Arg Glu Arg Ser Glu Ser Ser Gly Ile Lys Asn His Met Arg 85 90 95
- Ser Leu Ala Cys Ile Gln Ser Gly Arg Arg Lys Thr Ala Leu Glu Ile 100 105 110
- Thr Ser Ile Ser Lys Arg Ile Ser Lys Val Ile Gln Val Met Gln Thr 115 120 125
- Leu Gly Ile Gln Ser Asn Ile Ile Glu Gly Gly Tyr Leu Gln Ala Leu 130 135 140
- Gln Asp Arg Lys Arg Glu Met Arg His Thr Phe Pro Ile Glu Thr Glu 145 150 155 160
- Ser Asn Leu Val Gly Leu Glu Thr Asn Val Glu Lys Leu Val Glu Ala 165 170 175
- Leu Val Gly Asn Asp Ser Ser His Gly Val Ser Ile Thr Gly Leu Gly 180 185 190
- Gly Leu Gly Lys Thr Thr Leu Ala Arg Gln Val Phe Asn His Thr Lys
 195 200 205

 Val
 Lys
 Asp
 His
 Phe
 Asp
 Ala
 Leu
 Ala
 Trp
 Val
 Cys
 Val
 Ser
 Glu
 Glu

 Phe
 Thr
 Arg
 Lys
 His
 Val
 Trp
 Glu
 Thr
 Ile
 Leu
 Lys
 Lys
 Leu
 Ser
 His

 225
 230
 230
 235
 235
 240
 240

 Gly
 Asp
 Tyr
 Val
 Ala
 Asp
 Met
 Asn
 Glu
 Gly
 Glu
 Leu
 Gln
 Lys
 Leu

 Ile
 Gln
 Leu
 Glu
 Thr
 Lys
 Ala
 Leu
 Ile
 Val
 Phe
 Asp
 Val

 Ile
 Gln
 Leu
 Glu
 Thr
 Lys
 Lys
 Ala
 Leu
 Ile
 Val
 Phe
 Asp
 Val

 Ile
 Gln
 Leu
 Glu
 Thr
 Lys
 Lys
 Ala
 Leu
 Ile
 Val
 Phe
 Asp
 Val

 Ile
 Gln
 Leu
 Leu
 L

- (2) INFORMATION FOR SEQ ID NO:851:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..235
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594546
- Met
 Leu
 Met
 Ser
 Phe
 Leu
 Ser
 Asp
 Ala
 Asp
 Ala
 Arg
 Gln
 Thr
 Thr
 Thr

 1
 1
 5
 2
 10
 10
 15
 15

 Glu
 Leu
 Arg
 Asp
 Asp
 Val
 Lys
 Glu
 Thr
 Tyr
 Asp

 Ala
 Glu
 Asp
 Ile
 Ile
 Glu
 Thr
 Tyr
 Leu
 Leu
 Lys
 Arg
 Glu
 Arg
 Ser
 Glu

 35
 40
 40
 45
 45
 45
- Ser Ser Gly Ile Lys Asn His Met Arg Ser Leu Ala Cys Ile Gln Ser
 50 55 60
- Gly Arg Arg Lys Thr Ala Leu Glu Ile Thr Ser Ile Ser Lys Arg Ile 65 70 75 80

 Ser Lys Val Ile Gln Val Met Gln Thr Leu Gly Ile Gln Ser Asn Ile
- 85 90 95
 Ile Glu Gly Gly Tyr Leu Gln Ala Leu Gln Asp Arg Lys Arg Glu Met
- 100 105 110

 Arg His Thr Phe Pro Ile Glu Thr Glu Ser Asn Leu Val Gly Leu Glu
 115 120 125
- Thr Asn Val Glu Lys Leu Val Glu Ala Leu Val Gly Asn Asp Ser Ser 130 135 140
- His Gly Val Ser Ile Thr Gly Leu Gly Gly Leu Gly Lys Thr Thr Leu 145 150 150 160
- Ala Arg Gln Val Phe Asn His Thr Lys Val Lys Asp His Phe Asp Ala 165 170 175
- Leu Ala Trp Val Cys Val Ser Gln Glu Phe Thr Arg Lys His Val Trp
 180 185 190
- Glu Thr Ile Leu Lys Lys Leu Ser His Gly Asp Tyr Val Ala Asp Met 195 200 205
- Asn Glu Gly Glu Leu Gln Glu Lys Leu Ile Gln Leu Leu Glu Thr Lys 210 215 220
- Lys Ala Leu Ile Val Phe Asp Asp Val Trp Lys 225 230 235
- (2) INFORMATION FOR SEQ ID NO:852:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1712 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

- (B) LOCATION: 1..1712
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852: ctggcgattc tctagggttt aaacccggat ccactatccg aattggtcga atcgtccgtg 60 gtaatgaaat cgccatcaaa gacgccggaa tctccaccaa gcacctccgg atcgtttccg 120 attccgagaa ctggataatc cacgatcttg gttcttccaa cggcaccata ttgaactctg 180 240 acactatcqa ctcaqatacq cccqtcaatc ttagccatgg agacgaaatt aagcttggtg 300 agtacactic cattitggtg aactitggga gtgatgttgt tcaggcgccg caggagcata 360 agcttccgcc caggccaagg aggaacaaca agcggcttgc tgcttcggat ccggatccgg atcctattga gtcggttcag gagaaaccaa agcgcacgcg tggatcgtcg aagcaagagg 420 aaaatgaact gcccaagagt actagggctt cgaggaaaaa gaatctggac gatatcgccg 480 ataaagaaga ggaattggat gtggaaattg agaaggtggt caaagctagg gttgggaggc 540 ctcggaagaa cgcaggcagt gcaattgcga aggaagaaga agttgtggag gagaaaaaaa 600 gggttgggag gccccggaag aacgcaagta gtgcaattac ggaggaagaa gaagttgtgg 660 aggagaaaaa aggcaactct agggctcgga gaggtaagaa cagtgagatt gtccagaaat 720 caatcaaatt ggaagttgag gatactccca aggcagtgga aatctcagag gtgaaaagca 780 ggaagagagt gacaaggagc aagcagatag aaaatgaatg ttttggattg gaggttaaag 840 900 atgagaagag aactacaagg tctaccagaa gcaagacgac tgaaattggt ggagagtctt ttctggagtt ggagatggtc ctgaaccaag cccggaaaaag ccgtgcaaag aggaagaaaa 960 1020 tggatgagga gccatccaag gagactagaa atgatgatgc cggagaagag gttttgaaga actgtcatgt tgaagaagat aaggaaaatg aagctcagga aggttgcagt ggaagaagtg 1080 1140 atgacatatg tgatcaagaa gatgagaagg aatgcgatgg atctaagagg gtagagcagg 1200 tgqaqattqa gttaaggaag aaaagcacag tagaaggcct gaaatgcact gataaagaag atqqaqaaac aqagaactca caagatattg aaagagaaag agaaaatgaa aatgaaaatg 1260 1320 aaqctcaaqa aqqttqcaqt gaaagaagtg ataaagaata tgagagggtt ggtggtgggg 1380 ctaaqaqqqt aqaqcaggtg gagattgagt taaggaagaa aagcaccgta ggagaagatg 1440 acctgaactg tactgttaga gaagatggag agacagaaaa cttacaagaa attgaagaag 1500 agtqtcacqa cqaqqaaaqt qactqcaaqq tcgaggaggc tggatttgcg acattagatg 1560 aqqaaaaqqt tqqqcaqqqa tqqaacaata aqaaaqtaga gagggtagaa gtatatttag aaaaaatgaa actaaqagaa tqqtttqatq ccataqaggt tcaactgcca aaacagacaa 1620 1680 ttqaaqaaac aqaqaaqatq attgagccca tgagaagtaa gagtatgaga gttcacaagc atattqcaqa qcaaaaqqaa aagggcgact aa
- (2) INFORMATION FOR SEQ ID NO:853:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 569 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..569
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594563
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:
- Gly Asp Ser Leu Gly Phe Lys Pro Gly Ser Thr Ile Arg Ile Gly Arg
 1 5 10 15
- Ile Val Arg Gly Asn Glu Ile Ala Ile Lys Asp Ala Gly Ile Ser Thr 20 25 30
- Lys His Leu Arg Ile Val Ser Asp Ser Glu Asn Trp Ile Ile His Asp 35 40 45
- Leu Gly Ser Ser Asn Gly Thr Ile Leu Asn Ser Asp Thr Ile Asp Ser 50 55 60
- Asp Thr Pro Val Asn Leu Ser His Gly Asp Glu Ile Lys Leu Gly Glu 65 70 75 80
- Tyr Thr Ser Ile Leu Val Asn Phe Gly Ser Asp Val Val Gln Ala Pro 85 90 95
- Gln Glu His Lys Leu Pro Pro Arg Pro Arg Arg Asn Asn Lys Arg Leu 100 105 110
- Ala Ala Ser Asp Pro Asp Pro Asp Pro Ile Glu Ser Val Gln Glu Lys
 115 120 125
- Pro Lys Arg Thr Arg Gly Ser Ser Lys Gln Glu Glu Asn Glu Leu Pro

	130					135					140				
Lys 145		Thr	Arg	Ala	Ser 150		Lys	Lys	Asn	Leu 155		Asp	Ile	Ala	Asp 160
	Glu	Glu	Glu	Leu 165	Asp	Val	Glu	Ile	Glu 170	Lys	Val	Val	Lys	Ala 175	Arg
Val	Gly	Arg	Pro 180	Arg	Lys	Asn	Ala	Gly 185	Ser	Ala	Ile	Ala	Lys 190	Glu	Glu
		195	Glu				200					205			
	210		Ile			215					220				
225			Ala		230					235					240
			Glu	245					250					255	
			Arg 260					265					270		
		275	Leu				280					285			
	290		Thr			295					300				
305			Asn		310					315					320
_			Pro	325					330					335	
		_	Asn 340					345					350		
		355	Ser				360					365			
	370		Asp			375					380				
385			Ser		390					395					400
			Glu	405					410					415	
			Glu 420					425					430		
		435	Val				440					445			
	450		Lys			455					460				
465					470					475					Glu 480
_				485					490					495	Ala
			500					505					510		Val
		515	Glu				520					525			
_	530					535					540				Glu
545					550				ser	Met 555	Arg	va⊥	нlS	ьуѕ	His 560
11e			Gln	565											

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1789
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594667
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854: 60 atggetteet getteeacce ttetgetatg getacaagee accgegagga agacteeate attetttet cagcatcaaa eteteetgat gaatteteet etgetteete tteetttet 120 tottcaccac toccaaccoc taaccgctac totttaaccg toactaacct atoctacacc 180 atcaatcaca coccaatact caattoogtt toattagotg otgaatcoto taaaaatcota 240 gccgtggttg gaccgagtgg aacaggaaaa tccactcttt taaagatcat ttcaggaaga 300 gtgaaccaca aggcactaga teegtettee geggttttga tgaacaateg taaaatcact 360 gactataacc aactacgaag gctatgcggg tttgtcccgc aggacgatga cctactgcct 420 ctacttaccg tgaaagagac gttaatgtat agcgccaaat tcagtttgag agattcaacg 480 gctaaggaaa gagaagaga agtggagagc ttgttgagtg atctcggtct tgttctcgtc 540 600 caaqacagct tcgtgggaga aggagacgaa gaggatcgtg gcgtttcggg tggagagagg 660 aaqaqaqtct ctataqccqt tqaqatgatt cgtgatccac caattctgct tcttgacgaa 720 ccaacctctq qtttqqataq tcqaaactcq cttcaggttg ttgagctttt ggctactatg 780 gcgaaatcca aacagagaac cgtcctcttc tccatccacc aaccaagtta taggatcctc gattacatct ccgattacct gattctttct cgcggatcgg ttatccactt gggaagtctt 840 gaacatctcg aggactcgat agcgaaacta gggtttcaga ttccagaaca gctgaatcct 900 atagaattcg ccatggaaat agttgagtcc ttgagaactt ttaagccaaa ctcggtagct 960 gtcgtagaat catcatcaat gtggcctgaa aacaacgaaa acgatgggat tatctctaag 1020 aaagaagcgt ttcgtgtcct agacgtcacc gagatctcat acctctgctc aagattctgc 1080 aagatcatct atagaacaaa gcagttgttc ctggcgcgaa caatgcaagc ggttgtagct 1140 ggattaggtc taggtagcgt ctacacaaga ctcaagcgtg acgaagaagg cgttgcagag 1200 cggcttggac tctttgcctt cagcttaagc ttcctcctct cttcaacagt cgaagcactt 1260 cccatttacc tccgagaacg tcgcgttctg atgaaagaat catctcgtgg atcctaccga 1320 atctcatcct acatgatagc caacaccatc gcatttgtac cgttcctctt cgttgtatct 1380 ctcctcttct ccatcccagt ctactggatc gtaggcctaa acccatcgat tcaagccttc 1440 teettetttg teetetgggt ttggeteate atteteatgg ceagttetet ggtgetttte 1500 ctcagcgctg tttctcctga cttcatctct ggtaactccc tcatatgcac tgttcttgga 1560 geettettee tetteteegg etaetttate ecaaaagaga agateecaaa accatggatg 1620 ttcatgtact atgtgtcctt gtaccgttac ccgctggagt cnnnggtggt gaatgagtac 1680 1740 tggagcatgc gagaggaatg cttctccagt gggaacatgg gctgcttgat gaccggagag gatgtgttga aggagagag gcttgacaag gatacgagat ggatcaacg
- (2) INFORMATION FOR SEQ ID NO:855:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 596 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..596
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594668
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:
- Met Ala Ser Cys Phe His Pro Ser Ala Met Ala Thr Ser His Arg Glu

 1 10 15
- Glu Asp Ser Ile Ile Leu Phe Ser Ala Ser Asn Ser Pro Asp Glu Phe 20 25 30
- Ser Ser Ala Ser Ser Ser Phe Ser Ser Pro Leu Pro Thr Pro Asn
 35 40 45
- Arg Tyr Ser Leu Thr Val Thr Asn Leu Ser Tyr Thr Ile Asn His Thr 50 55 60
- Pro Ile Leu Asn Ser Val Ser Leu Ala Ala Glu Ser Ser Lys Ile Leu 65 70 75 80
- Ala Val Val Gly Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Ile 85 90 95
- Ile Ser Gly Arg Val Asn His Lys Ala Leu Asp Pro Ser Ser Ala Val

105 100 Leu Met Asn Asn Arg Lys Ile Thr Asp Tyr Asn Gln Leu Arg Arg Leu 120 Cys Gly Phe Val Pro Gln Asp Asp Leu Leu Pro Leu Leu Thr Val 135 140 Lys Glu Thr Leu Met Tyr Ser Ala Lys Phe Ser Leu Arg Asp Ser Thr 150 155 Ala Lys Glu Arg Glu Glu Arg Val Glu Ser Leu Leu Ser Asp Leu Gly 165 170 Leu Val Leu Val Gln Asp Ser Phe Val Gly Glu Gly Asp Glu Glu Asp 185 180 Arg Gly Val Ser Gly Gly Glu Arg Lys Arg Val Ser Ile Ala Val Glu 200 Met Ile Arg Asp Pro Pro Ile Leu Leu Leu Asp Glu Pro Thr Ser Gly 215 Leu Asp Ser Arg Asn Ser Leu Gln Val Val Glu Leu Leu Ala Thr Met 230 235 Ala Lys Ser Lys Gln Arg Thr Val Leu Phe Ser Ile His Gln Pro Ser 250 245 Tyr Arg Ile Leu Asp Tyr Ile Ser Asp Tyr Leu Ile Leu Ser Arg Gly 265 260 Ser Val Ile His Leu Gly Ser Leu Glu His Leu Glu Asp Ser Ile Ala 280 Lys Leu Gly Phe Gln Ile Pro Glu Gln Leu Asn Pro Ile Glu Phe Ala 300 295 Met Glu Ile Val Glu Ser Leu Arg Thr Phe Lys Pro Asn Ser Val Ala 315 310 Val Val Glu Ser Ser Ser Met Trp Pro Glu Asn Asn Glu Asn Asp Gly 325 330 Ile Ile Ser Lys Lys Glu Ala Phe Arg Val Leu Asp Val Thr Glu Ile 340 345 350 Ser Tyr Leu Cys Ser Arg Phe Cys Lys Ile Ile Tyr Arg Thr Lys Gln 360 365 Leu Phe Leu Ala Arg Thr Met Gln Ala Val Val Ala Gly Leu Gly Leu 380 375 Gly Ser Val Tyr Thr Arg Leu Lys Arg Asp Glu Glu Gly Val Ala Glu 395 400 390 Arg Leu Gly Leu Phe Ala Phe Ser Leu Ser Phe Leu Leu Ser Ser Thr 410 415 Val Glu Ala Leu Pro Ile Tyr Leu Arg Glu Arg Arg Val Leu Met Lys 425 430 Glu Ser Ser Arg Gly Ser Tyr Arg Ile Ser Ser Tyr Met Ile Ala Asn 440 Thr Ile Ala Phe Val Pro Phe Leu Phe Val Val Ser Leu Leu Phe Ser 460 455 Ile Pro Val Tyr Trp Ile Val Gly Leu Asn Pro Ser Ile Gln Ala Phe 475 470 Ser Phe Phe Val Leu Trp Val Trp Leu Ile Ile Leu Met Ala Ser Ser 490 485 Leu Val Leu Phe Leu Ser Ala Val Ser Pro Asp Phe Ile Ser Gly Asn 505 500 Ser Leu Ile Cys Thr Val Leu Gly Ala Phe Phe Leu Phe Ser Gly Tyr 520 525 Phe Ile Pro Lys Glu Lys Ile Pro Lys Pro Trp Met Phe Met Tyr Tyr 540 535 Val Ser Leu Tyr Arg Tyr Pro Leu Glu Xaa Xaa Val Val Asn Glu Tyr 555 550 Trp Ser Met Arg Glu Glu Cys Phe Ser Ser Gly Asn Met Gly Cys Leu 570 Met Thr Gly Glu Asp Val Leu Lys Glu Arg Gly Leu Asp Lys Asp Thr 580

Arg Trp Ile Asn 595

- (2) INFORMATION FOR SEQ ID NO:856:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 587 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..587
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594670
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:
- Met Ala Thr Ser His Arg Glu Glu Asp Ser Ile Ile Leu Phe Ser Ala 1 5 10 15
- Ser Asn Ser Pro Asp Glu Phe Ser Ser Ala Ser Ser Ser Phe Ser Ser 20 25 30
- Ser Pro Leu Pro Thr Pro Asn Arg Tyr Ser Leu Thr Val Thr Asn Leu 35 40 45
- Ser Tyr Thr Ile Asn His Thr Pro Ile Leu Asn Ser Val Ser Leu Ala 50 55 60
- Ala Glu Ser Ser Lys Ile Leu Ala Val Val Gly Pro Ser Gly Thr Gly 65 70 75 80
- Lys Ser Thr Leu Leu Lys Ile Ile Ser Gly Arg Val Asn His Lys Ala 85 90 95
- Leu Asp Pro Ser Ser Ala Val Leu Met Asn Asn Arg Lys Ile Thr Asp 100 105 110
- Tyr Asn Gln Leu Arg Arg Leu Cys Gly Phe Val Pro Gln Asp Asp Asp 115 120 125
- Leu Leu Pro Leu Leu Thr Val Lys Glu Thr Leu Met Tyr Ser Ala Lys 130 135 140
- Phe Ser Leu Arg Asp Ser Thr Ala Lys Glu Arg Glu Glu Arg Val Glu 145 150 155 160
- Ser Leu Leu Ser Asp Leu Gly Leu Val Leu Val Gln Asp Ser Phe Val 165 170 175
- Gly Glu Gly Asp Glu Glu Asp Arg Gly Val Ser Gly Gly Glu Arg Lys 180 185 190
- Arg Val Ser Ile Ala Val Glu Met Ile Arg Asp Pro Pro Ile Leu Leu 195 200 205
- Leu Asp Glu Pro Thr Ser Gly Leu Asp Ser Arg Asn Ser Leu Gln Val 210 215 220
- Val Glu Leu Leu Ala Thr Met Ala Lys Ser Lys Gln Arg Thr Val Leu 225 230 235 235
- Phe Ser Ile His Gln Pro Ser Tyr Arg Ile Leu Asp Tyr Ile Ser Asp 245 250 255
- Tyr Leu Ile Leu Ser Arg Gly Ser Val Ile His Leu Gly Ser Leu Glu 260 265 270
- His Leu Glu Asp Ser Ile Ala Lys Leu Gly Phe Gln Ile Pro Glu Gln 275 280 285
- Leu Asn Pro Ile Glu Phe Ala Met Glu Ile Val Glu Ser Leu Arg Thr 290 295 300
- Phe Lys Pro Asn Ser Val Ala Val Val Glu Ser Ser Ser Met Trp Pro 305 310 315 320
- Glu Asn Asn Glu Asn Asp Gly Ile Ile Ser Lys Lys Glu Ala Phe Arg
 325 330 335
- Val Leu Asp Val Thr Glu Ile Ser Tyr Leu Cys Ser Arg Phe Cys Lys 340 345 350
- Ile Ile Tyr Arg Thr Lys Gln Leu Phe Leu Ala Arg Thr Met Gln Ala 355 360 365
- Val Val Ala Gly Leu Gly Leu Gly Ser Val Tyr Thr Arg Leu Lys Arg

1260

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380
                       375
    370
Asp Glu Glu Gly Val Ala Glu Arg Leu Gly Leu Phe Ala Phe Ser Leu
                                       395
                    390
Ser Phe Leu Leu Ser Ser Thr Val Glu Ala Leu Pro Ile Tyr Leu Arg
                405
                                    410
Glu Arg Arg Val Leu Met Lys Glu Ser Ser Arg Gly Ser Tyr Arg Ile
                               425
           420
Ser Ser Tyr Met Ile Ala Asn Thr Ile Ala Phe Val Pro Phe Leu Phe
                            440
                                                445
       435
Val Val Ser Leu Leu Phe Ser Ile Pro Val Tyr Trp Ile Val Gly Leu
                        455
                                            460
Asn Pro Ser Ile Gln Ala Phe Ser Phe Phe Val Leu Trp Val Trp Leu
                                        475
                    470
Ile Ile Leu Met Ala Ser Ser Leu Val Leu Phe Leu Ser Ala Val Ser
                                                        495
                                    490
                485
Pro Asp Phe Ile Ser Gly Asn Ser Leu Ile Cys Thr Val Leu Gly Ala
                                505
            500
Phe Phe Leu Phe Ser Gly Tyr Phe Ile Pro Lys Glu Lys Ile Pro Lys
                            520
        515
Pro Trp Met Phe Met Tyr Tyr Val Ser Leu Tyr Arg Tyr Pro Leu Glu
                                            540
                        535
Xaa Xaa Val Val Asn Glu Tyr Trp Ser Met Arg Glu Glu Cys Phe Ser
                    550
                                        555
Ser Gly Asn Met Gly Cys Leu Met Thr Gly Glu Asp Val Leu Lys Glu
                                    570
                565
Arg Gly Leu Asp Lys Asp Thr Arg Trp Ile Asn
                                585
            580
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- (2) INFORMATION FOR SEQ ID NO:857:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

tcagaatttg

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594695
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:857: 60 gattatgtcc gaggaacatg gataccaaag gagtgggaag aaatgcagag agaagtttga 120 gaatctgtac aaatactata ggaagactaa agaaggcaaa gccggaagac aagacggaaa 180 acattacaga tttttccggc agctcgaagc gctatacggg gattctaata acttggtttc ttgtcccaat cataacacgc agttcatgag cagtgctctt catggtttcc atactcaaaa 240 ccctatgaac gttactacaa caacgtccaa catccataac gttgatagtg ttcatggttt 300 tcatcaaagc cttagtcttt ctaacaacta caactcctcc gagcttgagc tgatgacttc 360 ctcttcggaa gggaatgatt ctagtagtag aaggaaaaag aggagttgga aagcgaagat 420 480 aaaggagttc attgatacga acatgaaaag gttgatagag aggcaagatg tttggcttga gaagttgaca aaggttattg aagacaaaga ggaacaacgg atgatgaaag aagaggaatg 540 gaggaagatt gaagctgcaa ggattgataa agagcatttg ttttgggcta aagagagggc 600 gaggatggaa gctagggatg ttgcggtgat tgaggcattg caatacttga caggaaagcc 660 attgataaag ccgctgtgtt catccccgga agagaggaca aatggtaata atgagatccg 720 aaacaatagt gagacacaga atgagaatgg aagcgatcaa acgatgacta acaatgtttg 780 840 tgttaaagga agtagtagct gctggggtga gcaagagatt ttaaagctta tggagataag 900 aacgagcatg gactcgacct ttcaagagat attaggaggg tgctcggatg agtttctatg ggaggaaatc gcagcgaagt tgattcagtt agggtttgat cagagaagtg ccttattatq 960 caaggaaaag tgggaatgga taagcaatgg aatgaggaaa gaaaagaagc aaatcaacaa 1020 gaaaagaaag gataattcgt ccagctgcgg cgtgtactac ccgagaaacg aagaaaatcc 1080 aatctacaat aatcgagaaa gtggatataa tgataatgat ccgcatcaaa tcaacgaaca 1140

aggcaatgta ggttcttcaa catcaaacgc aaacgcaaac gcaaacctaa ccactggaaa

tccgancggt gcaatggctg ctactacaaa ctgcttcccg ttcttcatgg gagatggaga

- (2) INFORMATION FOR SEQ ID NO:858:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..423
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594696
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:
- Ile Met Ser Glu Glu His Gly Tyr Gln Arg Ser Gly Lys Lys Cys Arg

 1 10 15
- Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Arg Lys Thr Lys Glu Gly
 20 25 30
- Lys Ala Gly Arg Gln Asp Gly Lys His Tyr Arg Phe Phe Arg Gln Leu 35 40 45
- Glu Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn His 50 60
- Asn Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn 65 70 75 80
- Pro Met Asn Val Thr Thr Thr Ser Asn Ile His Asn Val Asp Ser 85 90 95
- Val His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser 100 105 110
- Ser Glu Leu Glu Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser 115 120 125
- Ser Arg Arg Lys Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile 130 135 140
- Asp Thr Asn Met Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu 145 150 155 160
- Lys Leu Thr Lys Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys
- 165 170 175
 Glu Glu Glu Trp Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His
 180 185 190
- Leu Phe Trp Ala Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala 195 200 205
- Val Ile Glu Ala Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro 210 215 220
- Leu Cys Ser Ser Pro Glu Glu Arg Thr Asn Gly Asn Asn Glu Ile Arg 225 230 235 240
- Asn Asn Ser Glu Thr Gln Asn Glu Asn Gly Ser Asp Gln Thr Met Thr

 245 250 255
 240
 250 255
- Asn Asn Val Cys Val Lys Gly Ser Ser Ser Cys Trp Gly Glu Glu 260 265 270
- Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe Gln 275 280 285
- Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala 290 295 300
- Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys
- 305 310 315 320 Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys Lys
- 325 330 335 Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr
- 355 360 365

 Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly 370 375 380
- Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu Thr Thr Gly Asn

385 390 395 Pro Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe Pro Phe Met 405 410

Gly Asp Gly Asp Gln Asn Leu

420

- (2) INFORMATION FOR SEQ ID NO:859:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..422
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594697
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:
- Met Ser Glu Glu His Gly Tyr Gln Arg Ser Gly Lys Lys Cys Arg Glu 5 10
- Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Arg Lys Thr Lys Glu Gly Lys 20 2.5
- Ala Gly Arg Gln Asp Gly Lys His Tyr Arg Phe Phe Arg Gln Leu Glu 4.5 40
- Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn His Asn 50 55 60
- Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn Pro 75 70
- Met Asn Val Thr Thr Thr Ser Asn Ile His Asn Val Asp Ser Val 85 90
- His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser Ser 100 105
- Glu Leu Glu Leu Met Thr Ser Ser Glu Gly Asn Asp Ser Ser Ser 115 120 125
- Arg Arg Lys Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp 130 135 140
- Thr Asn Met Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys 150 155 160
- Leu Thr Lys Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu 170 175
- Glu Glu Trp Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu 185 190
- Phe Trp Ala Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val 200 205
- Ile Glu Ala Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu 220 215
- Cys Ser Ser Pro Glu Glu Arg Thr Asn Gly Asn Asn Glu Ile Arg Asn 230 235
- Asn Ser Glu Thr Gln Asn Glu Asn Gly Ser Asp Gln Thr Met Thr Asn 245 250
- Asn Val Cys Val Lys Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu Ile 265
- Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe Gln Glu 280
- Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala Ala 300 295
- Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys Lys 315 310
- Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys Lys Gln 325 330
- Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr Tyr 340 345

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Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly Tyr 355 360 365
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Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly Ser 370 380

Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu Thr Thr Gly Asn Pro 385 390 395 400

Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe Pro Phe Met Gly $405 \hspace{1cm} 410 \hspace{1cm} 415$

Asp Gly Asp Gln Asn Leu

420

- (2) INFORMATION FOR SEQ ID NO:860:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..355
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594698
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn Pro Met Asn Val 1 5 10 15

Thr Thr Thr Ser Asn Ile His Asn Val Asp Ser Val His Gly Phe 20 25 30

His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser Ser Glu Leu Glu 35 40 45

Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser Ser Arg Arg Lys 50 55 60

Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp Thr Asn Met
65 70 75 80

Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys Leu Thr Lys 85 90 95 Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu Glu Glu Trp

100 105 110

Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu Phe Trp Ala

115 120 125

Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val Ile Glu Ala 130 135 140

Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu Cys Ser Ser 145 150 155 160
Pro Glu Glu Arg Thr Asn Gly Asn Asn Glu Ile Arg Asn Asn Ser Glu

Thr Gln Asn Glu Asn Gly Ser Asp Gln Thr Met Thr Asn Asn Val Cys 180 185 190

Val Lys Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu Ile Leu Lys Leu 195 200 205

Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe Gln Glu Ile Leu Gly 210 215 220

Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala Ala Lys Leu Ile 225 230 235 240

Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys Lys Glu Lys Trp 245 250 255

Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys Lys Gln Ile Asn Lys 260 265 270

Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr Tyr Pro Arg Asn 275 280 285

Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly Tyr Asn Asp Asn 290 295 300

Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly Ser Ser Thr Ser

305 310 315 320
Asn Ala Asn Ala Asn Ala Asn Leu Thr Thr Gly Asn Pro Xaa Gly Ala 325
Met Ala Ala Thr Thr Asn Cys Phe Pro Phe Phe Met Gly Asp Gly Asp 340 345 350

Gln Asn Leu 355

- (2) INFORMATION FOR SEQ ID NO:861:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1185
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594699
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861: gattatgtcc gaggaacatg gataccaaag gagtgggaag aaatgcagag agaagtttga gaatctgtac aaatactata ggaagactaa agaaggcaaa gccggaagac aagacggaaa acattacaga tttttccggc agctcgaagc gctatacggg gattctaata acttggtttc

180 240 ttgtcccaat cataacacgc agttcatgag cagtgctctt catggtttcc atactcaaaa 300 ccctatgaac gttactacaa caacgtccaa catccataac gttgatagtg ttcatggttt tcatcaaagc cttagtcttt ctaacaacta caactcctcc gagcttgagc tgatgacttc 360 420 ctcttcggaa gggaatgatt ctagtagtag aaggaaaaag aggagttgga aagcgaagat aaaggagttc attgatacga acatgaaaag gttgatagag aggcaagatg tttggcttga 480 qaagttgaca aaggttattg aagacaaaga ggaacaacgg atgatgaaag aagaggaatg 540 qaqqaaqatt qaaqctqcaa qqattqataa aqaqcatttq ttttqqqcta aaqaqaqqqc 600 qaqqatqqaa qctaqqqatq ttqcqqtqat tqaqqcattq caatacttqa caqqaaaqcc 660 attgataaaq ccgctgtgtt catccccgga agagaggaca aatggaagta gtagctgctg 720 qqqtqaqcaa qaqattttaa aqcttatqqa qataaqaacq aqcatqqact cqacctttca 780 agagatatta qqaqqqtqct cqqatqaqtt tctatqqqaq qaaatcqcaq cqaaqttqat 840 tcagttaggg tttgatcaga gaagtgcctt attatgcaag gaaaagtggg aatggataag 900 caatggaatg aggaaagaaa agaagcaaat caacaagaaa agaaaggata attcgtccag 960

ctgcggcgtg tactacccga gaaacgaaga aaatccaatc tacaataatc gagaaagtgg 1020 atataatgat aatgatccgc atcaaatcaa cgaacaaggc aatgtaggtt cttcaacatc 1080 aaacgcaaac gcaaacgcaa acctaaccac tggaaatccg ancggtgcaa tggctgctac 1140

tacaaactgc ttcccgttct tcatgggaga tggagatcag aattt

- (2) INFORMATION FOR SEQ ID NO:862:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..394
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594700
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Arg Lys Thr Lys Glu Gly 20 25 30

Lys Ala Gly Arg Gln Asp Gly Lys His Tyr Arg Phe Phe Arg Gln Leu 35 40 45

Glu Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn His 50 55 60

Asn Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn 65 70 75 80

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Pro Met Asn Val Thr Thr Thr Ser Asn Ile His Asn Val Asp Ser
          85
                  90
Val His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser
     100 105 110
Ser Glu Leu Glu Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser
                                   125
115 120
Ser Arg Arg Lys Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile
130 135 140
Asp Thr Asn Met Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu
   150 155 160
Lys Leu Thr Lys Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys
         165 170 175
Glu Glu Glu Trp Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His
        180 185 190
Leu Phe Trp Ala Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala
         200 205
Val Ile Glu Ala Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro
  210 215 220
Leu Cys Ser Ser Pro Glu Glu Arg Thr Asn Gly Ser Ser Ser Cys Trp
   230 235 240
Gly Glu Gln Glu Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp
                250 255
           245
Ser Thr Phe Gln Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp
            265
        260
Glu Glu Ile Ala Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser
                    280
                        285
Ala Leu Leu Cys Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg
                                300
                 295
Lys Glu Lys Lys Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser
              310
                             315 320
Cys Gly Val Tyr Tyr Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn
                          330 335
            325
Arg Glu Ser Gly Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln
        340
                       345
Gly Asn Val Gly Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu
                    360
                                   365
Thr Thr Gly Asn Pro Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe
   370 375
Pro Phe Phe Met Gly Asp Gly Asp Gln Asn
              390
(2) INFORMATION FOR SEQ ID NO:863:
   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 393 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
```

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..393
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594701
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:
- Met Ser Glu Glu His Gly Tyr Gln Arg Ser Gly Lys Lys Cys Arg Glu 10 5
- Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Arg Lys Thr Lys Glu Gly Lys 25
- Ala Gly Arg Gln Asp Gly Lys His Tyr Arg Phe Phe Arg Gln Leu Glu 40
- Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn His Asn 55 60
- Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn Pro

```
65
                70
                                 75
Met Asn Val Thr Thr Thr Ser Asn Ile His Asn Val Asp Ser Val
                          90
          85
His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser Ser
         100 105
Glu Leu Glu Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser Ser
                      120
Arg Arg Lys Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp
       135
                                    140
Thr Asn Met Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys
                                155
   150
Leu Thr Lys Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu
             165
                             170 175
Glu Glu Trp Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu
                          185
Phe Trp Ala Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val
           200
Ile Glu Ala Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu
                   215
Cys Ser Ser Pro Glu Glu Arg Thr Asn Gly Ser Ser Ser Cys Trp Gly
                230
                                 235
Glu Glu Glu Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser
            245
                             250
Thr Phe Gln Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu
       260
                          265
Glu Ile Ala Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala
                      280 285
Leu Leu Cys Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys
                295
Glu Lys Lys Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Cys
                310 315 320
Gly Val Tyr Tyr Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg
            325 330 335
Glu Ser Gly Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly
         340 345 350
Asn Val Gly Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu Thr
355 360 365
Thr Gly Asn Pro Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe Pro
 370 375
Phe Phe Met Gly Asp Gly Asp Gln Asn
             390
(2) INFORMATION FOR SEQ ID NO:864:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 326 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..326
        (D) OTHER INFORMATION: / Ceres Seq. ID 1594702
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:
Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn Pro Met Asn Val
            5
                             10
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Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp Thr Asn Met
Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys Leu Thr Lys
                           90
           85
Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu Glu Glu Trp
                        105
        100
Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu Phe Trp Ala
                    120 125
    115
Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val Ile Glu Ala
  130 135
                      140
Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu Cys Ser Ser
            150 155
Pro Glu Glu Arg Thr Asn Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu
               170
           165
                                          175
Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe Gln
                       185
                                       190
       180
Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala
                                   205
     195 200
Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys
                                 220
                 215
Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys Lys
     230 235
Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr
           245 250
Tyr Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly
        260 265
Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly
                    280
                                    285
Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu Thr Thr Gly Asn
                  295 300
Pro Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe Pro Phe Phe Met
               310 315 320
Gly Asp Gly Asp Gln Asn
            325
```

- (2) INFORMATION FOR SEQ ID NO:865:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..512
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594703
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

gcatcgcaga gctgggaatt atgatgacta caacaatttt ggtgaccctt atcatgcttc 60 ttatctggca gacgaacatc atagtttcga actggttttc ttctcatccg tnttgttcaa 120 gtgtggctga tggaagttgg ataatcttgg tttttgctac aattatgttt ctcataatgt 180 ttgtttggaa ctacgggagt aaactgaagt atgaaactga agtccagaaa aagctaccaa 240 tggacctact acgagaactn ggcagtaacc ttgggacaat tagangcacc cgtatgtccc 300 tgttccaagt gtgcctcaga ncgagagatt tcttttcaga cgtgtatgcc caagaagcta 360 tcantttatt ccgctgtgta gccaggtatg gatacaaaga tgtgcggaag gaaagtcacc 420 aggcgtttga gcagatactg attgagagtc tagaaaaatt tatacgtnaq qaagcacaqq 480 agcgtgcact tgngagtgac ggagnaccat aa

- (2) INFORMATION FOR SEQ ID NO:866:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..169
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594704
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:
- Ile Ala Glu Leu Gly Ile Met Met Thr Thr Ile Leu Val Thr Leu 1 5 10 15
- Ser Ser His Pro Xaa Cys Ser Ser Val Ala Asp Gly Ser Trp Ile Ile 35 40 45
- Leu Val Phe Ala Thr Ile Met Phe Leu Ile Met Phe Val Trp Asn Tyr 50 55 60
- Gly Ser Lys Leu Lys Tyr Glu Thr Glu Val Gln Lys Lys Leu Pro Met 70 75 80
- Asp Leu Leu Arg Glu Xaa Gly Ser Asn Leu Gly Thr Ile Arg Xaa Thr 85 90 95
- Arg Met Ser Leu Phe Gln Val Cys Leu Arg Xaa Arg Asp Phe Phe Ser 100 105 110
- Asp Val Tyr Ala Gln Glu Ala Ile Xaa Leu Phe Arg Cys Val Ala Arg 115 120 125
- Tyr Gly Tyr Lys Asp Val Arg Lys Glu Ser His Gln Ala Phe Glu Gln 130 135 140
- Arg Ala Leu Xaa Ser Asp Gly Xaa Pro 165
- (2) INFORMATION FOR SEQ ID NO:867:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..163
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594705
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:
- Met Met Thr Thr Ile Leu Val Thr Leu Ile Met Leu Leu Ile Trp 1 5 10 15 15
- Gln Thr Asn Ile Ile Val Ser Asn Trp Phe Ser Ser His Pro Xaa Cys 20 25 30
- Ser Ser Val Ala Asp Gly Ser Trp Ile Ile Leu Val Phe Ala Thr Ile
 35 40 45
- Met Phe Leu Ile Met Phe Val Trp Asn Tyr Gly Ser Lys Leu Lys Tyr 50 55 60
- Glu Thr Glu Val Gln Lys Lys Leu Pro Met Asp Leu Leu Arg Glu Xaa 65 70 75 80
- Gly Ser Asn Leu Gly Thr Ile Arg Xaa Thr Arg Met Ser Leu Phe Gln 85 90 95
- Val Cys Leu Arg Xaa Arg Asp Phe Phe Ser Asp Val Tyr Ala Gl
n Glu 100 105 110
- Ala Ile Xaa Leu Phe Arg Cys Val Ala Arg Tyr Gly Tyr Lys Asp Val
- Arg Lys Glu Ser His Gln Ala Phe Glu Gln Ile Leu Ile Glu Ser Leu 130 135 140
- Gly Xaa Pro

- (2) INFORMATION FOR SEQ ID NO:868:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594706
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

Met Thr Thr Thr Ile Leu Val Thr Leu Ile Met Leu Leu Ile Trp Gln $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Thr Asn Ile Ile Val Ser Asn Trp Phe Ser Ser His Pro Xaa Cys Ser 20 25 30

Ser Val Ala Asp Gly Ser Trp Ile Ile Leu Val Phe Ala Thr Ile Met 35 40 45

Phe Leu Ile Met Phe Val Trp Asn Tyr Gly Ser Lys Leu Lys Tyr Glu 50 55 60

Thr Glu Val Gln Lys Lys Leu Pro Met Asp Leu Leu Arg Glu Xaa Gly 65 70 75 80

Ser Asn Leu Gly Thr Ile Arg Xaa Thr Arg Met Ser Leu Phe Gln Val 85 90 95

Cys Leu Arg Xaa Arg Asp Phe Phe Ser Asp Val Tyr Ala Gln Glu Ala 100 105 110

Ile Xaa Leu Phe Arg Cys Val Ala Arg Tyr Gly Tyr Lys Asp Val Arg 115 120 125

Lys Glu Ser His Gln Ala Phe Glu Gln Ile Leu Ile Glu Ser Leu Glu 130 135 140

Lys Phe Ile Arg Xaa Glu Ala Gln Glu Arg Ala Leu Xaa Ser Asp Gly 145 150 155 160

Xaa Pro

- (2) INFORMATION FOR SEQ ID NO:869:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1614
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594752
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

()	- <u> </u>		_			
atgtctcgct	cccagaacga	ggagtttcaa	caatggtgga	acaagcaacg	agataggaac	60
aatcacgacg	ttctttacgc	cggcgacgat	gaagcattcc	tcaccgttga	aatccgtact	120
		taaggatcgg				180
cgtctctacc	tcctcaagtt	caagcaactc	gcatcttcct	tcctctggat	cggtaactct	240
ttcctttacc	ttqqatttct	cgttgntgtt	gtgcttcttc	tctgtttcga	gcttgccgct	300
tatttcaagg	gatggcactt	cacacctccc	tctgttgcct	ccgccgaggt	cgctgtggag	360
ataatttaca	cttagtagtt	ggagatcagg	gcatcttacc	ttgcgccacc	gcttcagagc	420
		tctcttcttg				480
		gctccgccgt				540
		agttagattg				600
ccaatgtgca	atgaaaagga	ggtttaccaa	caatctattq	gagctgtgtg	tatgcttgac	660
taaccaaaaa	aaagaatgct	agttcaggtt	cttgatgact	ccagtgaatt	ggatgttcan	720
		acaaaaatgg				780
nccacctaca	gatttcttga	agaaaactgt	gcctcanttt	taaqqaqaat	gttaggtgac	840
	5-22-06094	5	J 	22 2	2 22 2	

cagttggctt tagaaagtgg ttataccctg agcttaatgt tgaacagcag gtcaatggtg 960 ntttttatta acttctttgg ctttaatgga actgctggtg tttggagaat caaagccctc gaggattgcg ggggatggtt ggagcgaaca actgttgagg acatggatat tgccgttcgt 1020 gcgcatcntt gtggatggaa gttcatttat ctgaatgatg ttaaggtgag tgctgccaag 1080 aaagcaaata tganantnnn ctcttnntct tgctacggaa gcttantcnn gccattctac 1140 tcattcacgc tcttctgcgt cattcttcca ttaacgatgt tcttcccaga agctaactta 1200 1260 ccatcttggg ttgtttgcta tatccctggg atcatgtcca tcttaaacat catcccagcc 1320 ccaagateet teeettteat agtteegtat eteettteg aaaaennenn nnnnnnnnn 1380 aaatttggag ccatgatctc tgagtccggc tctttggttg agtccacaac catccaacga 1440 tcatcctctg attcaggtct gaccgagctt agcaaactag gagcagcaaa gaaagctggc aaaaccaaaa gaaaccgtct gtacagaacg gaaatcgcac tcgcgtttat cctcttggca 1500 qcctcqqtqa gaagcttgtt gtctgcgcaa gggatccatt tctatttcct cttgttccaa 1560 qqaatcacqt tcqttattgt cggtctagat ttgatcgggg aacaggtcag ttag

- (2) INFORMATION FOR SEQ ID NO:870:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..537
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594753
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:
- Met Ser Arg Ser Gln Asn Glu Glu Phe Gln Gln Trp Trp Asn Lys Gln 1 10 15
- Arg Asp Arg Asn Asn His Asp Val Leu Tyr Ala Gly Asp Asp Glu Ala 20 25 30
- Phe Leu Thr Val Glu Ile Arg Thr Pro Ala Thr Val Asp Pro Asp Lys 35 40 45
- Asp Arg Ile Arg Thr Arg Thr Val Arg Gln Leu Ser Arg Leu Tyr Leu 50 55 60
- Leu Lys Phe Lys Gln Leu Ala Ser Ser Phe Leu Trp Ile Gly Asn Ser 65 70 75 80
- Phe Leu Tyr Leu Gly Phe Leu Val Xaa Val Val Leu Leu Cys Phe 85 90 95
- Glu Leu Ala Ala Tyr Phe Lys Gly Trp His Phe Thr Pro Pro Ser Val
- Ala Ser Ala Glu Val Ala Val Glu Val Val Tyr Ala Trp Trp Leu Glu 115 120 125
- Ile Arg Ala Ser Tyr Leu Ala Pro Pro Leu Gln Ser Leu Thr Asn Val 130 135 140
- Cys Ile Val Leu Phe Leu Ile Gln Ser Val Asp Arg Leu Val Leu Val 145 150 155 160
- Leu Gly Cys Phe Trp Ile Lys Leu Arg Arg Ile Lys Pro Val Ala Ser 165 170 175
- Met Glu Tyr Pro Thr Lys Leu Val Gly Glu Gly Val Arg Leu Glu Asp 180 185 190
- Tyr Pro Met Val Ile Val Gln Ile Pro Met Cys Asn Glu Lys Glu Val 195 200 205
- Tyr Gln Gln Ser Ile Gly Ala Val Cys Met Leu Asp Trp Pro Arg Glu 210 215 220
- Arg Met Leu Val Gln Val Leu Asp Asp Ser Ser Glu Leu Asp Val Xaa 225 230 235 240
- Gln Leu Ile Lys Ala Glu Val Gln Lys Trp Gln Gln Arg Gly Val Arg
 245
 250
 255
 The Wal Die Day Van Minn Gwa Gly Dho Lou Gly Gly Asp Cys Ala Ser
- Ile Val Phe Pro Xaa Thr Cys Gly Phe Leu Glu Glu Asn Cys Ala Ser 260 265 270
- Xaa Leu Arg Arg Met Leu Gly Asp Gln Leu Ala Leu Glu Ser Gly Tyr 275 280 285

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Thr Leu Ser Leu Met Leu Asn Ser Arg Ser Met Val Xaa Phe Ile Asn
                    295
Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Lys Ala Leu
             310
                                 315
Glu Asp Cys Gly Gly Trp Leu Glu Arg Thr Thr Val Glu Asp Met Asp
             325
                              330
Ile Ala Val Arg Ala His Xaa Cys Gly Trp Lys Phe Ile Tyr Leu Asn
                                           350
                          345
         340
Asp Val Lys Val Ser Ala Ala Lys Lys Ala Asn Met Xaa Xaa Xaa Ser
     355
                       360
                               365
Xaa Ser Cys Tyr Gly Ser Leu Xaa Xaa Pro Phe Tyr Ser Phe Thr Leu
                    375
                                  380
Phe Cys Val Ile Leu Pro Leu Thr Met Phe Phe Pro Glu Ala Asn Leu
              390
                               395
Pro Ser Trp Val Val Cys Tyr Ile Pro Gly Ile Met Ser Ile Leu Asn
                             410
             405
Ile Ile Pro Ala Pro Arg Ser Phe Pro Phe Ile Val Pro Tyr Leu Leu
         420
                                           430
                       425
Phe Glu Asn Xaa Xaa Xaa Xaa Lys Phe Gly Ala Met Ile Ser Glu
                      440
Ser Gly Ser Leu Val Glu Ser Thr Thr Ile Gln Arg Ser Ser Ser Asp
                           460
  450 455
Ser Gly Leu Thr Glu Leu Ser Lys Leu Gly Ala Ala Lys Lys Ala Gly
                     475
     470
Lys Thr Lys Arg Asn Arg Leu Tyr Arg Thr Glu Ile Ala Leu Ala Phe
                    490
            485
Ile Leu Leu Ala Ala Ser Val Arg Ser Leu Leu Ser Ala Gln Gly Ile
   500 505 510
His Phe Tyr Phe Leu Leu Phe Gln Gly Ile Thr Phe Val Ile Val Gly
                               525
    515 520
Leu Asp Leu Ile Gly Glu Gln Val Ser
                   535
```

- (2) INFORMATION FOR SEQ ID NO:871:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..361
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871: Met Glu Tyr Pro Thr Lys Leu Val Gly Glu Gly Val Arg Leu Glu Asp

1 5 10 15

Tyr Pro Met Val Ile Val Gln Ile Pro Met Cys Asn Glu Lys Glu Val
20 25 30

Tyr Gln Gln Ser Ile Gly Ala Val Cys Met Leu Asp Trp Pro Arg Glu
35 40 45

Arg Met Leu Val Gln Val Leu Asp Asp Ser Ser Glu Leu Asp Val Xaa

50 55

Gln Leu Ile Lys Ala Glu Val Gln Lys Trp Gln Gln Arg Gly Val Arg 65 70 75 80

Ile Val Phe Pro Xaa Thr Cys Gly Phe Leu Glu Glu Asn Cys Ala Ser 85 90 95

Xaa Leu Arg Arg Met Leu Gly Asp Gln Leu Ala Leu Glu Ser Gly Tyr
100 105 110

Thr Leu Ser Leu Met Leu Asn Ser Arg Ser Met Val Xaa Phe Ile Asn 115 120 125

Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Lys Ala Leu

						105					1.40					
Glu	130 Asp	Cvs	Glv	Glv	Trp	135 Leu	Glu	Arq	Thr	Thr	140 Val	Glu	Asp	Met	Asp	
145					150					155					160	
Ile	Ala	Val	Arg	Ala 165	His	Xaa	Cys	Gly	Trp 170	Lys	Phe	Ile	Tyr	Leu 175	Asn	
Asp	Val	Lys	Val 180		Ala	Ala	Lys	Lys 185		Asn	Met	Xaa	Xaa 190	Xaa	Ser	
Xaa	Ser	Cys 195		Gly	Ser	Leu	Xaa 200		Pro	Phe	Tyr	Ser 205		Thr	Leu	
Phe	Cys 210		Ile	Leu	Pro	Leu 215		Met	Phe	Phe	Pro 220	Glu	Ala	Asn	Leu	
225					230					235				Leu	240	
				245					250					Leu 255		
			260					265					270	Ser		
		275					280					285		Ser		
	290					295					300			Ala		
Lys 305	Thr	Lys	Arg	Asn	Arg 310	Leu	Tyr	Arg	Thr	Glu 315	Ile	Ala	Leu	Ala	Pne 320	
	Leu	Leu	Ala	Ala 325		Val	Arg	Ser	Leu 330		Ser	Ala	Gln	Gly 335		
His	Phe	Tyr	Phe 340		Leu	Phe	Gln	Gly 345		Thr	Phe	Val	Ile 350	Val	Gly	
Leu	Asp	Leu 355		Gly	Glu	Gln	Val 360	Ser								
(2) INFORMATION FOR SEQ ID NO:872: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 1291 (D) OTHER INFORMATION: / Ceres Seq. ID 1594760																
	(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:87	2:					
atg	gggn	ngg	gtaa	ccag	tt g	gaag	aagt	c ag	ctac	atca	aca	acaa	.cca	gggt	ggctac	60 120
aaaggataca acaacttcaa aaccaacaat cccaacctct cctaccgtag caccancgtt 120 gctaatcctc aggatcaggt gtatcccgtg caacaacaac aaggtcagaa caaacctttt 180																
gttetetaca accaaggttt egttentaag cageaatttn tggggaacta eeageegeea 240																
ccaccacctg gatttgcaca tcagcaaaac catggtccta nttgctactg a (2) INFORMATION FOR SEQ ID NO:873:																
(i) SEQUENCE CHARACTERISTICS:																
(A) LENGTH: 96 amino acids																
(B) TYPE: amino acid (C) STRANDEDNESS:																
(D) TOPOLOGY: linear																
(ii) MOLECULE TYPE: peptide (ix) FEATURE:																
	(12		(A) 1	JAME/)								
(B) LOCATION: 196 (D) OTHER INFORMATION: / Ceres Seq. ID 1594761																
	(xi	L) SI	(U) (OTHEF OCE I	ESCF	URPT!	ON:	SEQ	ID 1	10:8	73:	. D 1.	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	<u> </u>		
Mo+												11e	e Ası	n Asr	n Asn	

Met Gly Xaa Gly Asn Gln Leu Glu Glu Val Ser Tyr Ile Asn Asn Asn

Gln Gly Gly Tyr Lys Gly Tyr Asn Asn Phe Lys Thr Asn Asn Pro Asn

5

10

- (2) INFORMATION FOR SEQ ID NO:874:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594763
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

Trp Xaa Xaa Val Thr Ser Trp Lys Lys Ser Ala Thr Ser Thr Thr Thr 1 5 10 15

Arg Val Ala Thr Lys Asp Thr Thr Thr Ser Lys Pro Thr Ile Pro Thr 20 25 30

Ser Pro Thr Val Ala Pro Xaa Leu Leu Ile Leu Arg Ile Arg Cys Ile 35 40 45

Pro Cys Asn Asn Asn Lys Val Arg Thr Asn Leu Leu Phe Ser Thr Thr 50 55 60

Lys Val Ser Phe Xaa Ser Ser Asn Xaa Trp Gly Thr Thr Ser Arg His 65 70 80

His His Leu Asp Leu His Ile Ser Lys Thr Met Val Leu Xaa Ala Thr 85 90 95

- (2) INFORMATION FOR SEQ ID NO:875:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..276
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594807
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

atgtcgccaa ccctcaggac caagtctacg ctcagcagca gcagcagcag aaccaanccc 60 aaaccgtttg ttccttacaa ccaaaaccaa gggttcattc caaagcagca gtttcaagga 120 ggatatcaac aacagcagcc acaacctggt ttcacaccac aacaacaaca tgcacctacg cctcagaatn cagacataat gattatgctc cagcagctca ttcaagnaca agnccacagg 240 agcaatggaa atcngctaag aagttgtgtg aagtaa

- (2) INFORMATION FOR SEQ ID NO:876:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

120

180

240

300

360 420

480

```
(ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..91
         (D) OTHER INFORMATION: / Ceres Seq. ID 1594808
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:
Met Ser Pro Thr Leu Arg Thr Lys Ser Thr Leu Ser Ser Ser Ser Ser
                                   10
Arg Thr Xaa Pro Lys Pro Phe Val Pro Tyr Asn Gln Asn Gln Gly Phe
                              25
          20
Ile Pro Lys Gln Gln Phe Gln Gly Gly Tyr Gln Gln Gln Pro Gln
                          40
       35
Pro Gly Phe Thr Pro Gln Gln Gln His Ala Pro Thr Pro Gln Asn Xaa
         55
Asp Ile Met Ile Met Leu Gln Gln Leu Ile Gln Xaa Gln Xaa His Arg
           70
                                       75
Ser Asn Gly Asn Xaa Leu Arg Ser Cys Val Lys
              85
(2) INFORMATION FOR SEQ ID NO:877:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 91 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..91
          (D) OTHER INFORMATION: / Ceres Seq. ID 1594810
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:
Val Ala Asn Pro Gln Asp Gln Val Tyr Ala Gln Gln Gln Gln Gln
               5
                                   10
Asn Gln Xaa Gln Thr Val Cys Ser Leu Gln Pro Lys Pro Arg Val His
                                                   30
                              25
Ser Lys Ala Ala Val Ser Arg Arg Ile Ser Thr Thr Ala Ala Thr Thr
                                               4.5
                           40
Trp Phe His Thr Thr Thr Thr Cys Thr Tyr Ala Ser Glu Xaa Arg
                                          60
                       55
His Asn Asp Tyr Ala Pro Ala Ala His Ser Xaa Thr Xaa Pro Gln Glu
                                       75
                   70
Gln Trp Lys Xaa Ala Lys Lys Leu Cys Glu Val
               85
(2) INFORMATION FOR SEQ ID NO:878:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 606 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..606
          (D) OTHER INFORMATION: / Ceres Seq. ID 1594833
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:
atgtttccgt ccaatttctg ggaaagaaac agtctccgct tctctcctca actccgagat
ttctcactgt tatcgccatg gctccaccta aacccggagg caaagctaaa aaagttgtng
ggagttatca aacttgcttt agaggcgggn aaagcaactc cggcaccacc ggttggtccg
gcgcttggtt ctaagggagt taacattatg gctttttgca aggattataa tgcaagaact
```

gctgataaag ctggttatat cattcctgtt gaaatcactg tcttcgatat tggtgatgtg

tttcgagntt ttaggataag agcttcacgt ttattctcaa gaccccgcct gcttcggttt

tgttgcttaa agctgcaggt ttatctctgt agaattgatc ttaagggatc aaaagatcca

cagcaagata aagttggggt gataacaata gaccagctac gcacaattgc agcagagaag

ctacccgacc tgaactgcac gaccattgaa tccgctatga gaatcattgc aggaactnca 540 gctaacatgg ggatagacat tgaccctccg attcttgaac ccaaaaagaa agcagtttta 600 ttgtaa

- (2) INFORMATION FOR SEQ ID NO:879:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..201
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594834
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

Met Phe Pro Ser Asn Phe Trp Glu Arg Asn Ser Leu Arg Phe Ser Pro 1 5 10 15

Gln Leu Arg Asp Phe Ser Leu Leu Ser Pro Trp Leu His Leu Asn Pro 20 25 30

Glu Ala Lys Leu Lys Leu Xaa Gly Val Ile Lys Leu Ala Leu Glu
35 40 45

Ala Xaa Lys Ala Thr Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ser 50 55 60

Lys Gly Val Asn Ile Met Ala Phe Cys Lys Asp Tyr Asn Ala Arg Thr 65 70 75 80

Ala Asp Lys Ala Gly Tyr Ile Ile Pro Val Glu Ile Thr Val Phe Asp 85 90 95

Ile Gly Asp Val Phe Arg Xaa Phe Arg Ile Arg Ala Ser Arg Leu Phe 100 105 110

Ser Arg Pro Arg Leu Leu Arg Phe Cys Cys Leu Lys Leu Gln Val Tyr 115 120 125

Leu Cys Arg Ile Asp Leu Lys Gly Ser Lys Asp Pro Gln Gln Asp Lys 130 135 140

Val Gly Val Ile Thr Ile Asp Gln Leu Arg Thr Ile Ala Ala Glu Lys 145 150 155 160

Leu Pro Asp Leu Asn Cys Thr Thr Ile Glu Ser Ala Met Arg Ile Ile 165 170 175

Ala Gly Thr Xaa Ala Asn Met Gly Ile Asp Ile Asp Pro Pro Ile Leu 180 185 190

Glu Pro Lys Lys Lys Ala Val Leu Leu 195 200

- (2) INFORMATION FOR SEQ ID NO:880:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594836
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Met Ala Phe Cys Lys Asp Tyr Asn Ala Arg Thr Ala Asp Lys Ala Gly

Tyr Ile Ile Pro Val Glu Ile Thr Val Phe Asp Ile Gly Asp Val Phe

Arg Xaa Phe Arg Ile Arg Ala Ser Arg Leu Phe Ser Arg Pro Arg Leu 35 40 45

Leu Arg Phe Cys Cys Leu Lys Leu Gln Val Tyr Leu Cys Arg Ile Asp 50 55 60

Leu Lys Gly Ser Lys Asp Pro Gln Gln Asp Lys Val Gly Val Ile Thr 75 70 Ile Asp Gln Leu Arg Thr Ile Ala Ala Glu Lys Leu Pro Asp Leu Asn 90 85 Cys Thr Thr Ile Glu Ser Ala Met Arg Ile Ile Ala Gly Thr Xaa Ala 110 100 105 Asn Met Gly Ile Asp Ile Asp Pro Pro Ile Leu Glu Pro Lys Lys 120 115 Ala Val Leu Leu 130 (2) INFORMATION FOR SEQ ID NO:881: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 633 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..633
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594860
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

60 aaaqaaacga aattaagaga aggagaaggt tttacgccgg agttggagac tgatctagat ccgccggcga aaaagcagag ccgtcacatt catcgtcgga aatcaagaaa gggtaattct 120 ctgtaggata gagagacatg gaagccaagt ttttccggtt cttgaagatt gttggagttg 180 gatacaaagc tagagctgag gaagcagggc gtttcttata cctcaaattg ggttacagtc 240 acgaagtnna acttgcggtt cctccagcgg ttcgngtctt ttgtttcaag aacaatgtgg 300 tttgctgcac tggaatcgac aagcaaagag tgcatcagtt tgctgcaacg gtaaggagtt 360 420 gcaaaccccc tgaaccttat aagggcaaag gcataatgta cactgatgna agtcgncaag aagaaacaag gnanngnngt nnnaaatgat ctctctttgt atgcttcttc ttccttctta 480 ctctgcagag acaactttca tctatctgtg gtagattatg gttggatttt tatcaataag 540 ttttatttgg ttgtatgaga catcattttg ttgttaagtc tctttcaatg aaacaaaatg 600 agaagagttc gtcttggaaa tatttatgtt ttg

- (2) INFORMATION FOR SEQ ID NO:882:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594861
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

Met Glu Ala Lys Phe Phe Arg Phe Leu Lys Ile Val Gly Val Gly Tyr
1 5 10 15

Lys Ala Arg Ala Glu Glu Ala Gly Arg Phe Leu Tyr Leu Lys Leu Gly 20 25 30

Tyr Ser His Glu Xaa Xaa Leu Ala Val Pro Pro Ala Val Xaa Val Phe 35 40 45

Cys Phe Lys Asn Asn Val Val Cys Cys Thr Gly Ile Asp Lys Gln Arg
50 60

Val His Gln Phe Ala Ala Thr Val Arg Ser Cys Lys Pro Pro Glu Pro 65 70 75 80

Tyr Lys Gly Lys Gly Ile Met Tyr Thr Asp Xaa Ser Xaa Gln Glu Glu 85 90 95

Thr Arg Xaa Xaa Xaa Lys

100

- (2) INFORMATION FOR SEQ ID NO:883:
 - (i) SEQUENCE CHARACTERISTICS:

120

180

240

300

360

- (A) LENGTH: 367 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..367 (D) OTHER INFORMATION: / Ceres Seq. ID 1594936 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:883: gcatttatcg aaatcggaga tttggtcgtc gaaaatggga aagcagccgg tgaaattgaa ggcggtggtt tacgcgttat cgncgtttca gcagaagatc atgacgggtc tttggaagga tetteeggag aagatteace acaaggtete agagaattgg ateagtaeta tteteetegt cgctcctgtc gtcggaacct actcgtatgc tcagtacttc aaagaacaag agaagctgga gcacaggttc taagcatgga gatatcttga ttccaattct ttcctcattt ttcattctcc aaaatgnggt ttattgacag ttttgtaatn nnnnnnncca aaatagaagc ggaaaagttg (2) INFORMATION FOR SEQ ID NO:884: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..89 (D) OTHER INFORMATION: / Ceres Seq. ID 1594937 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:884: Ala Phe Ile Glu Ile Gly Asp Leu Val Val Glu Asn Gly Lys Ala Ala 10 Gly Glu Ile Glu Gly Gly Leu Arg Val Ile Xaa Val Ser Ala Glu 30 25 20 Asp His Asp Gly Ser Leu Glu Gly Ser Ser Gly Glu Asp Ser Pro Gln 40 Gly Leu Arg Glu Leu Asp Gln Tyr Tyr Ser Pro Arg Arg Ser Cys Arg 55 60 Arg Asn Leu Leu Val Cys Ser Val Leu Gln Arg Thr Arg Glu Ala Gly 75 70 Ala Gln Val Leu Ser Met Glu Ile Ser 85 (2) INFORMATION FOR SEQ ID NO:885: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..83 (D) OTHER INFORMATION: / Ceres Seq. ID 1594938 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:885: His Leu Ser Lys Ser Glu Ile Trp Ser Ser Lys Met Gly Lys Gln Pro 10 Val Lys Leu Lys Ala Val Val Tyr Ala Leu Ser Xaa Phe Gln Gln Lys 25 20
 - Ile Met Thr Gly Leu Trp Lys Asp Leu Pro Glu Lys Ile His His Lys 35 40 45

 Val Ser Glu Asn Trp Ile Ser Thr Ile Leu Leu Val Ala Pro Val Val 50 60

Gly Thr Tyr Ser Tyr Ala Gln Tyr Phe Lys Glu Gln Glu Lys Leu Glu 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:886:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..72
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594939
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

Met Gly Lys Gln Pro Val Lys Leu Lys Ala Val Val Tyr Ala Leu Ser 1 5 10 15

Xaa Phe Gln Gln Lys Ile Met Thr Gly Leu Trp Lys Asp Leu Pro Glu 20 25 30

Lys Ile His His Lys Val Ser Glu Asn Trp Ile Ser Thr Ile Leu Leu 35 40 45

Val Ala Pro Val Val Gly Thr Tyr Ser Tyr Ala Gln Tyr Phe Lys Glu
50 55 60

Gln Glu Lys Leu Glu His Arg Phe

65 70

- (2) INFORMATION FOR SEQ ID NO:887:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..585
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594971
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

agatatagga gaagggagca gcagtaaggt ggtgatgcat aggtcgttga catgccggcg 60 gagtgagece tggaacteca acgaetecaa ecaeteegae gaegeeaegt aaggataaeg 120 tgtggaggag cgtctttaat ccgggaagca acctcgccac tagagccatc ggtccaacat 180 ctttgataaa cccacccatc caaattctcc ctccgtctac gactggttgt acagcggtga 240 ctcaaggagt cagcaccgtt aggatggtcc gatggagtgt gacatgcggg tgatgtaaat 300 atggtgacct gatcttccgc caccttactt tgtttttttt atattgtttt tgtqtacttt atcagagtgg ataaagtgac ggggaatgtt tttcttttgt acaaaaaact gtcttcccac 420 ctaagcaatg tgtgttagtt tctgttttgg gctgtgtttt gcaagttttt gtatttcaga 480 gttgtagtgt agttgcaagt ggcggttgga tctttcacta tcttgttgga ttttgatgat 540 ggttgatgct tttgctttaa tgttaaataa ataagcatac ttttg

- (2) INFORMATION FOR SEQ ID NO:888:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..36
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1594972
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val Met His Arg Ser Leu

```
10
Thr Cys Arg Arg Ser Glu Pro Trp Asn Ser Asn Asp Ser Asn His Ser
                                25
            20
Asp Asp Ala Thr
        35
(2) INFORMATION FOR SEQ ID NO:889:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 713 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..713
          (D) OTHER INFORMATION: / Ceres Seq. ID 1595173
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:
                                                                        60
agatatagga gaagggagca gcagtaaggt ggtgatgcat aggtcgttga catgccggcg
                                                                       120
gagtgagccc tggaactcca acgactccaa ccactccgac gacgccacgt aaggataacg
tgtggaggag cgtctttaat ccgggaagca acctcgccac tagagccatc ggtccaacat
                                                                       180
ctttgataaa cccacccatc caaattctcc ctccgtctac gactgcgttg ataatgaagc
                                                                       240
tcaaaggaag gaacatgtgg cactgtgttt agtgggcgcg tggattaagt gaatagttit
                                                                       300
attctgattt gaccaaatca accttccttt ttgtgcatat ggttgtacag cggtgactca
                                                                       360
aggagtcagc accgttagga tggtccgatg gagtgtgaca tgcgggtgat gtaaatatgg
                                                                       420
tgacctgatc ttccgccacc ttactttgtt ttttttatat tgtttttgtg tactttatca
                                                                       480
gagtggataa agtgacgggg aatgtttttc ttttgtacaa aaaactgtct tcccacctaa
                                                                       540
gcaatgtgtg ttagtttctg ttttgggctg tgttttgcaa gtttttgtat ttcagagttg
                                                                       600
tagtgtagtt gcaagtggcg gttggatctt tcactatctt gttggatttt gatgatggtt
                                                                       660
gatgcttttg ctttaatgtt aaataaataa gcatactttt gctaggtacc att
(2) INFORMATION FOR SEQ ID NO:890:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 36 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..36
           (D) OTHER INFORMATION: / Ceres Seq. ID 1595174
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:
Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val Met His Arg Ser Leu
                                     10
Thr Cys Arg Arg Ser Glu Pro Trp Asn Ser Asn Asp Ser Asn His Ser
                                                     30
            20
Asp Asp Ala Thr
         35
 (2) INFORMATION FOR SEQ ID NO:891:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 667 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..667
           (D) OTHER INFORMATION: / Ceres Seq. ID 1595550
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:
 atcaataaac acaaaaacaa aagaagaaga gaataaacaa aagaagaaaa aaaaaagtat
                                                                        60
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taaaacaaaa tcaataaaaa gagaataaaa aatggtgggt tetcacaaag caageggagt

gcttcttgtg ctactagtgg ttatggccac cacaatagca aacgggacac ctgttgtcga 180 240 tacagcaaaa aatgcagcta cagcagttga agatacagca aaaaatgcag ctacagcagt tggcggtgca gctgcatcag ttggtgctaa agtaacaggt gccaaaccag gcggtgcatc 300 acttgatgtt aaagcatcag gagccaaagg agacggcaaa actgatgata gtgcggcatt 360 420 tgcggctgca tggaaagaag cttgtgcagc agggagcacg attacagtgc caaaaggtga 480 gtatttggta gagagcctag agttcaaagg tccatgcaaa ggtccagtca ctttggaatt gaatggcaat tttaaggctc cggctacggt caagaccact aagcctcatg ccggatggat 540 tgatttcgaa aatctcgctg atttcacttt gaatggaaac aaagctattt ttgacggtca 600 agggtccctc gcttggaagg ccaatgactg cgccaaaacc ggcaaatgca actctctccc 660 tatcaac

- (2) INFORMATION FOR SEQ ID NO:892:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..192
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595551
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met Val Gly Ser His Lys Ala Ser Gly Val Leu Leu Val Leu Leu Val 1 5 5 10 5 15 Val Met Ala Thr Thr Ile Ala Asn Gly Thr Pro Val Val Asp Thr Ala

20 25 30

Lys Asn Ala Ala Thr Ala Val Glu Asp Thr Ala Lys Asn Ala Ala Thr
35 40 45

35
Ala Val Gly Gly Ala Ala Ala Ser Val Gly Ala Lys Val Thr Gly Ala
50
60

Lys Pro Gly Gly Ala Ser Leu Asp Val Lys Ala Ser Gly Ala Lys Gly 65 70 75 80

Asp Gly Lys Thr Asp Asp Ser Ala Ala Phe Ala Ala Ala Trp Lys Glu 85 90 95

115 120 125
Glu Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr Lys

130 135 140

Pro His Ala Gly Trp Ile Asp Phe Glu Asn Leu Ala Asp Phe Thr Leu 145 150 155 160

Asn Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp Lys
165 170 175

Ala Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile Asn 180 185 190

- (2) INFORMATION FOR SEQ ID NO:893:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..175
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595552
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:
- Met Ala Thr Thr Ile Ala Asn Gly Thr Pro Val Val Asp Thr Ala Lys

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10
               5
Asn Ala Ala Thr Ala Val Glu Asp Thr Ala Lys Asn Ala Ala Thr Ala
                               25
           2.0
Val Gly Gly Ala Ala Ala Ser Val Gly Ala Lys Val Thr Gly Ala Lys
Pro Gly Gly Ala Ser Leu Asp Val Lys Ala Ser Gly Ala Lys Gly Asp
                       55
Gly Lys Thr Asp Asp Ser Ala Ala Phe Ala Ala Ala Trp Lys Glu Ala
                   70
Cys Ala Ala Gly Ser Thr Ile Thr Val Pro Lys Gly Glu Tyr Leu Val
                                   90
               85
Glu Ser Leu Glu Phe Lys Gly Pro Cys Lys Gly Pro Val Thr Leu Glu
                                                  110
           100
                               105
Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr Lys Pro
                                               125
                           120
        115
His Ala Gly Trp Ile Asp Phe Glu Asn Leu Ala Asp Phe Thr Leu Asn
                      135
                                           140
Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp Lys Ala
                                       155
                  150
Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile Asn
                                   170
               165
```

- (2) INFORMATION FOR SEQ ID NO:894:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 950 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..950
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:894: gcscgsagrc cmtttcctag racatyytww ttgraaaaag aaacttaatc acaactctct ctttaatctc tttgtctctc tctctctc tctatctctc tctcatttta atggcgaccc 120 aagattotoa agggattaaa ototttggta aaaccataac attoaacgoo aacatcacac 180 agacgataaa aaaagaagag cagcaacaac aacaacagcc agagctacaa gcaacaacag 240 300 ccgttagatc accctcatcg gatctgacgg ctgagaagcg tccagacaag atcataccat gtccgagatg caagagcatg gagactaagt tttgttactt caacaactac aacgttaatc aaccaagaca cttctgcaaa ggttgtcaac gttactggac cgccggtgga gctctccgga 420 atgttcccgt cggtgccggt cgtcggaagt caaaacctcc cggacgtgtc ggtgggttcg 480 ctgagttgct tggagctgcg actggagctg ttgatcaggt cgagctagat gctttgctag 540 tggaagagtg gagagctgct acggcgtctc acggtggttt ccggcatgat tttccggtga 600 agaggeteeg ttgtttteeg etetttaaca teeatgateg gatgagggag tgggagagaa 660 agagaaagag agagagaga agagagagag cttataaaca tctatatata tttatatcaa 720 atttttttgt tacctttgga tgaatattga atccaaattt tttttttctg aactataaac 780 ctataatgat ttgcgtaaaa tgacactttt atgtggatta tgtcaaacct gggttttagt 840 ttgttgattc ctaagtgtgg caccctatgc ttgtttcgca tttaagggtt gaaatgtaaa 900 cctaatttat ttttcgcatg ctataataaa tctgagtgat agcttgcgcc
- (2) INFORMATION FOR SEQ ID NO:895:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..210
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595564
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

Met Ala Thr Gln Asp Ser Gln Gly Ile Lys Leu Phe Gly Lys Thr Ile 10 Thr Phe Asn Ala Asn Ile Thr Gln Thr Ile Lys Lys Glu Glu Gln Gln 20 25 Gln Gln Gln Gln Pro Glu Leu Gln Ala Thr Thr Ala Val Arg Ser Pro 40 Ser Ser Asp Leu Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Pro Cys 55 Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr 75 7.0 Asn Val Asn Gln Pro Arg His Phe Cys Lys Gly Cys Gln Arg Tyr Trp 90 85 Thr Ala Gly Gly Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg 105 100 Lys Ser Lys Pro Pro Gly Arg Val Gly Gly Phe Ala Glu Leu Leu Gly 120 125 Ala Ala Thr Gly Ala Val Asp Gln Val Glu Leu Asp Ala Leu Leu Val 140 135 Glu Glu Trp Arg Ala Ala Thr Ala Ser His Gly Gly Phe Arg His Asp 155 150 Phe Pro Val Lys Arg Leu Arg Cys Phe Pro Leu Phe Asn Ile His Asp 170 175 165 Arg Met Arg Glu Trp Glu Arg Lys Arg Lys Arg Glu Arg Glu Arg Glu 180 185 190 Arg Ala Tyr Lys His Leu Tyr Ile Phe Ile Ser Asn Phe Phe Val Thr 200 Phe Gly

- (2) INFORMATION FOR SEQ ID NO:896:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

210

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Val Asn Gln Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Arg His Phe Cys Lys Gly Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ala

Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro Pro

Gly Arg Val Gly Gly Phe Ala Glu Leu Leu Gly Ala Ala Thr Gly Ala 50 55 60

Val Asp Gln Val Glu Leu Asp Ala Leu Leu Val Glu Glu Trp Arg Ala 65 70 75 80

Ala Thr Ala Ser His Gly Gly Phe Arg His Asp Phe Pro Val Lys Arg 85 90 95

Leu Arg Cys Phe Pro Leu Phe Asn Ile His Asp Arg Met Arg Glu Trp 100 105 110

Glu Arg Lys Arg Lys Arg Glu Arg Glu Arg Glu Arg Ala Tyr Lys His
115 120 125

Leu Tyr Ile Phe Ile Ser Asn Phe Phe Val Thr Phe Gly
130 135 140

- (2) INFORMATION FOR SEQ ID NO:897:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1358 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1358
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897: ctaacttctc tgttcatctt tttctctctt tatttataaa tttatctgca tagtactctc 60 120 tgaatctata tcttcaaaaa aaaaaaacgt ccaagatcaa atcaagaaac ccattaaaaa aaaaaatcag gttttggttt cagttttaag ggtttaaggt ttcttgggga agaaacgatg 180 gagacttttt gtgggtttca aaaggaggaa gagcagatgg atttacctcc tgggttcagg 240 300 tttcatccaa cagatgaaga actcataact cactatctcc ataagaaggt tcttgacacc agcttctcag ctaaagctat cggtgaagtt gatttaaaca aatcagagcc atgggagtta 360 420 ccatggatgg caaaaatggg tgagaaagaa tggtattttt tctgtgtgag agacagaaag 480 tatcccaccg gtttaagaac taaccgagca actgaagccg gttattggaa ggcgaccggg aaggataaag agatataccg aggcaaatca cttgttggga tgaagaagac acttgttttc 540 tatagaggaa gagctcctaa aggtcagaaa accaactggg tgatgcatga gtacaggctt 600 gaaaaaaatt ctctgcccat aacttgccga aaaccgcaaa gaatgaatgg gtgatatgca 660 gggtgttcca aaagagtgct ggagggaaga agatcccgat ttcgagtcta atccgaatcg 720 gttcactcgg aaccgacttt aacccttcgc ttttgccctc tttaaccgat tcttcgcctt 780 acaacgataa aaccaaaaca gaaccggtct acgtgccctg cttctccaac caaacggatc 840 aaaaccaagg aaccacactc aattgcttca gcagccctgt tettaactcg atccaagccg 900 acatttttca caggattcca ctctatcaaa ctcagtccct ccaggtttct atgaatctac 960 agagcccggt tctcacgcaa gaacactcag ttctacatgc tatgatcgag aacaacagaa 1020 gacaaagtct caaaacgatg agtgtctcac aagaaaccgg agtttcaact gacatgaaca 1080 ctgatatctc atcggatttt gaatttggta agaggcggtt tgattctcaa gaagatccgt 1140 cttcctctac tggaccggtt gatcttgaac ctttctggaa ttactgaaga tgattcaaga 1200 ttctcatgtc cattaattta ctgtggtgtg ttaaagtttg tataggctat tgtcatatac 1260 tctcatatca acttccacta tatattataa caatttaaag aaacttaaaa atatgatttg 1320 atatatgact aaagtattat aatacaattt tgtacccc
- (2) INFORMATION FOR SEQ ID NO:898:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..158
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595582
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:
- Met Glu Thr Phe Cys Gly Phe Gln Lys Glu Glu Glu Gln Met Asp Leu 1 5 15
- Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile Thr His 20 25 30
- Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala Lys Ala Ile 35 40 45
- Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu Pro Trp Met
 50 55 60
- Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp Arg 65 70 75 80
- Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly Tyr
 85 90 95
- Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser Leu
 100 105 110
- Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys 115 120 125
- Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Lys Asn

135 130 Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn Gly 150 155 (2) INFORMATION FOR SEQ ID NO:899: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..145 (D) OTHER INFORMATION: / Ceres Seq. ID 1595583 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899: Met Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu 10 5 Ile Thr His Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala 25 20 Lys Ala Ile Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu 45 40 Pro Trp Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val 60 55 Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu 75 70 Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly 90 Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg 100 105 110 Ala Pro Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu 120 125 Glu Lys Asn Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn 135 Gly 145 (2) INFORMATION FOR SEQ ID NO:900: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..95 (D) OTHER INFORMATION: / Ceres Seq. ID 1595584 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900: Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp 10 Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly 25 20 Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser 40 35 Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro 55 Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Lys 75 70 Asn Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn Gly 90 85

(2) INFORMATION FOR SEQ ID NO:901: (i) SEQUENCE CHARACTERISTICS:

1380

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1425
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901: aatggcgtcg acgaagcccg attccgcaat caaccttgaa gaagaggctg aaggcgacgg tgtagccqta gacgatccga ttttcatacc ggagaccacg aacttactcg tccgttactc

tgtagccgta gacgatccga ttttcatacc ggagaccacg aacttactcg tccgttactc 120 gccattcgac gacagggaca tcgattgcaa tccttatttc cctttcacag gcccgatttc 180 agattetgga teaggttett acteggatte tgagecegat eecaacaget gteecatega 240 300 tttcttcgat cgagattctt ccgatgttga cgtggctgag tacttggaat caggagggct 360 gaccgccggt gattataata tttggggctt ttatgacccc aaggaagacg aggaagaga ggagatagtt ttggggactt ccgggtcgga tctgcaaccg ggtgattcag gggagcaagg 420 480 gcttcgagtg accggtatcg attcagattc cgattgtgaa gatggcgtgt ttgattttat 540 ctctgaggat agtagcggga ataggggaaa tgattcgggt cgggtcgagg ttggtacggg 600 tetteeteet gigtgggate atetettegg agagggaace gigtiggetg atgaagaatg ggaggaggtg cagaacgcga ttaactggac agcttttagt ggacccgaag atgaggacga 660 agaagatgaa ttgtcttcac tatcaaggga tgatgaagaa gaagatcatg aactggactg 720 780 gcaggttttg ttaactgtta acaatgttgt taattatatc gaacaagctg aaggaatcat gctaaatcct gatgatatcg atccggatta ttacctgtat ctatctggtt tggatgaatt 840 tgatgaaaat cagagtggac attatgatgc tgatgctatt cttgggcaaa tgtttgatga 900 960 cgagactgga atcaggggaa atcctccagc agccaaaagt gtaattcagg atcttccggt tgtggagctt gctgtggaag agttagacaa agggaacaat gtttgtgcgg tatgcaaaga 1020 tgaaatgtta gtggaggaga aagtaaggag gcttccttgt agtcatttct atcatggaga 1080 gtgtatcata ccttggttgg ggataaggaa tacttgcccg gtttgtcggt atgagctgcc 1140 1200 tactgatgat cttgagtatg aaagacataa gagctcagaa aggggcgata ctggtttggc aaggaacgtg ttgccgggta gatatagtta attgaatatt tgaagtgatc tattcttcaa 1260 gttaatagac atggtttcag aggcaagatc cttgaaccac tttgtttwtg gtaagcactt 1320

- (2) INFORMATION FOR SEQ ID NO:902:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 amino acids

gttaaacttt gaacccttat cttgaagtgt ttgtgaagtt aattc

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..409
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595586

atcgtgaatg tgataatgtt taagttgtat atattccttt tgttttgtga aataaatcat

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:
- Met Ala Ser Thr Lys Pro Asp Ser Ala Ile Asn Leu Glu Glu Glu Ala

 1 5 10 15

 15 10 Pro Clu Thr
- Glu Gly Asp Gly Val Ala Val Asp Asp Pro Ile Phe Ile Pro Glu Thr 20 25 30
- Thr Asn Leu Leu Val Arg Tyr Ser Pro Phe Asp Asp Arg Asp Ile Asp 35 40 45
- Cys Asn Pro Tyr Phe Pro Phe Thr Gly Pro Ile Ser Asp Ser Gly Ser 50 55 60
- Gly Ser Tyr Ser Asp Ser Glu Pro Asp Pro Asn Ser Cys Pro Ile Asp 65 70 75 80
- Phe Phe Asp Arg Asp Ser Ser Asp Val Asp Val Ala Glu Tyr Leu Glu 85 90 95
- Ser Gly Gly Leu Thr Ala Gly Asp Tyr Asn Ile Trp Gly Phe Tyr Asp
 100 105 110
- Pro Lys Glu Asp Glu Glu Glu Glu Ile Val Leu Gly Thr Ser Gly

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120
        115
Ser Asp Leu Gln Pro Gly Asp Ser Gly Glu Gln Gly Leu Arg Val Thr
                                            140
                        135
    130
Gly Ile Asp Ser Asp Ser Asp Cys Glu Asp Gly Val Phe Asp Phe Ile
                                        155
                    150
Ser Glu Asp Ser Ser Gly Asn Arg Gly Asn Asp Ser Gly Arg Val Glu
                                    170
                165
Val Gly Thr Gly Leu Pro Pro Val Trp Asp His Leu Phe Gly Glu Gly
                                                   190
                                185
            180
Thr Val Leu Ala Asp Glu Glu Trp Glu Glu Val Gln Asn Ala Ile Asn
                                                205
                            200
Trp Thr Ala Phe Ser Gly Pro Glu Asp Glu Asp Glu Glu Asp Glu Leu
                                            220
                        215
Ser Ser Leu Ser Arg Asp Asp Glu Glu Glu Asp His Glu Leu Asp Trp
                                        235
                    230
Gln Val Leu Leu Thr Val Asn Asn Val Val Asn Tyr Ile Glu Gln Ala
                                    250
                245
Glu Gly Ile Met Leu Asn Pro Asp Asp Ile Asp Pro Asp Tyr Tyr Leu
                                                    270
                                265
            260
Tyr Leu Ser Gly Leu Asp Glu Phe Asp Glu Asn Gln Ser Gly His Tyr
                                                285
                            280
Asp Ala Asp Ala Ile Leu Gly Gln Met Phe Asp Asp Glu Thr Gly Ile
                        295
                                            300
Arg Gly Asn Pro Pro Ala Ala Lys Ser Val Ile Gln Asp Leu Pro Val
                                        315
                    310
Val Glu Leu Ala Val Glu Glu Leu Asp Lys Gly Asn Asn Val Cys Ala
                                                        335
                                    330
                325
Val Cys Lys Asp Glu Met Leu Val Glu Glu Lys Val Arg Arg Leu Pro
                                                     350
                                345
            340
Cys Ser His Phe Tyr His Gly Glu Cys Ile Ile Pro Trp Leu Gly Ile
                                                 365
                            360
Arg Asn Thr Cys Pro Val Cys Arg Tyr Glu Leu Pro Thr Asp Asp Leu
                                            380
                        375
Glu Tyr Glu Arg His Lys Ser Ser Glu Arg Gly Asp Thr Gly Leu Ala
                                         395
                                                             400
                    390
Arg Asn Val Leu Pro Gly Arg Tyr Ser
                405
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- (2) INFORMATION FOR SEQ ID NO:903:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2547 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2547
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:903: atcatcactc tctctctttc gttacagttc cctaatcaag caagttgcat atcacgagct

ctctcaactc tcaatccaat ccatctctc ctcacgcatt ttcgtttgtt tcttcgtttt cctcttttca gattcttct ttcgattct cacattgata aaacttgtct atggtggttg tacgtcgat tgagtagatg aagttcaccg gaaaatcaaa tttgacggct acattacccg gcaactgtccc aaatatcagg gctattcata gaaggagagc gcggaaaccg agcttcactc gtcaacgaag atctggcgtg tctgtcagga ggctaagcag gcggagact cctcaattga aacattgagc ggaggatcaa aacattgagc gatgcggcg ggttgaagat gatgataacg aggaggataa acttgctgcc ggagtgtgc ggaggatca gatgcggagata acttgggtcc tctgtttat tatcaccacc atgatgaca acattctggc tctgtttat tatcaccacc atgatgaca acattctggc tctgtttat tatcaccacc atgatgaca acattctggc tttcaagaca acattctggc tctgtttat tatcaccacc atgatgaca acattctggc tttcaagaca acattctggc tttcaagaca acattctggc tctgtttat tatcaccacc atgatgaca acattctggc tttcaagaca acattctggc tttcaagaca acattctggc tttcaagaca acattctggc tttcaagaca

acaattcaag aaacaagcat agtggattct tgtgtaagca tgagccttca gttccatttc

cccactgcgc gatggaggga gcaacaaaat gggatcccat ctgcttggat acaagggatg 780 atgtacacca aatctatagc aacgtgaagt ggaataatca acaagtgaat gatgtttcat 840 900 tagcttcttc tattgaattg aaacttcagg aagctcgtgc ttgcatcaag gatcttgaga gtgagaagcg atctcagaaa aagaagcttg agcagttcct gaagaaagtt agcgaggaga 960 gggcagettg geggageaga gageatgaga aggteegage aattattgat gaeatgaaag 1020 ctgacatgaa ccaggaaaag aagactcgtc agagattaga aatcgtcaat tcaaaattag 1080 tcaatgagct tgcagattca aagttagcag taaagcgtta catgcatgat taccaacagg 1140 aaaggaaggc aagagaattg atcgaagaag tttgtgatga actggcaaag gaaatagaag 1200 aagataaagc tgagattgaa gcattgaaga gcgaatccat gaatctcaga gaggaagtag 1260 1320 acgatgaaag aagaatgctg cagatggctg aggtttggcg tgaggaacgt gtccagatga agcttattga tgccaaagta acactcgaga acaagtattc acaaatgaac aaactcgtag 1380 1440 gagatatgga agcetteete agtteaagaa ataetaeagg tgtgaaagag gtgaaagttg cggaattgtt aagagaaact gctgcatcag ttgataatat ccaagaaatc aaggaattta 1500 catatgaacc ctcaaagccg gacgatatcc tcatgttgtt tgaacaaatg aacatgggtg 1560 aaaaccagga tagagaaatc, gagcaatatg ttgcctacag tccggtcagc cacgcttcaa 1620 1680 aagctcacac ggtaagtcca gatgtcaatt tgattaacaa agggagacat tcgaatgctt tcactgatca gaatggtgaa tttgaagaag atgacagtgg ctgggaaact gtgagccatt 1740 1800 ctgaagaaca cggatccagt tactctccag atgagagcat ccctaatatt agcaacactc 1860 atcaccgtaa cagcaatgta tcgatgaatg gaacagagta tgaaaagact ctattgagag aaataaaaga agtgtgctcg gttccaagac gacaatccaa aaagttaccg tcaatggcaa 1920 agctctggag ttcattagaa ggtatgaatg gaagggtatc aaacgcgaga aaatcaacca 1980 tggagatggt ttcaccagag acaggctcaa acaaaggcgg attcaacaca ttggacctgg 2040 ttggtcaatg gagctcatca ccagactcgg ctaatgctaa tttaaatcga ggagggagga 2100 aagggtgcat agagtggcca agaggtgcac ataagaacag cttgaagaca aagctcatag 2160 2220 aagcacaaat cgagagccaa aaggttcagc tgaagcatgt ccttgagcat aagatctagg ccacaacata ttccaaaact accagtccta ggccatacta ctattctttg tggctgagca 2280 gcagaactgg atttttgatc ccgttctcct gctattgcca ttgtcgcgtg atctagcgct 2340 2400 ggtcaagcca atcaacgtgg tatattttcg ttagctaaaa gcaaaatgat ctttgtgatt gattgctgtc gtagcttggc tgggctagct acagccactt aattaccaac aacctcttgg 2460 ttgctaggaa cagaggcaca atggtgtttt cctttaatga attttgttcc tctttagtcc 2520 aacgctaggt caataatatc ttctttt

- (2) INFORMATION FOR SEQ ID NO:904:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..673
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595600
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

Met Lys Phe Thr Gly Lys Ser Asn Leu Thr Ala Thr Leu Pro Ala Thr 1 5 10 15

Val Pro Asn Ile Arg Ala Ile His Arg Arg Arg Ala Arg Lys Pro Ser 20 25 30

Phe Thr Arg Gln Arg Arg Ser Gly Val Ser Val Arg Arg Leu Ser Arg 35 40 45

Pro Glu Thr Pro Gln Leu Lys Ser Lys Val Glu Asp Gln Asn Ile Glu 50 55 60

Arg Cys Gly Gly Val Glu Asp Asp Asp Asp Glu Asp Asp Asp Cys Asn 65 70 75 80

Lys Met Arg Cys Gln Glu Arg Ser Arg Ser Val Arg Pro Asp Thr Val 85 90 95

Arg Lys Leu Ala Ala Gly Val Trp Gln Leu Arg Val Pro Asp Ala Val 100 105 110

Ser Ser Gly Gly Asp Lys Arg Ser Lys Asp Arg Leu Arg Phe Gln Glu 115 120 125

Thr Ala Gly Pro Ala Gly Asn Leu Gly Pro Leu Phe Tyr Tyr His His 130 135 140

His Asp Asp Lys His Ser Gly Phe Gln Ser Asn Asn Ser Arg Asn Lys 150 155 His Ser Gly Phe Leu Cys Lys His Glu Pro Ser Val Pro Phe Pro His 165 170 Cys Ala Met Glu Gly Ala Thr Lys Trp Asp Pro Ile Cys Leu Asp Thr 180 185 Arg Asp Asp Val His Gln Ile Tyr Ser Asn Val Lys Trp Asn Asn Gln 200 Gln Val Asn Asp Val Ser Leu Ala Ser Ser Ile Glu Leu Lys Leu Gln 210 215 220 Glu Ala Arg Ala Cys Ile Lys Asp Leu Glu Ser Glu Lys Arg Ser Gln 225 230 235 240 Lys Lys Leu Glu Gln Phe Leu Lys Lys Val Ser Glu Glu Arg Ala 245 250 255 Ala Trp Arg Ser Arg Glu His Glu Lys Val Arg Ala Ile Ile Asp Asp 265 270 260 Met Lys Ala Asp Met Asn Gln Glu Lys Lys Thr Arg Gln Arg Leu Glu 275 280 285 Ile Val Asn Ser Lys Leu Val Asn Glu Leu Ala Asp Ser Lys Leu Ala 290 295 Val Lys Arg Tyr Met His Asp Tyr Gln Glu Arg Lys Ala Arg Glu 305 310 315 Leu Ile Glu Glu Val Cys Asp Glu Leu Ala Lys Glu Ile Glu Glu Asp 325 330 Lys Ala Glu Ile Glu Ala Leu Lys Ser Glu Ser Met Asn Leu Arg Glu 340 345 Glu Val Asp Asp Glu Arg Arg Met Leu Gln Met Ala Glu Val Trp Arg 360 365 Glu Glu Arg Val Gln Met Lys Leu Ile Asp Ala Lys Val Thr Leu Glu 370 375 Asn Lys Tyr Ser Gln Met Asn Lys Leu Val Gly Asp Met Glu Ala Phe 385 390 395 Leu Ser Ser Arg Asn Thr Thr Gly Val Lys Glu Val Lys Val Ala Glu 405 410 Leu Leu Arg Glu Thr Ala Ala Ser Val Asp Asn Ile Gln Glu Ile Lys 420 425 430 Glu Phe Thr Tyr Glu Pro Ser Lys Pro Asp Asp Ile Leu Met Leu Phe 435 440 Glu Gln Met Asn Met Gly Glu Asn Gln Asp Arg Glu Ile Glu Gln Tyr 460 450 455 Val Ala Tyr Ser Pro Val Ser His Ala Ser Lys Ala His Thr Val Ser 470 475 Pro Asp Val Asn Leu Ile Asn Lys Gly Arg His Ser Asn Ala Phe Thr 485 490 Asp Gln Asn Gly Glu Phe Glu Glu Asp Asp Ser Gly Trp Glu Thr Val 505 Ser His Ser Glu Glu His Gly Ser Ser Tyr Ser Pro Asp Glu Ser Ile 520 Pro Asn Ile Ser Asn Thr His His Arg Asn Ser Asn Val Ser Met Asn 535 Gly Thr Glu Tyr Glu Lys Thr Leu Leu Arg Glu Ile Lys Glu Val Cys 555 Ser Val Pro Arg Arg Gln Ser Lys Leu Pro Ser Met Ala Lys Leu 570 Trp Ser Ser Leu Glu Gly Met Asn Gly Arg Val Ser Asn Ala Arg Lys 580 585 Ser Thr Met Glu Met Val Ser Pro Glu Thr Gly Ser Asn Lys Gly Gly 595 600 Phe Asn Thr Leu Asp Leu Val Gly Gln Trp Ser Ser Ser Pro Asp Ser 610 615 620 Ala Asn Ala Asn Leu Asn Arg Gly Gly Arg Lys Gly Cys Ile Glu Trp

635 625 630 Pro Arg Gly Ala His Lys Asn Ser Leu Lys Thr Lys Leu Ile Glu Ala 645 650 655 Gln Ile Glu Ser Gln Lys Val Gln Leu Lys His Val Leu Glu His Lys 660 665 Ile

- (2) INFORMATION FOR SEQ ID NO:905:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..592
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595601
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

Met Arg Cys Gln Glu Arg Ser Arg Ser Val Arg Pro Asp Thr Val Arg

10 5 Lys Leu Ala Ala Gly Val Trp Gln Leu Arg Val Pro Asp Ala Val Ser

25 20

Ser Gly Gly Asp Lys Arg Ser Lys Asp Arg Leu Arg Phe Gln Glu Thr 40

Ala Gly Pro Ala Gly Asn Leu Gly Pro Leu Phe Tyr Tyr His His His 55

Asp Asp Lys His Ser Gly Phe Gln Ser Asn Asn Ser Arg Asn Lys His 70 75

Ser Gly Phe Leu Cys Lys His Glu Pro Ser Val Pro Phe Pro His Cys 90 85

Ala Met Glu Gly Ala Thr Lys Trp Asp Pro Ile Cys Leu Asp Thr Arg 100 105

Asp Asp Val His Gln Ile Tyr Ser Asn Val Lys Trp Asn Asn Gln Gln 115 120 125

Val Asn Asp Val Ser Leu Ala Ser Ser Ile Glu Leu Lys Leu Gln Glu 130 140

Ala Arg Ala Cys Ile Lys Asp Leu Glu Ser Glu Lys Arg Ser Gln Lys 150 155 160

Lys Lys Leu Glu Gln Phe Leu Lys Lys Val Ser Glu Glu Arg Ala Ala 165 170

Trp Arg Ser Arg Glu His Glu Lys Val Arg Ala Ile Ile Asp Asp Met 190 180 185

Lys Ala Asp Met Asn Gln Glu Lys Lys Thr Arg Gln Arg Leu Glu Ile 200

Val Asn Ser Lys Leu Val Asn Glu Leu Ala Asp Ser Lys Leu Ala Val 220 215

Lys Arg Tyr Met His Asp Tyr Gln Gln Glu Arg Lys Ala Arg Glu Leu 235 230

Ile Glu Glu Val Cys Asp Glu Leu Ala Lys Glu Ile Glu Glu Asp Lys 245 250

Ala Glu Ile Glu Ala Leu Lys Ser Glu Ser Met Asn Leu Arg Glu Glu 260 265

Val Asp Asp Glu Arg Arg Met Leu Gln Met Ala Glu Val Trp Arg Glu 285 280

Glu Arg Val Gln Met Lys Leu Ile Asp Ala Lys Val Thr Leu Glu Asn 295 300

Lys Tyr Ser Gln Met Asn Lys Leu Val Gly Asp Met Glu Ala Phe Leu 310 315

Ser Ser Arg Asn Thr Thr Gly Val Lys Glu Val Lys Val Ala Glu Leu 330

Leu Arg Glu Thr Ala Ala Ser Val Asp Asn Ile Gln Glu Ile Lys Glu 340 345 350 Phe Thr Tyr Glu Pro Ser Lys Pro Asp Asp Ile Leu Met Leu Phe Glu 355 360 365 Gln Met Asn Met Gly Glu Asn Gln Asp Arg Glu Ile Glu Gln Tyr Val 370 375 380 Ala Tyr Ser Pro Val Ser His Ala Ser Lys Ala His Thr Val Ser Pro 385 390 395 400 Asp Val Asn Leu Ile Asn Lys Gly Arg His Ser Asn Ala Phe Thr Asp 405 410 415 Gln Asn Gly Glu Phe Glu Glu Asp Asp Ser Gly Trp Glu Thr Val Ser 420 425 430 His Ser Glu Glu His Gly Ser Ser Tyr Ser Pro Asp Glu Ser Ile Pro 435 440 445 Asn Ile Ser Asn Thr His His Arg Asn Ser Asn Val Ser Met Asn Gly 450 455 460 Thr Glu Tyr Glu Lys Thr Leu Leu Arg Glu Ile Lys Glu Val Cys Ser 465 470 475 480 Val Pro Arg Arg Gln Ser Lys Lyu Pro Ser Met Ala Lys Leu Trp 485 490 495 Ser Ser Leu Glu Gly Met Asn Gly Arq Val Ser Asn Ala Arq Lys Ser 500 505 510 Thr Met Glu Met Val Ser Pro Glu Thr Gly Ser Asn Lys Gly Gly Phe 515 520 525 Asn Thr Leu Asp Leu Val Gly Gln Trp Ser Ser Ser Pro Asp Ser Ala 530 535 540 Asn Ala Asn Leu Asn Arg Gly Gly Arg Lys Gly Cys Ile Glu Trp Pro 545 550 555 560 Arg Gly Ala His Lys Asn Ser Leu Lys Thr Lys Leu Ile Glu Ala Gln 565 570 575 Ile Glu Ser Gln Lys Val Gln Leu Lys His Val Leu Glu His Lys Ile 580 585 590

- (2) INFORMATION FOR SEQ ID NO:906:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..495
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595602
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:
- Met Glu Gly Ala Thr Lys Trp Asp Pro Ile Cys Leu Asp Thr Arg Asp 1 5 10 15
- Asp Val His Gln Ile Tyr Ser Asn Val Lys Trp Asn Asn Gln Gln Val 20 25 30
- Asn Asp Val Ser Leu Ala Ser Ser Ile Glu Leu Lys Leu Gln Glu Ala 35 40 45
- Arg Ala Cys Ile Lys Asp Leu Glu Ser Glu Lys Arg Ser Gln Lys Lys
- 50 55 60 Lys Leu Glu Gln Phe Leu Lys Lys Val Ser Glu Glu Arg Ala Ala Trp
- 65 70 75 80 Arg Ser Arg Glu His Glu Lys Val Arg Ala Ile Ile Asp Asp Met Lys
- 85 90 95 Ala Asp Met Asn Gln Glu Lys Lys Thr Arg Gln Arg Leu Glu Ile Val
- 100 105 110 Asn Ser Lys Leu Val Asn Glu Leu Ala Asp Ser Lys Leu Ala Val Lys

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115
                  120
Arg Tyr Met His Asp Tyr Gln Glu Arg Lys Ala Arg Glu Leu Ile
 130 135 140
Glu Glu Val Cys Asp Glu Leu Ala Lys Glu Ile Glu Glu Asp Lys Ala
   150 155 160
Glu Ile Glu Ala Leu Lys Ser Glu Ser Met Asn Leu Arg Glu Glu Val
          165 170 175
Asp Asp Glu Arg Arg Met Leu Gln Met Ala Glu Val Trp Arg Glu Glu
        180 185 190
Arg Val Gln Met Lys Leu Ile Asp Ala Lys Val Thr Leu Glu Asn Lys
    195 200 205
Tyr Ser Gln Met Asn Lys Leu Val Gly Asp Met Glu Ala Phe Leu Ser
               215
                              220
Ser Arg Asn Thr Thr Gly Val Lys Glu Val Lys Val Ala Glu Leu Leu
            230 235
Arg Glu Thr Ala Ala Ser Val Asp Asn Ile Gln Glu Ile Lys Glu Phe
          245 250 255
Thr Tyr Glu Pro Ser Lys Pro Asp Asp Ile Leu Met Leu Phe Glu Gln
       260 265 270
Met Asn Met Gly Glu Asn Gln Asp Arg Glu Ile Glu Gln Tyr Val Ala
275 280 285
Tyr Ser Pro Val Ser His Ala Ser Lys Ala His Thr Val Ser Pro Asp
290 295 300
Val Asn Leu Ile Asn Lys Gly Arg His Ser Asn Ala Phe Thr Asp Gln
305 310 315 320
Asn Gly Glu Phe Glu Glu Asp Asp Ser Gly Trp Glu Thr Val Ser His
          325 330 335
Ser Glu Glu His Gly Ser Ser Tyr Ser Pro Asp Glu Ser Ile Pro Asn
       340 345 350
Ile Ser Asn Thr His His Arg Asn Ser Asn Val Ser Met Asn Gly Thr
355 360 365
Glu Tyr Glu Lys Thr Leu Leu Arg Glu Ile Lys Glu Val Cys Ser Val
370 375 380
Pro Arg Arg Gln Ser Lys Lys Leu Pro Ser Met Ala Lys Leu Trp Ser
385 390 395 400
Ser Leu Glu Gly Met Asn Gly Arg Val Ser Asn Ala Arg Lys Ser Thr
          405
                        410 415
Met Glu Met Val Ser Pro Glu Thr Gly Ser Asn Lys Gly Gly Phe Asn
       420 425 430
Thr Leu Asp Leu Val Gly Gln Trp Ser Ser Ser Pro Asp Ser Ala Asn
                 440 445
Ala Asn Leu Asn Arg Gly Gly Arg Lys Gly Cys Ile Glu Trp Pro Arg
               455 460
Gly Ala His Lys Asn Ser Leu Lys Thr Lys Leu Ile Glu Ala Gln Ile
465 470 475 480
Glu Ser Gln Lys Val Gln Leu Lys His Val Leu Glu His Lys Ile
          485
                        490 495
(2) INFORMATION FOR SEQ ID NO:907:
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1835 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1835
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595607
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

acacaaccaa agcgtttaga aaaaaaacag cgataaaacc gaaacatcaa gcaaacaaaa aaaaagagga gaatttttt tttttgtttt cgttttcaaa aacaaaatct ttgaatttta

tggcaacccg tcttctccga acaaacttta tccggcgatc ttaccgttta cccgctttta 240 gcccggtggg tcctcccacc gtgactgctt ccaccgccgt cgtcccggag attctctcct ttggacaaca agcaccggaa ccacctcttc accacccaaa acccactgag caatctcacg 300 atggtctcga tctctccgat caagcccgtc ttttctcctc taccccaacc tctgatctcc 360 teegtteeae egeegtgttg eatgeggegg egataggtee tatggtegae etagggaegt 420 480 gggtcatgag ctctaaactt atggacgctt ccgtgacgcg tggcatggtt ttagggcttg 540 tgaaaagtac gttttatgac catttttgcg ccggtgaaga tgccgacgca gccgctgagc 600 gcgtgagaag cgtttatgaa gctaccggtc ttaaagggat gcttgtctat ggcgtcgaac 660 acgccgatga cgctgtatct tgtgatgata acatgcaaca attcattcga accattgaag 720 ctgccaaatc tttaccaaca tctcacttta gctcagtggt tgtgaagata actgccattt 780 qtccaattaq tcttctgaaa cgagtgagcg atctgcttcg gtgggaatac aaaagtccaa 840 acttcaaact ctcatggaag ctcaaatcgt ttccggtttt ctccgattcg agtcctctct accacacaaa ctcagaaccg gaaccgttaa ccgcggaaga agaacgggag ctcgaagcag 900 960 ctcatggaag gattcaagaa atctgtagga aatgccaaga gtccaatgta ccattgttga 1020 ttgatgcgga agacacaatc ctccaacccg cgatcgatta catggcttat tcatcggcga tcatgttcaa tgctgacaaa gaccgaccaa tcgtttacaa cacgattcag gcgtacttga 1080 gagacgccgg tgagagactg catttggcag tacaaaatgc tgagaaagag aatgttccta 1140 tggggttcaa gttggtgaga ggggcttaca tgtctagcga agctagcttg gcggattccc 1200 tgggttgcaa gtcgccagtc cacgacacaa ttcaggatac tcactcttgt tacaatgatt 1260 gtatgacatt cctgatggag aaagcatcaa acggttctgg tttcggtgtc gttctcgcaa 1320 cacataacgc tgattcgggg agacttgcgt cgaggaaagc gagtgacctc gggattgata 1380 aacagaacgg gaagatagag tttgcacagc tatatggtat gtcggatgca ttgtCcttcg 1440 gtttaaagag agccgggttc aatgttagca agtacatgcc gtttggaccc gtcgcaaccg 1500 ctataccgta tcttctccga cgcgcttatg agaaccgggg aatgatggcc accggagctc 1560 atgaccgtca actcatgagg atggaactta agaggagatt aatcgccggg attgcgtaaa 1620 gagagagtat ggagccatta aatgaaattg ggaaatgtag atgaataaat ttcttctatg 1680 taqtttaaga aattgaaaac aaaaaattat aatataagaa atggagtagg taagaacatt 1740 tcctgtggct aaatattttt catgagggac tatgttttta ctatcaatat atcattcaca 1800 aatgtatatt caccttatca ataaaaatgt ttttt

- (2) INFORMATION FOR SEQ ID NO:908:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 538 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

150

- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

Thr Thr Lys Ala Phe Arg Lys Lys Thr Ala Ile Lys Pro Lys His Gln 1.0 Ala Asn Lys Lys Lys Glu Glu Asn Phe Phe Phe Leu Phe Ser Phe Ser 20 Lys Thr Lys Ser Leu Asn Phe Met Ala Thr Arg Leu Leu Arg Thr Asn 40 Phe Ile Arg Arg Ser Tyr Arg Leu Pro Ala Phe Ser Pro Val Gly Pro 55 Pro Thr Val Thr Ala Ser Thr Ala Val Val Pro Glu Ile Leu Ser Phe 70 75 Gly Gln Gln Ala Pro Glu Pro Pro Leu His His Pro Lys Pro Thr Glu Gln Ser His Asp Gly Leu Asp Leu Ser Asp Gln Ala Arg Leu Phe Ser 105 100 Ser Thr Pro Thr Ser Asp Leu Leu Arg Ser Thr Ala Val Leu His Ala 120 Ala Ala Ile Gly Pro Met Val Asp Leu Gly Thr Trp Val Met Ser Ser 140 135 Lys Leu Met Asp Ala Ser Val Thr Arg Gly Met Val Leu Gly Leu Val

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Lys Ser Thr Phe Tyr Asp His Phe Cys Ala Gly Glu Asp Ala Asp Ala
                            170
            165
Ala Ala Glu Arg Val Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly
        180
                      185
                                        190
Met Leu Val Tyr Gly Val Glu His Ala Asp Asp Ala Val Ser Cys Asp
                     200
                                     205
Asp Asn Met Gln Gln Phe Ile Arg Thr Ile Glu Ala Ala Lys Ser Leu
 210 215
                                 220
Pro Thr Ser His Phe Ser Ser Val Val Val Lys Ile Thr Ala Ile Cys
    230 235
Pro Ile Ser Leu Leu Lys Arg Val Ser Asp Leu Leu Arg Trp Glu Tyr
           245 250
Lys Ser Pro Asn Phe Lys Leu Ser Trp Lys Leu Lys Ser Phe Pro Val
       260 265
Phe Ser Asp Ser Ser Pro Leu Tyr His Thr Asn Ser Glu Pro Glu Pro
     275 280
Leu Thr Ala Glu Glu Glu Arg Glu Leu Glu Ala Ala His Gly Arg Ile
        295 300
Gln Glu Ile Cys Arg Lys Cys Gln Glu Ser Asn Val Pro Leu Leu Ile
      310 315
Asp Ala Glu Asp Thr Ile Leu Gln Pro Ala Ile Asp Tyr Met Ala Tyr
            325 330
Ser Ser Ala Ile Met Phe Asn Ala Asp Lys Asp Arg Pro Ile Val Tyr
         340 345
Asn Thr Ile Gln Ala Tyr Leu Arg Asp Ala Gly Glu Arg Leu His Leu
                            365
      355 360
Ala Val Gln Asn Ala Glu Lys Glu Asn Val Pro Met Gly Phe Lys Leu
                      380
      375
Val Arg Gly Ala Tyr Met Ser Ser Glu Ala Ser Leu Ala Asp Ser Leu
               390 395
Gly Cys Lys Ser Pro Val His Asp Thr Ile Gln Asp Thr His Ser Cys
                410 415
Tyr Asn Asp Cys Met Thr Phe Leu Met Glu Lys Ala Ser Asn Gly Ser
         420 425
Gly Phe Gly Val Val Leu Ala Thr His Asn Ala Asp Ser Gly Arg Leu
          440
                                     445
Ala Ser Arg Lys Ala Ser Asp Leu Gly Ile Asp Lys Gln Asn Gly Lys
                  455 460
Ile Glu Phe Ala Gln Leu Tyr Gly Met Ser Asp Ala Leu Ser Phe Gly
               470 475 480
Leu Lys Arg Ala Gly Phe Asn Val Ser Lys Tyr Met Pro Phe Gly Pro
                           490 495
Val Ala Thr Ala Ile Pro Tyr Leu Leu Arg Arg Ala Tyr Glu Asn Arg
                        505 510
Gly Met Met Ala Thr Gly Ala His Asp Arg Gln Leu Met Arg Met Glu
                      520
Leu Lys Arg Arg Leu Ile Ala Gly Ile Ala
   530
(2) INFORMATION FOR SEQ ID NO:909:
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- - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..499
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595609
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:
- Met Ala Thr Arg Leu Leu Arg Thr Asn Phe Ile Arg Arg Ser Tyr Arg

10 Leu Pro Ala Phe Ser Pro Val Gly Pro Pro Thr Val Thr Ala Ser Thr 20 25 Ala Val Val Pro Glu Ile Leu Ser Phe Gly Gln Gln Ala Pro Glu Pro Pro Leu His His Pro Lys Pro Thr Glu Gln Ser His Asp Gly Leu Asp 55 Leu Ser Asp Gln Ala Arg Leu Phe Ser Ser Thr Pro Thr Ser Asp Leu 75 70 Leu Arg Ser Thr Ala Val Leu His Ala Ala Ile Gly Pro Met Val 90 85 Asp Leu Gly Thr Trp Val Met Ser Ser Lys Leu Met Asp Ala Ser Val 100 105 Thr Arg Gly Met Val Leu Gly Leu Val Lys Ser Thr Phe Tyr Asp His 120 125 115 Phe Cys Ala Gly Glu Asp Ala Asp Ala Ala Ala Glu Arg Val Arg Ser 135 140 Val Tyr Glu Ala Thr Gly Leu Lys Gly Met Leu Val Tyr Gly Val Glu 150 155 His Ala Asp Asp Ala Val Ser Cys Asp Asp Asn Met Gln Gln Phe Ile 170 165 Arg Thr Ile Glu Ala Ala Lys Ser Leu Pro Thr Ser His Phe Ser Ser 185 180 Val Val Val Lys Ile Thr Ala Ile Cys Pro Ile Ser Leu Leu Lys Arg 200 Val Ser Asp Leu Leu Arg Trp Glu Tyr Lys Ser Pro Asn Phe Lys Leu 210 215 220 Ser Trp Lys Leu Lys Ser Phe Pro Val Phe Ser Asp Ser Ser Pro Leu 230 235 Tyr His Thr Asn Ser Glu Pro Glu Pro Leu Thr Ala Glu Glu Glu Arg 250 245 Glu Leu Glu Ala Ala His Gly Arg Ile Gln Glu Ile Cys Arg Lys Cys 265 Gln Glu Ser Asn Val Pro Leu Leu Ile Asp Ala Glu Asp Thr Ile Leu 280 285 Gln Pro Ala Ile Asp Tyr Met Ala Tyr Ser Ser Ala Ile Met Phe Asn 295 300 Ala Asp Lys Asp Arg Pro Ile Val Tyr Asn Thr Ile Gln Ala Tyr Leu 310 315 Arg Asp Ala Gly Glu Arg Leu His Leu Ala Val Gln Asn Ala Glu Lys 330 Glu Asn Val Pro Met Gly Phe Lys Leu Val Arg Gly Ala Tyr Met Ser 345 340 Ser Glu Ala Ser Leu Ala Asp Ser Leu Gly Cys Lys Ser Pro Val His 365 360 Asp Thr Ile Gln Asp Thr His Ser Cys Tyr Asn Asp Cys Met Thr Phe 380 375 Leu Met Glu Lys Ala Ser Asn Gly Ser Gly Phe Gly Val Val Leu Ala 395 390 Thr His Asn Ala Asp Ser Gly Arg Leu Ala Ser Arg Lys Ala Ser Asp 405 410 Leu Gly Ile Asp Lys Gln Asn Gly Lys Ile Glu Phe Ala Gln Leu Tyr 425 420 Gly Met Ser Asp Ala Leu Ser Phe Gly Leu Lys Arg Ala Gly Phe Asn 440 435 Val Ser Lys Tyr Met Pro Phe Gly Pro Val Ala Thr Ala Ile Pro Tyr 460 455 Leu Leu Arg Arg Ala Tyr Glu Asn Arg Gly Met Met Ala Thr Gly Ala 475 470 His Asp Arg Gln Leu Met Arg Met Glu Leu Lys Arg Arg Leu Ile Ala 490

Gly Ile Ala

- (2) INFORMATION FOR SEQ ID NO:910:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..405
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595610
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:
- Met Val Asp Leu Gly Thr Trp Val Met Ser Ser Lys Leu Met Asp Ala 1 5 10 15
- Ser Val Thr Arg Gly Met Val Leu Gly Leu Val Lys Ser Thr Phe Tyr 20 25 30
- Asp His Phe Cys Ala Gly Glu Asp Ala Asp Ala Ala Ala Glu Arg Val 35 40 45
- Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly Met Leu Val Tyr Gly 50 60
- Val Glu His Ala Asp Asp Ala Val Ser Cys Asp Asp Asn Met Gln Gln 65 70 75 80
- Phe Ile Arg Thr Ile Glu Ala Ala Lys Ser Leu Pro Thr Ser His Phe 85 90 95
- Ser Ser Val Val Lys Ile Thr Ala Ile Cys Pro Ile Ser Leu Leu 100 105 110
- Lys Arg Val Ser Asp Leu Leu Arg Trp Glu Tyr Lys Ser Pro Asn Phe 115 120 125
- Lys Leu Ser Trp Lys Leu Lys Ser Phe Pro Val Phe Ser Asp Ser Ser 130 135 140
- Pro Leu Tyr His Thr Asn Ser Glu Pro Glu Pro Leu Thr Ala Glu Glu 145 150 155 160
- Glu Arg Glu Leu Glu Ala Ala His Gly Arg Ile Gln Glu Ile Cys Arg 165 170 175
- Lys Cys Gln Glu Ser Asn Val Pro Leu Leu Ile Asp Ala Glu Asp Thr 180 185 190
- Ile Leu Gln Pro Ala Ile Asp Tyr Met Ala Tyr Ser Ser Ala Ile Met 195 200 205
- Phe Asn Ala Asp Lys Asp Arg Pro Ile Val Tyr Asn Thr Ile Gln Ala 210 215 220
- Tyr Leu Arg Asp Ala Gly Glu Arg Leu His Leu Ala Val Gln Asn Ala 225 230 235 240
- Glu Lys Glu Asn Val Pro Met Gly Phe Lys Leu Val Arg Gly Ala Tyr 245 250 255
- Met Ser Ser Glu Ala Ser Leu Ala Asp Ser Leu Gly Cys Lys Ser Pro 260 265 270
- Val His Asp Thr Ile Gln Asp Thr His Ser Cys Tyr Asn Asp Cys Met 275 280 285
- Thr Phe Leu Met Glu Lys Ala Ser Asn Gly Ser Gly Phe Gly Val Val 290 295 300
- Leu Ala Thr His Asn Ala Asp Ser Gly Arg Leu Ala Ser Arg Lys Ala 305 310 315 320
- Ser Asp Leu Gly Ile Asp Lys Gln Asn Gly Lys Ile Glu Phe Ala Gln
- Leu Tyr Gly Met Ser Asp Ala Leu Ser Phe Gly Leu Lys Arg Ala Gly 340 345 350
- Phe Asn Val Ser Lys Tyr Met Pro Phe Gly Pro Val Ala Thr Ala Ile 355 360 365
- Pro Tyr Leu Leu Arg Arg Ala Tyr Glu Asn Arg Gly Met Met Ala Thr

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380
                       375
    370
Gly Ala His Asp Arg Gln Leu Met Arg Met Glu Leu Lys Arg Arg Leu
                                        395
                    390
Ile Ala Gly Ile Ala
                405
(2) INFORMATION FOR SEQ ID NO:911:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 590 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..590
          (D) OTHER INFORMATION: / Ceres Seq. ID 1595619
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:
aactcatcac ttacttaaca tactaagaga gttattagaa cttgcaaaaa atggcttcca
                                                                       60
aggetttgat tetgttaggt etetteteag ttettetegt egteteegaa gtgtetgeeg
                                                                      120
caaggcaatc gggcatggtg aagccagaga gtgaggaaac tgtgcaacct gaaggttatg
                                                                      180
gcggtggcca cggaggacat ggtggtcacg gagggggagg aggccacgga catggaggac
                                                                      240
acaacggagg agggggccac ggacttgacg gatacggagg aggtggagga cactatggag
                                                                      300
                                                                      360
gaggtggagg acactacgga ggaggtggag gacactacgg aggaggtgga ggacactacg
                                                                      420
gaggaggtgg tggaggacac ggaggtggag gacactacgg aggtggtgga ggaggatacg
gaggtggagg aggacaccac ggaggaggag gccacgggct aaacgaacct gttcagacta
                                                                      480
agccgggtgt ttaaaactat ataatatctt cactaccatg catgattgca tatatatat
                                                                      540
tacgcttatg tattatctat atgcctataa ataaaccatg gtgagtttgt
(2) INFORMATION FOR SEQ ID NO:912:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 147 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
           (B) LOCATION: 1..147
           (D) OTHER INFORMATION: / Ceres Seq. ID 1595620
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu
                                    10
 Val Val Ser Glu Val Ser Ala Ala Arg Gln Ser Gly Met Val Lys Pro
                                 25
            2.0
 Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly Gly Gly His Gly
                                                 45
 Gly His Gly Gly His Gly Gly Gly Gly His Gly His Gly Gly His
                                             60
                         55
 Asn Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly Gly
                                         75
                     70
 His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His Tyr
                                     90
                 85
 Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Gly Gly
                                 105
                                                     110
             100
 Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr Gly Gly Gly Gly Gly
                                                 125
                             120
 His His Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys
     130
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145 (2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

Pro Gly Val

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595621
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:913: Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly 10 5 Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly 2.0 25 His Gly Gly His Asn Gly Gly Gly His Gly Leu Asp Gly Tyr Gly 40 Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly 55 Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly 75 70 Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr Gly 90 Gly Gly Gly His His Gly Gly Gly His Gly Leu Asn Glu Pro 105 100

Val Gln Thr Lys Pro Gly Val

- (2) INFORMATION FOR SEQ ID NO:914:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595622
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:
- Met Ala Val Ala Thr Glu Asp Met Val Val Thr Glu Gly Glu Glu Ala

 5 10 15

 15 Thr Asp Leu Thr Asp
- Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp 20 25 30
- Thr Glu Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu

 35

 40

 45

 45

 45
- Glu Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val 50 55 60
 Val Glu Asp Thr Glu Val Glu Asp Thr Thr Glu Val Glu Asp
- 65 70 75
 Thr Glu Val Glu Glu Asp Thr Thr Glu Glu Glu Ala Thr Gly
 85 90
- (2) INFORMATION FOR SEQ ID NO:915:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1460
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915: gtgttagctt cctttacgtg tttctttcct ttctctctcc tctgtcacgc aagaacaata 60 aatactatga tcacttgatt ttctccgacg aaattttccc cagaaacaac aacagttcga 120 gcaacaaaac cctgaactct ctgtttctgt taaactcatt cacaatttta tgagaaattg 180 gacaaaaccc tgatgtcgga ttccgtcaaa acgacggtgg atccgctttt gaaagatttg 240 gatgggaaaa aagagagttt caggcggaac gttgtgtcta tggcagctga gttaaagcaa 300 gtgagaggtc gtttggtttc tcaagaacaa ttctttgtta aagaaagctt ttgtagaaaa 360 420 gaagcagaga agaaagctaa gaacatggaa atggagatct gtaaattgca gaagaagttg gaagatagaa attgtgaact tgtagcttca acttctgctg ctgaaaagtt tctagaagaa 480 gtggacgatc tgagatcaca gctagcttta acaaaggaca ttgcagaaac aagtgctgct 540 tctgctcaat ccgcacagct tcaatgctca gtgctaacag aacaacttga cgacaaaaca 600 660 cgttctctaa gaaacacgaa gaccgtgtaa ctcatctcgg tcaccagctt gataatcttc agagagattt gaagacaaga gaatgttctc aaaaacagct gagagaggaa gttatgagaa 720 780 tcgagcgtga gataactgaa gctgttgcaa agtctgggaa aggcacagaa tgtgagctca 840 ggaaacttct tgaagaggtt tctccaaaga actttgagag aatgaacatg ttattggcgg 900 taaaagacga agagattgca aagttaaaag atgatgtgaa gttaatgtca gctcattgga 960 aactcaaaac taaggaactt gaatctcagt tggagagaca aagaagagca gatcaagagt tgaagaagaa ggtactgaaa ctagagtttt gcctgcaaga agctcgtagt cagacaagaa 1020 agctacagag ggcgggggag agacgagaca aggcaatcaa agagctaagt gatcagatta 1080 ctggaaaaca gttgaatgaa tcggtttcag gggagaaaca aaacttctgg gatacttcag 1140 1200 ggttcaagat cgttgtgtca atgtcgatgt tgatattagt tattatctcc aaaagatgag ttcttttgtc ttgaactctc tttctttttg ttggtgtgta aatgcagtag ttgcagatag 1260 tagtcagata atggtgcata ttattactcc ttgaggttta gcgaagagaa atcttgcttc 1320 cctttgttaa gttataagtt tgttcatgtg tatttgaatc atttctcaaa aagaaaatgg 1380 gaaaaatgtc attcaaataa tcagtttacc attttcgttg gttttaaaca taaattttgg 1440 acctggtgat ttaaatcctc

- (2) INFORMATION FOR SEQ ID NO:916:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..145
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595624
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

Met Ser Asp Ser Val Lys Thr Thr Val Asp Pro Leu Leu Lys Asp Leu 1 5 10 15

Asp Gly Lys Lys Glu Ser Phe Arg Arg Asn Val Val Ser Met Ala Ala 20 25 30

Glu Leu Lys Gln Val Arg Gly Arg Leu Val Ser Gln Glu Gln Phe Phe 35 40 45

Val Lys Glu Ser Phe Cys Arg Lys Glu Ala Glu Lys Lys Ala Lys Asn 50 55 60

Met Glu Met Glu Ile Cys Lys Leu Gln Lys Lys Leu Glu Asp Arg Asn 65 70 75 80
Cys Glu Leu Val Ala Ser Thr Ser Ala Ala Glu Lys Phe Leu Glu Glu

85 90 95

Val Asp Asp Leu Arg Ser Gln Leu Ala Leu Thr Lys Asp Ile Ala Glu
100 105 110

Thr Ser Ala Ala Ser Ala Gln Ser Ala Gln Leu Gln Cys Ser Val Leu
115 120 125

Thr Glu Gln Leu Asp Asp Lys Thr Arg Ser Leu Arg Asn Thr Lys Thr 130 135 140

Val

- (2) INFORMATION FOR SEQ ID NO:917:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:
- Met Arg Ile Glu Arg Glu Ile Thr Glu Ala Val Ala Lys Ser Gly Lys
 1 5 10 15
- Gly Thr Glu Cys Glu Leu Arg Lys Leu Leu Glu Glu Val Ser Pro Lys 20 25 30
- Asn Phe Glu Arg Met Asn Met Leu Leu Ala Val Lys Asp Glu Glu Ile 35 40 45
- Ala Lys Leu Lys Asp Asp Val Lys Leu Met Ser Ala His Trp Lys Leu 50 55 60
- Lys Thr Lys Glu Leu Glu Ser Gln Leu Glu Arg Gln Arg Arg Ala Asp
 65 70 75 80
- Gln Glu Leu Lys Lys Lys Val Leu Lys Leu Glu Phe Cys Leu Gln Glu 85 90 95
- Ala Arg Ser Gln Thr Arg Lys Leu Gln Arg Ala Gly Glu Arg Arg Asp 100 105 110
- Lys Ala Ile Lys Glu Leu Ser Asp Gln Ile Thr Gly Lys Gln Leu Asn 115 120 125
- Glu Ser Val Ser Gly Glu Lys Gln Asn Phe Trp Asp Thr Ser Gly Phe 130 135 140
- Lys Ile Val Val Ser Met Ser Met Leu Ile Leu Val Ile Ile Ser Lys 145 150 155 160 Arg
- (2) INFORMATION FOR SEQ ID NO:918:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595626
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:
- Met Asn Met Leu Leu Ala Val Lys Asp Glu Glu Ile Ala Lys Leu Lys
 1 5 10 15
- Asp Asp Val Lys Leu Met Ser Ala His Trp Lys Leu Lys Thr Lys Glu 20 25 30
- Leu Glu Ser Gln Leu Glu Arg Gln Arg Arg Ala Asp Gln Glu Leu Lys
- Lys Lys Val Leu Lys Leu Glu Phe Cys Leu Gln Glu Ala Arg Ser Gln 50 55 60
- Thr Arg Lys Leu Gln Arg Ala Gly Glu Arg Arg Asp Lys Ala Ile Lys 65 70 75 80
- Glu Leu Ser Asp Gln Ile Thr Gly Lys Gln Leu Asn Glu Ser Val Ser 85 90 95
- Gly Glu Lys Gln Asn Phe Trp Asp Thr Ser Gly Phe Lys Ile Val Val 100 105 110
- Ser Met Ser Met Leu Ile Leu Val Ile Ile Ser Lys Arg 115 120 125
- (2) INFORMATION FOR SEQ ID NO:919:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1440
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919: 60 attgggattt catttagata atttttttt gggtcttgat ctaagttttg ttctttctaa 120 tttggtaagg caagaagagc attaagagca ttaaaagggt tagtgaagct acaagcattg 180 gtgaggggac ataatgtgag aaagcaagct aaaatgacat taaggtgtat gcaagctctg 240 gttcgagtcc agtctcgtgt gcttgaccaa cgcaaacgct tgtctcatga cggtagtcgc aaatccgcgt tcagtgactc tcacgctgtt tttgaatctc gctatcttca agatttgtca 300 gatcgacaat ccatgtcaag agaaggaagc agcgccgcgg aagattggga tgaccgacca 360 420 cacacgatag acgcagtgaa agtgatgcta caacggagac gggacacagc attgagacat gacaagacta atttgtcaca agctttctct caaaagatgt ggaggacggt tggtaaccaa 480 tccacggaag gacaccacga ggtagaactt gaagaggaaa ggccaaaatg gcttgaccgg 540 600 tggatggcta ctagaccgtg ggataaacga gctagtagta gagcttcggt tgaccaaagg 660 gtttcagtta aaaccgttga aatcgacact tctcagcctt actcaagaac aggagcagga 720 agcccgagtc gtggccaaag acctagttcc ccatcaagaa ctagccacca ttaccaatcc cgcaataatt tctcagccac tccatctccg gctaagtcta gaccaatact tattcggtca 780 gctagtccac ggtgccagag agacccgagg gaagaccgtg accgagcagc ttatagttat 840 acatcaaaca caccaagctt gagatccaat tatagtttca cagctaggag tggatgtaca 900 960 ttagtaccac aatggttaat aatgcatcat tgttgcctaa ttacatggcg agtacagagt 1020 cagetaaage gaggateegg teteatagtg caeegaggea aeggeeetea aetheegaga 1080 gggaccgtgc ggstttAgst AcaaGAaacg rytctsgtat ccggtaccac cgccagcgga 1140 gtatgaggac aataatagct taaggagtcc aagctttaag agtgtggctg gttcacattt tggtggaatg ttagagcagc aatcgaatta ctcttcatgt tgcactgagt ctaacggtgt 1200 tgagatctct ccagcttcta ctagtgactt taggaattgg cttagatgat tggtggtgat 1260 1320 gccaaatcaa ctgtcaagat ctttcatcat cctccaggaa aagaacgttt taaaatttta 1380 tattccagaa gaaaacaaac acttttatat tgtgtcgttg aggttgattt gtgtttggaa gataagttta ttgacctatt gatctgtaac ttcataagat tttgaaacgt tagaagattc 1440
- (2) INFORMATION FOR SEQ ID NO:920:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..294
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595628
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:
- Met Thr Leu Arg Cys Met Gln Ala Leu Val Arg Val Gln Ser Arg Val 1 5 10 15
- Leu Asp Gln Arg Lys Arg Leu Ser His Asp Gly Ser Arg Lys Ser Ala 20 25 30
- Phe Ser Asp Ser His Ala Val Phe Glu Ser Arg Tyr Leu Gln Asp Leu 35 40 45
- Ser Asp Arg Gln Ser Met Ser Arg Glu Gly Ser Ser Ala Ala Glu Asp 50 55 60
- Trp Asp Asp Arg Pro His Thr Ile Asp Ala Val Lys Val Met Leu Gln 65 70 75 80
- Arg Arg Arg Asp Thr Ala Leu Arg His Asp Lys Thr Asn Leu Ser Gln 85 90 95
- Ala Phe Ser Gln Lys Met Trp Arg Thr Val Gly Asn Gln Ser Thr Glu 100 105 110

Gly His His Glu Val Glu Leu Glu Glu Glu Arg Pro Lys Trp Leu Asp 115 120 125 Arg Trp Met Ala Thr Arg Pro Trp Asp Lys Arg Ala Ser Ser Arg Ala 130 135 140 Ser Val Asp Gln Arg Val Ser Val Lys Thr Val Glu Ile Asp Thr Ser 145 150 155 160 Gln Pro Tyr Ser Arg Thr Gly Ala Gly Ser Pro Ser Arg Gly Gln Arg 165 170 175 Pro Ser Ser Pro Ser Arg Thr Ser His His Tyr Gln Ser Arg Asn Asn 180 185 190 Phe Ser Ala Thr Pro Ser Pro Ala Lys Ser Arg Pro Ile Leu Ile Arg 195 200 205 Ser Ala Ser Pro Arg Cys Gln Arg Asp Pro Arg Glu Asp Arg Asp Arg 210 215 220 Ala Ala Tyr Ser Tyr Thr Ser Asn Thr Pro Ser Leu Arg Ser Asn Tyr 225 230 235 240 Ser Phe Thr Ala Arg Ser Gly Cys Thr Leu Val Pro Gln Trp Leu Ile 245 250 255 Met His His Cys Cys Leu Ile Thr Trp Arg Val Gln Ser Gln Leu Lys 260 265 270 Arg Gly Ser Gly Leu Ile Val His Arg Gly Asn Gly Pro Gln Xaa Pro 275 280 285

Arg Gly Thr Val Arg Xaa 290

- (2) INFORMATION FOR SEQ ID NO:921:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..289
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595629
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

Met Gln Ala Leu Val Arg Val Gln Ser Arg Val Leu Asp Gln Arg Lys 1 5 10 15 Arg Leu Ser His Asp Gly Ser Arg Lys Ser Ala Phe Ser Asp Ser His 20 25 30

Ala Val Phe Glu Ser Arg Tyr Leu Gln Asp Leu Ser Asp Arg Gln Ser 35 40 45

Met Ser Arg Glu Gly Ser Ser Ala Ala Glu Asp Trp Asp Asp Arg Pro 50 55 60

His Thr Ile Asp Ala Val Lys Val Met Leu Gln Arg Arg Arg Asp Thr 65 70 75 80

Ala Leu Arg His Asp Lys Thr Asn Leu Ser Gln Ala Phe Ser Gln Lys 85 90 95 Met Trp Arg Thr Val Gly Asn Gln Ser Thr Glu Gly His His Glu Val

100 105 110

Glu Leu Glu Glu Glu Arg Pro Lys Trp Leu Asp Arg Trp Met Ala Thr

115 120 125 Arg Pro Trp Asp Lys Arg Ala Ser Ser Arg Ala Ser Val Asp Gln Arg

arg Pro Trp Asp Lys Arg Ala Ser Ser Arg Ala Ser Val Asp Gln Arg 130 135 140

Thr Gly Ala Gly Ser Pro Ser Arg Gly Gln Arg Pro Ser Ser Pro Ser 165 170 175

Arg Thr Ser His His Tyr Gln Ser Arg Asn Asn Phe Ser Ala Thr Pro
180 185 190

Ser Pro Ala Lys Ser Arg Pro Ile Leu Ile Arg Ser Ala Ser Pro Arg

200 195 Cys Gln Arg Asp Pro Arg Glu Asp Arg Asp Arg Ala Ala Tyr Ser Tyr 220 215 Thr Ser Asn Thr Pro Ser Leu Arg Ser Asn Tyr Ser Phe Thr Ala Arg 235 230 Ser Gly Cys Thr Leu Val Pro Gln Trp Leu Ile Met His His Cys Cys 245 250 Leu Ile Thr Trp Arg Val Gln Ser Gln Leu Lys Arg Gly Ser Gly Leu 260 265 Ile Val His Arg Gly Asn Gly Pro Gln Xaa Pro Arg Gly Thr Val Arg 280 285 Xaa

- (2) INFORMATION FOR SEQ ID NO:922:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..241
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:
- Met Ser Arg Glu Gly Ser Ser Ala Ala Glu Asp Trp Asp Asp Arg Pro

 1 10 15
- His Thr Ile Asp Ala Val Lys Val Met Leu Gln Arg Arg Asp Thr 20 25 30
- Ala Leu Arg His Asp Lys Thr Asn Leu Ser Gln Ala Phe Ser Gln Lys 35 40 45
- Met Trp Arg Thr Val Gly Asn Gln Ser Thr Glu Gly His His Glu Val
 50 55 60
- Glu Leu Glu Glu Glu Arg Pro Lys Trp Leu Asp Arg Trp Met Ala Thr
 65 70 75 80
- Arg Pro Trp Asp Lys Arg Ala Ser Ser Arg Ala Ser Val Asp Gln Arg 85 90 95
- 115 120 125
 Arg Thr Ser His His Tyr Gln Ser Arg Asn Asn Phe Ser Ala Thr Pro
- Arg Thr Ser His His Tyr Gln Ser Arg Asn Asn Phe Ser Ala Thr Pio
- Ser Pro Ala Lys Ser Arg Pro Ile Leu Ile Arg Ser Ala Ser Pro Arg 145 150 155 160
- Cys Gln Arg Asp Pro Arg Glu Asp Arg Asp Arg Ala Ala Tyr Ser Tyr
 165 170 175
- Thr Ser Asn Thr Pro Ser Leu Arg Ser Asn Tyr Ser Phe Thr Ala Arg
 180
 185
 190
 Ser Cly Cys Thr Leu Val Pro Gln Tro Leu Ile Met His His Cys Cys
- Ser Gly Cys Thr Leu Val Pro Gln Trp Leu Ile Met His His Cys Cys 195 200 205
- Leu Ile Thr Trp Arg Val Gln Ser Gln Leu Lys Arg Gly Ser Gly Leu 210 215 220
- Ile Val His Arg Gly Asn Gly Pro Gln Xaa Pro Arg Gly Thr Val Arg 225 230 235 240
- (2) INFORMATION FOR SEQ ID NO:923:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1481 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1481
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595678
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:923: 60 gegttacact acaactetet atetetetet ettetttet geteattttt gggtaattet 120 tctggtttta tgttcttgtt cctattactg actcacaatc agccaacgca aatctttctt 180 tgaccatttt taatagattc tcttagtcac ttgttggatt tcaaatgcaa agttgacctc 240 atcttcttct tcttcgaggt tttatacaag ttactccata aaccttcgag cttccagcaa 300 ctttggcttc tctgttgtga attattgctt attatatcct caacacgaaa tcaaaatgcc 360 aagaccaaga gtttcagagt tgtctcagag gcaagctcca aggctgaggt catcgtcatc tacttctgat tccaatcatt ccaaccgtct gatcactacg gatcaaagtt ttaagcccgg 420 480 tgttgaccgt aaatctcctc gaagcggtgg acctaacagt gatccgcttg gtcagaagaa 540 acttggggga cgaatatcgg atctagagtc gcagttagga caagcgcaag aggaactgag attgctcaag gagcagttgg ctaatgctga agctgtgaag aaacaagctc aagatgagct 600 tcataagaag tccaagaaac caaacccgct ggctcgagtg gaggaatctg caactgaggc 660 720 tgagaggatt gatagagacg aaatccctgg tgatgtgcag aaagagactg atgtgtttga ggttcccgtt gaaaagattg cagtagaaga agaagaactg agaagcggca atgacgaagc 780 840 tgagaaattg gttgcaaagg aagatgagat aaagatgctg aaagctagac tctatgacat 900 qqaqaaagag catgaatcac taggcaaaga aaacgagagc ttgaagaatc agttgagcga ttcagcttca gagatttcta atgtgaaagc taatgaagat gagatggttt caaaggtgag 960 1020 taggattggg gaagagttag aagaaagcag agcaaagacg gctcacctga aggagaagct 1080 tgagtccatg gaagaagcaa aagatgcttt agaggctgag atgaagaagc tcagggttca 1140 aaccgagcag tggaggaagg cagcggatgc tgcagcagca gttctttctg gagagtttga gatgaatggt cgggatcgat ctgggtcaac tgagaagtat tatgcaggtg ggttctttga 1200 1260 cccgtcagct gggttcatgg atccaccggg aatggctgat gattatgatg atggactggg aagtggcaag aggaagagtt ctgggatgaa gatgtttggt gagttgtgga ggaagaaagg 1320 gcaaaagtga gttacagatt gtgtggagtg tcattcaaga aatggtgtgc tcaccgtttc 1380 1440 tctcttttat tttgctgtat ttacctggaa gtttttgtaa gtgggtccgc ttcatcagaa gctaactatc aatccaaatc aattgcaaaa acaatttcat g
- (2) INFORMATION FOR SEQ ID NO: 924:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..344
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595679
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:
- Met Pro Arg Pro Arg Val Ser Glu Leu Ser Gln Arg Gln Ala Pro Arg 1 5 10 15 Leu Arg Ser Ser Ser Ser Thr Ser Asp Ser Asn His Ser Asn Arg Leu
- 20 25 30

 Ile Thr Thr Asp Gln Ser Phe Lys Pro Gly Val Asp Arg Lys Ser Pro
- The Thr Asp Gin Ser Phe Lys Pio Gly Val Asp Aig Lys Der Fio 35 40 45
- Arg Ser Gly Gly Pro Asn Ser Asp Pro Leu Gly Gln Lys Lys Leu Gly 50 55 60
 Gly Arg Ile Ser Asp Leu Glu Ser Gln Leu Gly Gln Ala Gln Glu Glu
- 65 70 75 80 Leu Arg Leu Leu Lys Glu Gln Leu Ala Asn Ala Glu Ala Val Lys Lys
- 85 90 95
 Gln Ala Gln Asp Glu Leu His Lys Lys Ser Lys Lys Pro Asn Pro Leu
 100 105 110
- Ala Arg Val Glu Glu Ser Ala Thr Glu Ala Glu Arg Ile Asp Arg Asp 115 120 125

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Glu Ile Pro Gly Asp Val Gln Lys Glu Thr Asp Val Phe Glu Val Pro
                                           140
                       135
Val Glu Lys Ile Ala Val Glu Glu Glu Leu Arg Ser Gly Asn Asp
                                       155
                   150
Glu Ala Glu Lys Leu Val Ala Lys Glu Asp Glu Ile Lys Met Leu Lys
                                   170
               165
Ala Arg Leu Tyr Asp Met Glu Lys Glu His Glu Ser Leu Gly Lys Glu
                                                   190
                               185
Asn Glu Ser Leu Lys Asn Gln Leu Ser Asp Ser Ala Ser Glu Ile Ser
                           200
Asn Val Lys Ala Asn Glu Asp Glu Met Val Ser Lys Val Ser Arg Ile
                                           220
   210
                        215
Gly Glu Glu Leu Glu Glu Ser Arg Ala Lys Thr Ala His Leu Lys Glu
                                       235
                    230
Lys Leu Glu Ser Met Glu Glu Ala Lys Asp Ala Leu Glu Ala Glu Met
                                    250
                245
Lys Lys Leu Arg Val Gln Thr Glu Gln Trp Arg Lys Ala Ala Asp Ala
                                265
            260
Ala Ala Val Leu Ser Gly Glu Phe Glu Met Asn Gly Arg Asp Arg
                                                285
                            280
Ser Gly Ser Thr Glu Lys Tyr Tyr Ala Gly Gly Phe Phe Asp Pro Ser
                                            300
                        295
Ala Gly Phe Met Asp Pro Pro Gly Met Ala Asp Asp Tyr Asp Asp Gly
                                       315
                    310
Leu Gly Ser Gly Lys Arg Lys Ser Ser Gly Met Lys Met Phe Gly Glu
                                    330
                325
Leu Trp Arg Lys Lys Gly Gln Lys
            340
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- (2) INFORMATION FOR SEQ ID NO: 925:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1068
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595695
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

atttcatage aaaacaccaa aacagagtte acagaaacat attcaaagat ttttcacaaa 60 120 tattaccatt ttaaatctat aaacaatgac gaactcggtg gctaagttgg cactactagg gttttgcatt ctgcaagtga cgagcttact tgttccgcaa gcaaatgcta gggctttcct tgtgtttgga gatteteteg ttgacaatgg taacaatgae tttettgeta eeactgeteg 300 tgccgataat tacccttatg gtatcgattt tccaactcat cgtcctacgg gccgtttctc caatggtcta aacattccag atctcgtcaa ttctctcttc ctgactacgt tgtctttgtc atttctgaat accgcaaagt cttacggaaa atgtacgatt tgggtgctcg acgtgtcctt 420 gtgactggaa caggaccaat gggttgcgtc ccggccgagc tggcgcaacg tagccgcaac 480 540 ggcgagtgtg ctaccgaact ccaacgagcc gcgtcactat tcaacccaca actaattcaa atgataacag acctcaacaa cgaagttgga tcttcggcct tcattgccgc taatactcaa 600 caaatgcaca tggacttcat tagcgaccca caagcatatg gattcgtcac gtcgaaggtg gcttgttgtg gacaagggcc gtacaatggg atagggctat gcactccatt atcaaatctt tgcccaaaca gagatctctt tgccttttgg gatccttttc acccatcaga aaaagcaagt agaatcatag ctcaacaaat cctcaatggc tctcctgaat acatgcatcc catgaatctt agcaccatcc tcaccgttga ttccatgacc taagcttcta ttcctcatct atcccaaatc cactttatgc tttgtttttg ttttgccttt ctcgtttatt atatatttt acattggtgc 960 tttaattagt ttccttgagt tatgttgtga gttttgtgtt gttcatcaat aattagtcac 1020 caattgtgag ctgagaagta atattcaaca atcttacgaa tgttcact

- (2) INFORMATION FOR SEQ ID NO: 926:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met Thr Asn Ser Val Ala Lys Leu Ala Leu Leu Gly Phe Cys Ile Leu 5 10

Gln Val Thr Ser Leu Leu Val Pro Gln Ala Asn Ala Arg Ala Phe Leu 20 25

Val Phe Gly Asp Ser Leu Val Asp Asn Gly Asn Asn Asp Phe Leu Ala 40

Thr Thr Ala Arg Ala Asp Asn Tyr Pro Tyr Gly Ile Asp Phe Pro Thr 55

His Arg Pro Thr Gly Arg Phe Ser Asn Gly Leu Asn Ile Pro Asp Leu 70 75

Val Asn Ser Leu Phe Leu Thr Thr Leu Ser Leu Ser Phe Leu Asn Thr 85 90

Ala Lys Ser Tyr Gly Lys Cys Thr Ile Trp Val Leu Asp Val Ser Leu 105 100

- (2) INFORMATION FOR SEQ ID NO:927:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595697
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Tyr Asp Leu Gly Ala Arg Arg Val Leu Val Thr Gly Thr Gly Pro 5 10

Met Gly Cys Val Pro Ala Glu Leu Ala Gln Arg Ser Arg Asn Gly Glu 20 25

Cys Ala Thr Glu Leu Gln Arg Ala Ala Ser Leu Phe Asn Pro Gln Leu 45 40

Ile Gln Met Ile Thr Asp Leu Asn Asn Glu Val Gly Ser Ser Ala Phe 60 55

Ile Ala Ala Asn Thr Gln Gln Met His Met Asp Phe Ile Ser Asp Pro 75 70

Gln Ala Tyr Gly Phe Val Thr Ser Lys Val Ala Cys Cys Gly Gln Gly 90

Pro Tyr Asn Gly Ile Gly Leu Cys Thr Pro Leu Ser Asn Leu Cys Pro 100 105 110

Asn Arg Asp Leu Phe Ala Phe Trp Asp Pro Phe His Pro Ser Glu Lys 115 120 125

Ala Ser Arg Ile Ile Ala Gln Gln Ile Leu Asn Gly Ser Pro Glu Tyr 130 135 140

Met His Pro Met Asn Leu Ser Thr Ile Leu Thr Val Asp Ser Met Thr 155 145

- (2) INFORMATION FOR SEQ ID NO: 928:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595698
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

Met Gly Cys Val Pro Ala Glu Leu Ala Gln Arg Ser Arg Asn Gly Glu
1 10 15

Cys Ala Thr Glu Leu Gln Arg Ala Ala Ser Leu Phe Asn Pro Gln Leu 20 25 30

Ile Gln Met Ile Thr Asp Leu Asn Asn Glu Val Gly Ser Ser Ala Phe

Ile Ala Ala Asn Thr Gln Gln Met His Met Asp Phe Ile Ser Asp Pro
50 55 60

Gln Ala Tyr Gly Phe Val Thr Ser Lys Val Ala Cys Cys Gly Gln Gly
65 70 75 80

Pro Tyr Asn Gly Ile Gly Leu Cys Thr Pro Leu Ser Asn Leu Cys Pro 85 90 95

Asn Arg Asp Leu Phe Ala Phe Trp Asp Pro Phe His Pro Ser Glu Lys 100 105 110

Ala Ser Arg Ile Ile Ala Gln Gln Ile Leu Asn Gly Ser Pro Glu Tyr
115 120 125

Met His Pro Met Asn Leu Ser Thr Ile Leu Thr Val Asp Ser Met Thr

- (2) INFORMATION FOR SEQ ID NO: 929:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2164 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2164
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595707
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

atcaaaaaca cgaatatcga tagtacactt ctacgtgcaa ttttctcctt tctcttcctg 60 gacatctgtc tgtttattac attttcttgt aatctttctt ttgggggattt gaaatatcta 120 tcccctaaag tttcggaaaa ttctgttttt ctgttctcat tcttcgtgat ctttttcact 180 240 ttcttctaaa aaaacatgtg tggaatactt gccgtgttag gatgttccga tgattctcag 300 gccaagagag ttcgtgttct cgagctttct cgcagattga ggcacagagg acctgactgg agtggattat atcagaacgg agataattac ttggcccatc aacgtcttgc cgtcatcgat 360 cctgcttccg gtgatcaacc tcttttcaac gaggacaaga ccattgttgt cacggtgaac 420 ggagagattt ataaccatga ggagctgaga aaacgtctga agaatcacaa gttccgtact 480 540 ggtagtgatt gtgaagtcat tgctcacttg tacgaggagt atggtgtgga ttttgttgat atgttggatg gaatcttctc ctttgtgttg ctcgacacac gagataactc cttcatggtg gctcgtgatg cgattggtgt cacttcgctc tacattggtt ggggactaga cggatctgtg 660 tggatatett cagagatgaa aggettaaac gatgattgtg agcatttega aacgttteet 720 780 ccaggtcatt tttattcaag caagttagga gggtttaagc aatggtataa tcctccttgg ttcaatgaat ctgttccttc aacgccttat gagcctcttg cgataagacg cgcctttgaa 840 aacgctgtga ttaagcggtt gatgactgat gttccatttg gagttttgct ctctggtggt 900 cttgattctt cccttgttgc ctccatcact gcacgtcact tggccggtac taaggcggct 960 aagcaatggg gtcctcagct ccattccttt tgcgttggtc ttgagggctc accggacttg 1020 1080 aaggcaggga aagaggtggc ggaatatttg gggacggtgc accacgagtt ccacttctcg gtgcaggacg ggattgatgc gattgaggat gtgatttacc atgttgagac ctatgatgtg 1140

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acgactatca gagcgagcac accgatgttc ttgatgtccc ggaaaatcaa gtctctaggg
                                                                      1200
gtcaagatgg ttctctccgg cgaaggtgcg gacgagatct ttggagggta cctctatttc
                                                                      1260
cacaaggcac ctaacaagaa agagtttcac caagaaactt gtcgcaagat caaggctctt
                                                                      1320
cacaagtatg actgtctaag agccaacaaa tctacctctg cctttggact agaggcacgt
gttcctttcc ttgacaaaga cttcatcaac acagctatgt ctctcgaccc tgaatccaag
atgatcaagc cagaggaagg aaggatcgag aaatgggttc taaggagagc ctttgacgac
gaagaacgtc cttatctacc aaaacacatt ctctacagac agaaagaaca gttcagtgat
ggtgttggct acagttggat cgatggcctg aaagatcvcg ctgctcaaaa tgtcaatgac
                                                                      1620
aagatgatgt cgaacgcggg gcatatcttc cctcacaaca ctccaaacac taaagaagct
                                                                      1680
                                                                      1740
tactactaca gaatgatctt tgaaaggttc ttcccgcaga actctgcgag actaacggtt
                                                                      1800
cctggaggtg ccaccgtggc ttgttcgact gcaaaggcag tggagtggga tgcaagctgg
                                                                      1860
tccaacaata tggatccatc aggaagagcc gctatcggag ttcacctttc ggcctacgat
                                                                      1920
ggcaagaacg tggcattgac cataccacca cttaaggcaa ttgacaacat gccgatgatg
atgggtcaag gagttgtgat tcagtcataa cttcgaagga gaaatggatg aaatatgtgt
                                                                      1980
tatatcttcc caatgggtga agtgttttgt atgattttaa taataagaat gtgatccttt
                                                                      2040
ttttttccta tgaagatctg aatgtattat ctatcttgta aaaatttgtt tctttgtaag
                                                                      2100
atttgaatgt accgctttta cgtagatcga tgtacatcaa tcttataagt ttcaattatg
                                                                      2160
tatc
```

- (2) INFORMATION FOR SEQ ID NO:930:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..584
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595708
- Lys Arg Val Arg Val Leu Glu Leu Ser Arg Arg Leu Arg His Arg Gly
 20 25 30
- Pro Asp Trp Ser Gly Leu Tyr Gln Asn Gly Asp Asn Tyr Leu Ala His
- Gln Arg Leu Ala Val Ile Asp Pro Ala Ser Gly Asp Gln Pro Leu Phe
 50 60
- Asn Glu Asp Lys Thr Ile Val Val Thr Val Asn Gly Glu Ile Tyr Asn 65 70 75 80
 His Glu Glu Leu Arg Lys Arg Leu Lys Asn His Lys Phe Arg Thr Gly
- 85 90 95

 Ser Asp Cys Glu Val Ile Ala His Leu Tyr Glu Glu Tyr Gly Val Asp
- 100 105 110 Phe Val Asp Met Leu Asp Gly Ile Phe Ser Phe Val Leu Leu Asp Thr
- 115 120 125

 Arg Asp Asn Ser Phe Met Val Ala Arg Asp Ala Ile Gly Val Thr Ser
- Leu Tyr Ile Gly Trp Gly Leu Asp Gly Ser Val Trp Ile Ser Ser Glu
 145 150 155 160
- Met Lys Gly Leu Asn Asp Asp Cys Glu His Phe Glu Thr Phe Pro Pro
- Gly His Phe Tyr Ser Ser Lys Leu Gly Gly Phe Lys Gln Trp Tyr Asn 180 185 190
- Pro Pro Trp Phe Asn Glu Ser Val Pro Ser Thr Pro Tyr Glu Pro Leu 195 200 205
- Ala Ile Arg Arg Ala Phe Glu Asn Ala Val Ile Lys Arg Leu Met Thr 210 215 220
- Asp Val Pro Phe Gly Val Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu 225 230 230 235 235 240 Val Ala Ser Ile Thr Ala Arg His Leu Ala Gly Thr Lys Ala Ala Lys

250 245 Gln Trp Gly Pro Gln Leu His Ser Phe Cys Val Gly Leu Glu Gly Ser 260 265 Pro Asp Leu Lys Ala Gly Lys Glu Val Ala Glu Tyr Leu Gly Thr Val 280 His His Glu Phe His Phe Ser Val Gln Asp Gly Ile Asp Ala Ile Glu 300 290 295 Asp Val Ile Tyr His Val Glu Thr Tyr Asp Val Thr Thr Ile Arg Ala 310 315 Ser Thr Pro Met Phe Leu Met Ser Arg Lys Ile Lys Ser Leu Gly Val 325 330 Lys Met Val Leu Ser Gly Glu Gly Ala Asp Glu Ile Phe Gly Gly Tyr 340 345 350 Leu Tyr Phe His Lys Ala Pro Asn Lys Lys Glu Phe His Gln Glu Thr 365 355 360 Cys Arg Lys Ile Lys Ala Leu His Lys Tyr Asp Cys Leu Arg Ala Asn 375 380 Lys Ser Thr Ser Ala Phe Gly Leu Glu Ala Arg Val Pro Phe Leu Asp 390 395 Lys Asp Phe Ile Asn Thr Ala Met Ser Leu Asp Pro Glu Ser Lys Met 410 405 Ile Lys Pro Glu Glu Gly Arg Ile Glu Lys Trp Val Leu Arg Arg Ala 425 430 420 Phe Asp Asp Glu Glu Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg 435 440 Gln Lys Glu Gln Phe Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly 450 455 460 Leu Lys Asp Xaa Ala Ala Gln Asn Val Asn Asp Lys Met Met Ser Asn 465 470 475 Ala Gly His Ile Phe Pro His Asn Thr Pro Asn Thr Lys Glu Ala Tyr 485 490 Tyr Tyr Arg Met Ile Phe Glu Arg Phe Phe Pro Gln Asn Ser Ala Arg 505 Leu Thr Val Pro Gly Gly Ala Thr Val Ala Cys Ser Thr Ala Lys Ala 520 525 Val Glu Trp Asp Ala Ser Trp Ser Asn Asn Met Asp Pro Ser Gly Arg 530 535 540 Ala Ala Ile Gly Val His Leu Ser Ala Tyr Asp Gly Lys Asn Val Ala 550 555 560 Leu Thr Ile Pro Pro Leu Lys Ala Ile Asp Asn Met Pro Met Met Met 565 570 Gly Gln Gly Val Val Ile Gln Ser

(2) INFORMATION FOR SEQ ID NO:931:

580

(i) SEQUENCE CHARACTERISTICS:

- - (A) LENGTH: 469 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..469
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931: Met Leu Asp Gly Ile Phe Ser Phe Val Leu Leu Asp Thr Arg Asp Asn

10 Ser Phe Met Val Ala Arg Asp Ala Ile Gly Val Thr Ser Leu Tyr Ile

25 Gly Trp Gly Leu Asp Gly Ser Val Trp Ile Ser Ser Glu Met Lys Gly

```
Leu Asn Asp Asp Cys Glu His Phe Glu Thr Phe Pro Pro Gly His Phe
                       55
Tyr Ser Ser Lys Leu Gly Gly Phe Lys Gln Trp Tyr Asn Pro Pro Trp
                                      75
                  70
Phe Asn Glu Ser Val Pro Ser Thr Pro Tyr Glu Pro Leu Ala Ile Arg
                                  90
              85
Arg Ala Phe Glu Asn Ala Val Ile Lys Arg Leu Met Thr Asp Val Pro
                              105
Phe Gly Val Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu Val Ala Ser
                          120
       115
Ile Thr Ala Arg His Leu Ala Gly Thr Lys Ala Ala Lys Gln Trp Gly
                      135
                                         140
Pro Gln Leu His Ser Phe Cys Val Gly Leu Glu Gly Ser Pro Asp Leu
                                     155
       150
Lys Ala Gly Lys Glu Val Ala Glu Tyr Leu Gly Thr Val His His Glu
                                  170
              165
Phe His Phe Ser Val Gln Asp Gly Ile Asp Ala Ile Glu Asp Val Ile
          180
                              185
Tyr His Val Glu Thr Tyr Asp Val Thr Thr Ile Arg Ala Ser Thr Pro
                          200
  195
Met Phe Leu Met Ser Arg Lys Ile Lys Ser Leu Gly Val Lys Met Val
                                          220
                      215
Leu Ser Gly Glu Gly Ala Asp Glu Ile Phe Gly Gly Tyr Leu Tyr Phe
      230
                                      235
His Lys Ala Pro Asn Lys Lys Glu Phe His Gln Glu Thr Cys Arg Lys
                                  250
              245
Ile Lys Ala Leu His Lys Tyr Asp Cys Leu Arg Ala Asn Lys Ser Thr
                              265
Ser Ala Phe Gly Leu Glu Ala Arg Val Pro Phe Leu Asp Lys Asp Phe
                                             285
                          280
Ile Asn Thr Ala Met Ser Leu Asp Pro Glu Ser Lys Met Ile Lys Pro
                                          300
                       295
Glu Glu Gly Arg Ile Glu Lys Trp Val Leu Arg Arg Ala Phe Asp Asp
                                       315
                   310
Glu Glu Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg Gln Lys Glu
                                   330
               325
Gln Phe Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly Leu Lys Asp
                               345
           340
Xaa Ala Ala Gln Asn Val Asn Asp Lys Met Met Ser Asn Ala Gly His
                360
Ile Phe Pro His Asn Thr Pro Asn Thr Lys Glu Ala Tyr Tyr Tyr Arg
                                          380
                       375
Met Ile Phe Glu Arg Phe Phe Pro Gln Asn Ser Ala Arg Leu Thr Val
                                       395
                  390
 Pro Gly Gly Ala Thr Val Ala Cys Ser Thr Ala Lys Ala Val Glu Trp
                                   410
               405
Asp Ala Ser Trp Ser Asn Asn Met Asp Pro Ser Gly Arg Ala Ala Ile
                               425
 Gly Val His Leu Ser Ala Tyr Asp Gly Lys Asn Val Ala Leu Thr Ile
                                              445
                           440
 Pro Pro Leu Lys Ala Ile Asp Asn Met Pro Met Met Gly Gln Gly
                       455
 Val Val Ile Gln Ser
 465
```

(2) INFORMATION FOR SEQ ID NO:932:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 amino acids

 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932: Met Val Ala Arg Asp Ala Ile Gly Val Thr Ser Leu Tyr Ile Gly Trp 10 Gly Leu Asp Gly Ser Val Trp Ile Ser Ser Glu Met Lys Gly Leu Asn 25 Asp Asp Cys Glu His Phe Glu Thr Phe Pro Pro Gly His Phe Tyr Ser 40 Ser Lys Leu Gly Gly Phe Lys Gln Trp Tyr Asn Pro Pro Trp Phe Asn 55 Glu Ser Val Pro Ser Thr Pro Tyr Glu Pro Leu Ala Ile Arg Arg Ala

70 75 Phe Glu Asn Ala Val Ile Lys Arg Leu Met Thr Asp Val Pro Phe Gly

85 90 Val Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu Val Ala Ser Ile Thr

105 Ala Arg His Leu Ala Gly Thr Lys Ala Ala Lys Gln Trp Gly Pro Gln

120 Leu His Ser Phe Cys Val Gly Leu Glu Gly Ser Pro Asp Leu Lys Ala 140 135

Gly Lys Glu Val Ala Glu Tyr Leu Gly Thr Val His His Glu Phe His 150 155

Phe Ser Val Gln Asp Gly Ile Asp Ala Ile Glu Asp Val Ile Tyr His 165 170 175

Val Glu Thr Tyr Asp Val Thr Thr Ile Arg Ala Ser Thr Pro Met Phe 190 180 185 Leu Met Ser Arg Lys Ile Lys Ser Leu Gly Val Lys Met Val Leu Ser

195 200 205 Gly Glu Gly Ala Asp Glu Ile Phe Gly Gly Tyr Leu Tyr Phe His Lys

215 220 Ala Pro Asn Lys Lys Glu Phe His Gln Glu Thr Cys Arg Lys Ile Lys

230 235 240 Ala Leu His Lys Tyr Asp Cys Leu Arg Ala Asn Lys Ser Thr Ser Ala 245 250

Phe Gly Leu Glu Ala Arg Val Pro Phe Leu Asp Lys Asp Phe Ile Asn 260 265

Thr Ala Met Ser Leu Asp Pro Glu Ser Lys Met Ile Lys Pro Glu Glu 275 280

Gly Arg Ile Glu Lys Trp Val Leu Arg Arg Ala Phe Asp Asp Glu Glu 290 295 300

Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg Gln Lys Glu Gln Phe 315 310

Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly Leu Lys Asp Xaa Ala 325 330

Ala Gln Asn Val Asn Asp Lys Met Met Ser Asn Ala Gly His Ile Phe 345

Pro His Asn Thr Pro Asn Thr Lys Glu Ala Tyr Tyr Tyr Arg Met Ile 365 360

Phe Glu Arg Phe Phe Pro Gln Asn Ser Ala Arg Leu Thr Val Pro Gly 380 375

Gly Ala Thr Val Ala Cys Ser Thr Ala Lys Ala Val Glu Trp Asp Ala 390 395

Ser Trp Ser Asn Asn Met Asp Pro Ser Gly Arg Ala Ala Ile Gly Val 410

His Leu Ser Ala Tyr Asp Gly Lys Asn Val Ala Leu Thr Ile Pro Pro 430 425

Leu Lys Ala Ile Asp Asn Met Pro Met Met Gly Gln Gly Val Val 440

Ile Gln Ser

450

- (2) INFORMATION FOR SEQ ID NO:933:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2217
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595725
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

60 atagagattt ggttttttga ttcttccart ctcactctct ctgtctttct ctctccatca 120 aataccaaat tatctggaag ctgagtacat cttgttttct gctcattcct ctgtttcaac aatggagagt actattgtta tgatgatgat gataacaaga tctttctttt gcttcttggg 180 atttttatgc cttctctgct cttctgttca cggattgctt tctcctaaag gtgttaactt 240 tgaagtgcaa gctttgatgg acataaaagc ttcattacat gatcctcatg gtgttcttga 300 360 taactgggat agagatgctg ttgatccttg tagttggaca atggtcactt gttcttctga 420 aaactttgtc attggcttag gcacaccaag tcagaattta tctggtacac tatctccaag 480 cattaccaac ttaacaaatc ttcggattgt gctgttgcag aacaacaaca taacagggaa 540 aattcctgct gagattggtc ggcttacgag gcttgagact cttgatcttt ctgataattt cttccacggt gaaattcctt tttcagtagg ctatctacaa agcctgcaat atctgaggct 600 taacaacaat tototototg gagtgtttoc totgtoacta totaatatga otcaacttgo 660 720 ctttcttgat ttatcataca acaatcttag tggtcctgtt ccaagatttg ctgcaaagac 780 gtttagcatc gttgggaacc cgctgatatg tccaacgggt accgaaccag actgcaatgg 840 aacaacattg atacctatgt ctatgaactt gaatcaaact ggagttcctt tatacgccgg 900 tggatcgagg aatcacaaaa tggcaatcgc tgttggatcc agcgttggga ctgtatcatt 960 aatcttcatt gctgttggtt tgtttctctg gtggagacaa agacataacc aaaacacatt ctttgatgtt aaagatggga atcatcatga ggaagtttca cttggaaacc tgaggagatt 1020 tggtttcagg gagcttcaga ttgcgaccaa taacttcagc agtaagaact tattggggaa 1080 1140 aggtggctat ggaaatgtat acaaaggaat acttggagat agtacagtga ttgcagtgaa aaggettaaa gatggaggag cattgggagg agagatteag ttteagaeag aagttgaaat 1200 1260 gatcagttta gctgttcatc gaaatctctt aagactctac ggtttctgca tcacacaaac tgagaagctt ctagtttatc cttatatgtc taatggaagc gttgcatctc gaatgaaagc 1320 aaaacctgtt cttgactgga gcataaggaa gaggatagcc ataggagctg caagagggct 1380 tgtgtatctc catgagcaat gtgatccgaa gattatccac cgcgatgtca aagcagcgaa 1440 1500 tatacttctt gatgactact gtgaagctgt ggttggcgat tttggtttag ctaaactctt ggatcatcaa gattctcatg tgacaaccgc ggttagaggc acggtgggtc acattgctcc 1560 agagtatete teaactggte aateetetga gaaaacagat gtttttgget tegggattet 1620 1680 tcttcttgag cttgtaaccg gacaaagagc ttttgagttt ggtaaagcgg ctaaccagaa aggtgtgatg cttgattggg ttaaaaagat tcatcaagag aagaaacttg agctacttgt 1740 ggataaagag ttgttgaaga agaagagcta cgatgagatt gagttagacg aaatggtaag 1800 1860 agtagctttg ttgtgcacac agtacctgcc aggacataga ccaaaaatgt ctgaagttgt tegaatgetg gaaggagatg gacttgeaga gaaatgggaa getteteaaa gateagaeag 1920 tgtttcaaaa tgtagcaaca ggataaatga attgatgtca tcttcagaca gatactctga 1980 tettacegat gactetagtt tacttgtgca agcaatggag etetetggte etagatgaaa 2040 tctatacatg aatctgaaga agaagaagaa catgcatctg tttcttgaat caagagggat 2100 tcttgttttt ttgtataata gagaggtttt ttggagggaa atgttgtgtc tctgtaactg 2160 tataggettg ttgtgtaaga agttattact geacttaggg ttaatteaaa gttettt

- (2) INFORMATION FOR SEQ ID NO:934:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 638 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..638

(D) OTHER INFORMATION: / Ceres Seq. ID 1595726 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:934: Met Glu Ser Thr Ile Val Met Met Met Ile Thr Arg Ser Phe Phe 10 Cys Phe Leu Gly Phe Leu Cys Leu Leu Cys Ser Ser Val His Gly Leu 20 25 Leu Ser Pro Lys Gly Val Asn Phe Glu Val Gln Ala Leu Met Asp Ile 40 Lys Ala Ser Leu His Asp Pro His Gly Val Leu Asp Asn Trp Asp Arg 5.5 Asp Ala Val Asp Pro Cys Ser Trp Thr Met Val Thr Cys Ser Ser Glu 70 75 Asn Phe Val Ile Gly Leu Gly Thr Pro Ser Gln Asn Leu Ser Gly Thr 90 85 Leu Ser Pro Ser Ile Thr Asn Leu Thr Asn Leu Arg Ile Val Leu Leu 100 105 110 Gln Asn Asn Ile Thr Gly Lys Ile Pro Ala Glu Ile Gly Arg Leu 120 125 Thr Arg Leu Glu Thr Leu Asp Leu Ser Asp Asn Phe Phe His Gly Glu 135 140 Ile Pro Phe Ser Val Gly Tyr Leu Gln Ser Leu Gln Tyr Leu Arg Leu 155 150 Asn Asn Asn Ser Leu Ser Gly Val Phe Pro Leu Ser Leu Ser Asn Met 165 170 Thr Gln Leu Ala Phe Leu Asp Leu Ser Tyr Asn Asn Leu Ser Gly Pro 190 185 180 Val Pro Arg Phe Ala Ala Lys Thr Phe Ser Ile Val Gly Asn Pro Leu 200 205 Ile Cys Pro Thr Gly Thr Glu Pro Asp Cys Asn Gly Thr Thr Leu Ile 220 215 Pro Met Ser Met Asn Leu Asn Gln Thr Gly Val Pro Leu Tyr Ala Gly 230 235 Gly Ser Arg Asn His Lys Met Ala Ile Ala Val Gly Ser Ser Val Gly 250 245 Thr Val Ser Leu Ile Phe Ile Ala Val Gly Leu Phe Leu Trp Trp Arg 265 260 Gln Arg His Asn Gln Asn Thr Phe Phe Asp Val Lys Asp Gly Asn His 280 His Glu Glu Val Ser Leu Gly Asn Leu Arg Arg Phe Gly Phe Arg Glu 295 300 Leu Gln Ile Ala Thr Asn Asn Phe Ser Ser Lys Asn Leu Leu Gly Lys 315 310 Gly Gly Tyr Gly Asn Val Tyr Lys Gly Ile Leu Gly Asp Ser Thr Val 330 Ile Ala Val Lys Arg Leu Lys Asp Gly Gly Ala Leu Gly Gly Glu Ile 345 350 340 Gln Phe Gln Thr Glu Val Glu Met Ile Ser Leu Ala Val His Arg Asn 365 360 Leu Leu Arg Leu Tyr Gly Phe Cys Ile Thr Gln Thr Glu Lys Leu Leu 380 375 Val Tyr Pro Tyr Met Ser Asn Gly Ser Val Ala Ser Arg Met Lys Ala 395 390 Lys Pro Val Leu Asp Trp Ser Ile Arg Lys Arg Ile Ala Ile Gly Ala 410 Ala Arg Gly Leu Val Tyr Leu His Glu Gln Cys Asp Pro Lys Ile Ile 425 420 His Arg Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Asp Tyr Cys Glu 445 440 Ala Val Val Gly Asp Phe Gly Leu Ala Lys Leu Leu Asp His Gln Asp 460 455 Ser His Val Thr Thr Ala Val Arg Gly Thr Val Gly His Ile Ala Pro

475 470 465 Glu Tyr Leu Ser Thr Gly Gln Ser Ser Glu Lys Thr Asp Val Phe Gly 490 485 Phe Gly Ile Leu Leu Glu Leu Val Thr Gly Gln Arg Ala Phe Glu 505 Phe Gly Lys Ala Ala Asn Gln Lys Gly Val Met Leu Asp Trp Val Lys 520 Lys Ile His Gln Glu Lys Lys Leu Glu Leu Leu Val Asp Lys Glu Leu 540 535 Leu Lys Lys Lys Ser Tyr Asp Glu Ile Glu Leu Asp Glu Met Val Arg 550 555 Val Ala Leu Leu Cys Thr Gln Tyr Leu Pro Gly His Arg Pro Lys Met 565 570 Ser Glu Val Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp 580 585 Glu Ala Ser Gln Arg Ser Asp Ser Val Ser Lys Cys Ser Asn Arg Ile 605 600 Asn Glu Leu Met Ser Ser Ser Asp Arg Tyr Ser Asp Leu Thr Asp Asp 620 615 Ser Ser Leu Leu Val Gln Ala Met Glu Leu Ser Gly Pro Arg 630

- (2) INFORMATION FOR SEQ ID NO:935:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 632 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..632
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595727
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

Met Met Met Ile Thr Arg Ser Phe Phe Cys Phe Leu Gly Phe Leu 10 5 Cys Leu Leu Cys Ser Ser Val His Gly Leu Leu Ser Pro Lys Gly Val

25 20 Asn Phe Glu Val Gln Ala Leu Met Asp Ile Lys Ala Ser Leu His Asp

40 Pro His Gly Val Leu Asp Asn Trp Asp Arg Asp Ala Val Asp Pro Cys

55 Ser Trp Thr Met Val Thr Cys Ser Ser Glu Asn Phe Val Ile Gly Leu

75 70 Gly Thr Pro Ser Gln Asn Leu Ser Gly Thr Leu Ser Pro Ser Ile Thr

90 Asn Leu Thr Asn Leu Arg Ile Val Leu Leu Gln Asn Asn Asn Ile Thr

105 110 Gly Lys Ile Pro Ala Glu Ile Gly Arg Leu Thr Arg Leu Glu Thr Leu 125 120

Asp Leu Ser Asp Asn Phe Phe His Gly Glu Ile Pro Phe Ser Val Gly 140 135

Tyr Leu Gln Ser Leu Gln Tyr Leu Arg Leu Asn Asn Asn Ser Leu Ser 150 155

Gly Val Phe Pro Leu Ser Leu Ser Asn Met Thr Gln Leu Ala Phe Leu 170 165

Asp Leu Ser Tyr Asn Asn Leu Ser Gly Pro Val Pro Arg Phe Ala Ala 190 185

Lys Thr Phe Ser Ile Val Gly Asn Pro Leu Ile Cys Pro Thr Gly Thr 195 200 205

Glu Pro Asp Cys Asn Gly Thr Thr Leu Ile Pro Met Ser Met Asn Leu 220 215

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Asn Gln Thr Gly Val Pro Leu Tyr Ala Gly Gly Ser Arg Asn His Lys
                230
                                 235
Met Ala Ile Ala Val Gly Ser Ser Val Gly Thr Val Ser Leu Ile Phe
                    250
           245
Ile Ala Val Gly Leu Phe Leu Trp Trp Arg Gln Arg His Asn Gln Asn
                          265
          260
Thr Phe Phe Asp Val Lys Asp Gly Asn His His Glu Glu Val Ser Leu
                       280
Gly Asn Leu Arg Arg Phe Gly Phe Arg Glu Leu Gln Ile Ala Thr Asn
                 295
                                    300
Asn Phe Ser Ser Lys Asn Leu Leu Gly Lys Gly Gly Tyr Gly Asn Val
                                 315
               310
Tyr Lys Gly Ile Leu Gly Asp Ser Thr Val Ile Ala Val Lys Arg Leu
                           330
             325
Lys Asp Gly Gly Ala Leu Gly Gly Glu Ile Gln Phe Gln Thr Glu Val
                          345
          340
Glu Met Ile Ser Leu Ala Val His Arg Asn Leu Leu Arg Leu Tyr Gly
                       360
Phe Cys Ile Thr Gln Thr Glu Lys Leu Leu Val Tyr Pro Tyr Met Ser
                            380
                    375
Asn Gly Ser Val Ala Ser Arg Met Lys Ala Lys Pro Val Leu Asp Trp
                        395
    390
Ser Ile Arg Lys Arg Ile Ala Ile Gly Ala Ala Arg Gly Leu Val Tyr
                              410
             405
Leu His Glu Gln Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala
       420
                          425
Ala Asn Ile Leu Leu Asp Asp Tyr Cys Glu Ala Val Val Gly Asp Phe
                                        445
 435 440
Gly Leu Ala Lys Leu Leu Asp His Gln Asp Ser His Val Thr Thr Ala
                            460
                    455
Val Arg Gly Thr Val Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly
                               475
                470
Gln Ser Ser Glu Lys Thr Asp Val Phe Gly Phe Gly Ile Leu Leu
             485 490 495
Glu Leu Val Thr Gly Gln Arg Ala Phe Glu Phe Gly Lys Ala Ala Asn
   500
                           505
Gln Lys Gly Val Met Leu Asp Trp Val Lys Lys Ile His Gln Glu Lys
      515 520
                                        525
Lys Leu Glu Leu Leu Val Asp Lys Glu Leu Leu Lys Lys Ser Tyr
   530 535 540
Asp Glu Ile Glu Leu Asp Glu Met Val Arg Val Ala Leu Leu Cys Thr
     550
                                 555
Gln Tyr Leu Pro Gly His Arg Pro Lys Met Ser Glu Val Val Arg Met
                               570
             565
Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Glu Ala Ser Gln Arg Ser
          580 585
Asp Ser Val Ser Lys Cys Ser Asn Arg Ile Asn Glu Leu Met Ser Ser
           600 605
 Ser Asp Arg Tyr Ser Asp Leu Thr Asp Asp Ser Ser Leu Leu Val Gln
                   615
 Ala Met Glu Leu Ser Gly Pro Arg
                 630
 (2) INFORMATION FOR SEQ ID NO:936:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 631 amino acids
         (B) TYPE: amino acid
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- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..631

(D) OTHER INFORMATION: / Ceres Seq. ID 1595728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936: Met Met Met Ile Thr Arg Ser Phe Phe Cys Phe Leu Gly Phe Leu Cys 10 Leu Leu Cys Ser Ser Val His Gly Leu Leu Ser Pro Lys Gly Val Asn 25 Phe Glu Val Gln Ala Leu Met Asp Ile Lys Ala Ser Leu His Asp Pro 40 His Gly Val Leu Asp Asn Trp Asp Arg Asp Ala Val Asp Pro Cys Ser 55 Trp Thr Met Val Thr Cys Ser Ser Glu Asn Phe Val Ile Gly Leu Gly 75 70 Thr Pro Ser Gln Asn Leu Ser Gly Thr Leu Ser Pro Ser Ile Thr Asn 90 Leu Thr Asn Leu Arg Ile Val Leu Leu Gln Asn Asn Ile Thr Gly 105 Lys Ile Pro Ala Glu Ile Gly Arg Leu Thr Arg Leu Glu Thr Leu Asp 120 125 Leu Ser Asp Asn Phe Phe His Gly Glu Ile Pro Phe Ser Val Gly Tyr 135 140 Leu Gln Ser Leu Gln Tyr Leu Arg Leu Asn Asn Asn Ser Leu Ser Gly 145 150 155 Val Phe Pro Leu Ser Leu Ser Asn Met Thr Gln Leu Ala Phe Leu Asp 165 170 175 Leu Ser Tyr Asn Asn Leu Ser Gly Pro Val Pro Arg Phe Ala Ala Lys 180 185 Thr Phe Ser Ile Val Gly Asn Pro Leu Ile Cys Pro Thr Gly Thr Glu 195 200 205 Pro Asp Cys Asn Gly Thr Thr Leu Ile Pro Met Ser Met Asn Leu Asn 220 215 Gln Thr Gly Val Pro Leu Tyr Ala Gly Gly Ser Arg Asn His Lys Met 230 235 Ala Ile Ala Val Gly Ser Ser Val Gly Thr Val Ser Leu Ile Phe Ile 250 255 245 Ala Val Gly Leu Phe Leu Trp Trp Arg Gln Arg His Asn Gln Asn Thr 260 265 270 Phe Phe Asp Val Lys Asp Gly Asn His His Glu Glu Val Ser Leu Gly 280 285 Asn Leu Arg Arg Phe Gly Phe Arg Glu Leu Gln Ile Ala Thr Asn Asn 290 295 300 Phe Ser Ser Lys Asn Leu Leu Gly Lys Gly Gly Tyr Gly Asn Val Tyr 310 315 Lys Gly Ile Leu Gly Asp Ser Thr Val Ile Ala Val Lys Arg Leu Lys 330 325 Asp Gly Gly Ala Leu Gly Gly Glu Ile Gln Phe Gln Thr Glu Val Glu 340 345 Met Ile Ser Leu Ala Val His Arg Asn Leu Leu Arg Leu Tyr Gly Phe 360 Cys Ile Thr Gln Thr Glu Lys Leu Leu Val Tyr Pro Tyr Met Ser Asn 375 Gly Ser Val Ala Ser Arg Met Lys Ala Lys Pro Val Leu Asp Trp Ser 395 390 Ile Arg Lys Arg Ile Ala Ile Gly Ala Ala Arg Gly Leu Val Tyr Leu 410 405 His Glu Gln Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala Ala 425 Asn Ile Leu Leu Asp Asp Tyr Cys Glu Ala Val Val Gly Asp Phe Gly 440 445 Leu Ala Lys Leu Leu Asp His Gln Asp Ser His Val Thr Thr Ala Val 455

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Arg Gly Thr Val Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly Gln
                                      475
                   470
Ser Ser Glu Lys Thr Asp Val Phe Gly Phe Gly Ile Leu Leu Glu
                                 490
               485
Leu Val Thr Gly Gln Arg Ala Phe Glu Phe Gly Lys Ala Ala Asn Gln
                              505
           500
Lys Gly Val Met Leu Asp Trp Val Lys Lys Ile His Gln Glu Lys Lys
                                             525
                          520
       515
Leu Glu Leu Leu Val Asp Lys Glu Leu Leu Lys Lys Ser Tyr Asp
                                         540
                      535
Glu Ile Glu Leu Asp Glu Met Val Arg Val Ala Leu Leu Cys Thr Gln
                   550
                                     555
Tyr Leu Pro Gly His Arg Pro Lys Met Ser Glu Val Val Arg Met Leu
                                 570
               565
Glu Gly Asp Gly Leu Ala Glu Lys Trp Glu Ala Ser Gln Arg Ser Asp
                                                 590
                             585
           580
Ser Val Ser Lys Cys Ser Asn Arg Ile Asn Glu Leu Met Ser Ser Ser
                         600
                                            605
Asp Arg Tyr Ser Asp Leu Thr Asp Asp Ser Ser Leu Leu Val Gln Ala
                       615
                                          620
Met Glu Leu Ser Gly Pro Arg
                   630
```

- (2) INFORMATION FOR SEQ ID NO:937:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1755
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595741
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

atctcacaca ccgaaagtta ttttcgaatc cactaacgaa tcttccacag caaaaaactt 60 tcgtgttcct ctgtaatttc tcagtatata tagataccaa atcgagcagt gaaaaaatgg 120 ctatggcgag tttatatcgg cgatctcttc cttctcctcc ggccattgac ttttcttccg 180 240 ccqaaqgcaa gctaatcttc aatgaagege ttcagaaagg aactatggaa ggattttca 300 ggttgatttc gtattttcag acacaatccg aacctgcgta ttgtggtttg gctagtctct 360 cagtggtgtt gaatgctctt tctatcgatc ctggacgtaa atggaaaggg ccttggaggt ggtttgatga atcaatgttg gattgctgcg aacctctgga agtagtgaag gaaaaaggca 420 480 tttcatttgg aaaagttgtc tgtttggctc attgttcagg agcaaaagtt gaggctttcc gtacaagtca gagcaccatt gatgatttcc gcaaatttgt cgtgaaatgc acgagttctg 540 agaattgcca tatgatctca acatatcaca gaggtgtatt taagcagact gggactggtc 600 acttttcacc tattggtggc tataatgctg agagagatat ggctttgatt cttgatgttg 660 ctcqtttcaa gtatcccct cactgggttc ctcttaaact tctttgggaa gccatggaca 720 gtattgatca gtcaacaggg aaacgtagag ggttcatgct catatctaga ccacacagag 780 aacccggatt gctctatact ctgagctgca aggatgaaag ctggatcgaa atagccaagt 840 atttgaagga agatgttcct cgtcttgtaa gttcacagca tgtagattct gtggagaaaa 900 tcatatcagt tgtgttcaag tcacttccat caaatttcaa ccaattcatc agatgggtgg 960 ctgagatccg aattacagag gactcaaacc aaaatctcag cgcagaggag aagtctaggc 1020 tgaaactaaa gcaattggtg ctgaaggaag tgcacgaaac tgaactgttc aaacacatca 1080 ataagttott atocacagtg ggttatgaag acagtotgac ttatgctgct gcaaaggott 1140 gttgccaagg agctgaaatc ttatccggaa gctcatcaaa agagttttgt tgtcgggaaa 1200 cttgcgtgaa atgcatcaaa ggtcctgatg actctgaagg cacagtggtg actggagttg 1260 tggtgcgtga tgggaatgaa caaaaggttg atctgttagt gccatcgacg caaactgagt 1320 gtgaatgtgg tcctgaagca acttatccag caggaaacga tgtgttcact gcacttctat 1380 tggctttacc tccacagaca tggtcaggga tcaaagacca agctcttatg catgaaatga 1440 agcageteat ttecatgget teecteecaa etttgettea agaagaggta ttgeatette 1500 gacggcaact tcagctgcta aaacgatgcc aagagaacaa ggaagaggat gatctcgctg 1560 ctcctgccta ttagttcatt gtcccaaatc cactctcttc cccatttgaa tcccacgttc 1620 tcaacacttg attgttagaa agtctcttta ttgtctgtac gattcaaact ctatttgcaa tgagagatat ttgtaaacat attcattcta tgaattgtta atcacaataa gtaaagaatc 1740 ttagaatcat atttc

- (2) INFORMATION FOR SEQ ID NO:938:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 523 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..523
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595742
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:938: Leu Thr His Arg Lys Leu Phe Ser Asn Pro Leu Thr Asn Leu Pro Gln 5 10 Gln Lys Thr Phe Val Phe Leu Cys Asn Phe Ser Val Tyr Ile Asp Thr 25 Lys Ser Ser Ser Glu Lys Met Ala Met Ala Ser Leu Tyr Arg Arg Ser 40 Leu Pro Ser Pro Pro Ala Ile Asp Phe Ser Ser Ala Glu Gly Lys Leu 55 Ile Phe Asn Glu Ala Leu Gln Lys Gly Thr Met Glu Gly Phe Phe Arg 75 70 Leu Ile Ser Tyr Phe Gln Thr Gln Ser Glu Pro Ala Tyr Cys Gly Leu 90 8.5 Ala Ser Leu Ser Val Val Leu Asn Ala Leu Ser Ile Asp Pro Gly Arg 105 100 Lys Trp Lys Gly Pro Trp Arg Trp Phe Asp Glu Ser Met Leu Asp Cys 120 125 Cys Glu Pro Leu Glu Val Val Lys Glu Lys Gly Ile Ser Phe Gly Lys 135 140 Val Val Cys Leu Ala His Cys Ser Gly Ala Lys Val Glu Ala Phe Arg 155 150 Thr Ser Gln Ser Thr Ile Asp Asp Phe Arg Lys Phe Val Val Lys Cys 170 165 Thr Ser Ser Glu Asn Cys His Met Ile Ser Thr Tyr His Arg Gly Val 185 180 Phe Lys Gln Thr Gly Thr Gly His Phe Ser Pro Ile Gly Gly Tyr Asn 200 Ala Glu Arg Asp Met Ala Leu Ile Leu Asp Val Ala Arg Phe Lys Tyr 220 215 Pro Pro His Trp Val Pro Leu Lys Leu Leu Trp Glu Ala Met Asp Ser 235 230 Ile Asp Gln Ser Thr Gly Lys Arg Arg Gly Phe Met Leu Ile Ser Arg 250 Pro His Arg Glu Pro Gly Leu Leu Tyr Thr Leu Ser Cys Lys Asp Glu 265 Ser Trp Ile Glu Ile Ala Lys Tyr Leu Lys Glu Asp Val Pro Arg Leu 280 285 Val Ser Ser Gln His Val Asp Ser Val Glu Lys Ile Ile Ser Val Val 300 295 Phe Lys Ser Leu Pro Ser Asn Phe Asn Gln Phe Ile Arg Trp Val Ala 315 310 Glu Ile Arg Ile Thr Glu Asp Ser Asn Gln Asn Leu Ser Ala Glu Glu 330 Lys Ser Arg Leu Lys Leu Lys Gln Leu Val Leu Lys Glu Val His Glu 350 345 Thr Glu Leu Phe Lys His Ile Asn Lys Phe Leu Ser Thr Val Gly Tyr 360

Glu Asp Ser Leu Thr Tyr Ala Ala Ala Lys Ala Cys Cys Gln Gly Ala 375 Glu Ile Leu Ser Gly Ser Ser Ser Lys Glu Phe Cys Cys Arg Glu Thr 395 390 Cys Val Lys Cys Ile Lys Gly Pro Asp Asp Ser Glu Gly Thr Val Val 410 405 Thr Gly Val Val Val Arg Asp Gly Asn Glu Gln Lys Val Asp Leu Leu 425 Val Pro Ser Thr Gln Thr Glu Cys Glu Cys Gly Pro Glu Ala Thr Tyr 440 Pro Ala Gly Asn Asp Val Phe Thr Ala Leu Leu Leu Ala Leu Pro Pro 460 455 Gln Thr Trp Ser Gly Ile Lys Asp Gln Ala Leu Met His Glu Met Lys 475 470 Gln Leu Ile Ser Met Ala Ser Leu Pro Thr Leu Leu Gln Glu Glu Val 485 490 495 Leu His Leu Arg Arg Gln Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn 505

Lys Glu Glu Asp Asp Leu Ala Ala Pro Ala Tyr 520 515

- (2) INFORMATION FOR SEQ ID NO:939:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595743
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:939: Met Ala Met Ala Ser Leu Tyr Arg Arg Ser Leu Pro Ser Pro Pro Ala 10 5 Ile Asp Phe Ser Ser Ala Glu Gly Lys Leu Ile Phe Asn Glu Ala Leu 25 20 Gln Lys Gly Thr Met Glu Gly Phe Phe Arg Leu Ile Ser Tyr Phe Gln 45 40 Thr Gln Ser Glu Pro Ala Tyr Cys Gly Leu Ala Ser Leu Ser Val Val 55 Leu Asn Ala Leu Ser Ile Asp Pro Gly Arg Lys Trp Lys Gly Pro Trp 75 70 Arg Trp Phe Asp Glu Ser Met Leu Asp Cys Cys Glu Pro Leu Glu Val 85 Val Lys Glu Lys Gly Ile Ser Phe Gly Lys Val Val Cys Leu Ala His 105 100 Cys Ser Gly Ala Lys Val Glu Ala Phe Arg Thr Ser Gln Ser Thr Ile 120 Asp Asp Phe Arg Lys Phe Val Val Lys Cys Thr Ser Ser Glu Asn Cys 140 135 His Met Ile Ser Thr Tyr His Arg Gly Val Phe Lys Gln Thr Gly Thr 155 150 Gly His Phe Ser Pro Ile Gly Gly Tyr Asn Ala Glu Arg Asp Met Ala 170 165

Leu Ile Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp Val Pro 185

Leu Lys Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser Thr Gly

Lys Arg Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu Pro Gly

Leu Leu Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu Ile Ala

215 220

195 200

235 230 225 Lys Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val 245 250 255 Asp Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser 265 270 260 Asn Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu 280 285 Asp Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu 295 Lys Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His 315 320 305 310 Ile Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr 330 335 325 Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser 345 Ser Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys 360 Gly Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Arg 380 375 Asp Gly Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr Gln Thr 395 390 Glu Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val 405 410 415 Phe Thr Ala Leu Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser Gly Ile 420 425 Lys Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala 435 440 445 Ser Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln 450 455 460 Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu 475 465 470 Ala Ala Pro Ala Tyr 485

- (2) INFORMATION FOR SEQ ID NO:940:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..483
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595744
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

Met Ala Ser Leu Tyr Arg Arg Ser Leu Pro Ser Pro Pro Ala Ile Asp

1 5 10 15

Phe Ser Ser Ala Glu Gly Lys Leu Ile Phe Asn Glu Ala Leu Gln Lys 20 25 30

Gly Thr Met Glu Gly Phe Phe Arg Leu Ile Ser Tyr Phe Gln Thr Gln 35 40 45

Ser Glu Pro Ala Tyr Cys Gly Leu Ala Ser Leu Ser Val Val Leu Asn 50 55 60

Ala Leu Ser Ile Asp Pro Gly Arg Lys Trp Lys Gly Pro Trp Arg Trp 65 70 75 80

Phe Asp Glu Ser Met Leu Asp Cys Cys Glu Pro Leu Glu Val Val Lys
85 90 95

Glu Lys Gly Ile Ser Phe Gly Lys Val Val Cys Leu Ala His Cys Ser

Gly Ala Lys Val Glu Ala Phe Arg Thr Ser Gln Ser Thr Ile Asp Asp

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Phe Arg Lys Phe Val Val Lys Cys Thr Ser Ser Glu Asn Cys His Met
                                   140
                  135
Ile Ser Thr Tyr His Arg Gly Val Phe Lys Gln Thr Gly Thr Gly His
            150
                               155
Phe Ser Pro Ile Gly Gly Tyr Asn Ala Glu Arg Asp Met Ala Leu Ile
                            170 175
            165
Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp Val Pro Leu Lys
                         185
Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser Thr Gly Lys Arg
     195
                      200
Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu Pro Gly Leu Leu
                                   220
                 215
Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu Ile Ala Lys Tyr
                               235
             230
Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val Asp Ser
                   250
            245
Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser Asn Phe
                       265
Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu Asp Ser
                              285
                      280
Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu Lys Gln
                  295
                                   300
Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His Ile Asn
                               315
             310
Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr Ala Ala
                             330
            325
Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser Ser Ser
         340
                          345
Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys Gly Pro
                                      365
 355 360
Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Arg Asp Gly
 370 375
                                380
Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr Gln Thr Glu Cys
    390
                                395
Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val Phe Thr
                            410
             405
Ala Leu Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser Gly Ile Lys Asp
    420 425
Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala Ser Leu
      435 440 445
Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln Leu Gln
   450 455 460
Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu Ala Ala
               470 475
Pro Ala Tyr
```

- (2) INFORMATION FOR SEQ ID NO:941:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1195
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595748
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941: caaaaattc tctaaaaact caagaacttc atcatcttct tctcagaccc gtgtgagtga gtgaaagatt cgatttttc tcatctaaag atctttgtgt ttgctttaat ggagtgtatt gggaagagag tgaagtcccg gagctggcag cgtcttcagg ctgttaacaa gcggaagaag

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atggagactg tagctccggt gacatctccc ccaaagaaac gacggcagaa gaaacctaaa
                                                                      240
aactatgact ccgacattga ggacatcaca ccaacttgca acgacagtgt tcctcctcct
                                                                      300
caagtcagta acatgtactc tgtacctaac aactctgtaa aagagagttt ttctaggata
                                                                      360
atgagagatc tgaatgtgga gaagaaatca ggtcccagct cctctaggtt aacagatggg
                                                                      420
tctgagcaga acccatgtct gaaagagagg tcttttaggg ttagtgattt gggcgtggag
                                                                       480
                                                                      540
aagaaatgtt cccctgagat tacagatttg gatgttggga tacCtgttcc gagattttTT
ctaagttaaa ggatgtgtct gaacagaaga acacatgtct gatgcagaag agttctcctg
                                                                       600
agattgctga tttggatctt gtaatatcag ttccgagctc ttctgtgtta aaagatgtgt
                                                                       660
                                                                      720
cagaagaaat cagatttttg aaggacaagt gttcccctga gattagaggt ttggttttgg
                                                                      780
aaaaatcagt ccctgacgaa atagagattc tttcagattc tgagtctgaa actgaagcta
gaagaagagc ttcagccaag aagaagctat ttgaagaaag tagcagaatt gtagagtcta
                                                                       840
                                                                       900
tcagtgatgg tgaagatagc tcaagtgaaa ccgatgaaga ggaagaagaa aatcaagata
gtgaagataa taacaccaaa gataatgtaa cggtggagtc tttgtcttct gaggatccat
                                                                      960
cttcatcatc atcatcgtcg tcttcatctt cctcttcctc ctcgagtgac gatgaatcat
                                                                     1020
atgtaaagga ggtagttgga gataatagag atgatgatga cttgagaaag gccagttcac
                                                                     1080
caatcaagag agtctcttta gtggaaagga aggctttggt aaggtataag aggtctggtt
                                                                     1140
ctagcttaac caagcctaga gaaagagaca acaagattca gaaactaaac caccg
```

- (2) INFORMATION FOR SEQ ID NO:942:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942: Met Glu Cys Ile Gly Lys Arg Val Lys Ser Arg Ser Trp Gln Arg Leu

1 5 10 15
Gln Ala Val Asn Lys Arg Lys Lys Met Glu Thr Val Ala Pro Val Thr

20 25 30
Ser Pro Pro Lys Lys Arg Arg Gln Lys Lys Pro Lys Asn Tyr Asp Ser
35 40 45

Asp Ile Glu Asp Ile Thr Pro Thr Cys Asn Asp Ser Val Pro Pro 50 55 60

Gln Val Ser Asn Met Tyr Ser Val Pro Asn Asn Ser Val Lys Glu Ser 65 70 75 80

Phe Ser Arg Ile Met Arg Asp Leu Asn Val Glu Lys Lys Ser Gly Pro 85 90 95

Ser Ser Ser Arg Leu Thr Asp Gly Ser Glu Gln Asn Pro Cys Leu Lys
100 105 110

Glu Arg Ser Phe Arg Val Ser Asp Leu Gly Val Glu Lys Lys Cys Ser 115 120 125

Pro Glu Ile Thr Asp Leu Asp Val Gly Ile Pro Val Pro Arg Phe Phe 130 135 140

Leu Ser

- (2) INFORMATION FOR SEQ ID NO:943:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595750
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

```
Met Glu Thr Val Ala Pro Val Thr Ser Pro Pro Lys Lys Arg Arg Gln
                                   10
Lys Lys Pro Lys Asn Tyr Asp Ser Asp Ile Glu Asp Ile Thr Pro Thr
                               25
Cys Asn Asp Ser Val Pro Pro Pro Gln Val Ser Asn Met Tyr Ser Val
                           40
Pro Asn Asn Ser Val Lys Glu Ser Phe Ser Arg Ile Met Arg Asp Leu
                       55
Asn Val Glu Lys Lys Ser Gly Pro Ser Ser Ser Arg Leu Thr Asp Gly
                                       75
                   70
Ser Glu Gln Asn Pro Cys Leu Lys Glu Arg Ser Phe Arg Val Ser Asp
               85
                                  90
Leu Gly Val Glu Lys Lys Cys Ser Pro Glu Ile Thr Asp Leu Asp Val
          100
                           105
Gly Ile Pro Val Pro Arg Phe Phe Leu Ser
                           120
       115
```

- (2) INFORMATION FOR SEQ ID NO:944:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..204
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595751 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:
- Met Gln Lys Ser Ser Pro Glu Ile Ala Asp Leu Asp Leu Val Ile Ser 1 5 10 15 Val Pro Ser Ser Val Leu Lys Asp Val Ser Glu Glu Ile Arg Phe

20 25 30
Leu Lys Asp Lys Cys Ser Pro Glu Ile Arg Gly Leu Val Leu Glu Lys

35 40 45

Ser Val Pro Asp Glu Ile Glu Ile Leu Ser Asp Ser Glu Ser Glu Thr
50 55 60

Glu Ala Arg Arg Arg Ala Ser Ala Lys Lys Leu Phe Glu Glu Ser

Ser Arg Ile Val Glu Ser Ile Ser Asp Gly Glu Asp Ser Ser Ser Glu 85 90 95

Thr Asp Glu Glu Glu Glu Glu Asp Gln Asp Ser Glu Asp Asn Asn Thr
100 105 110

Lys Asp Asn Val Thr Val Glu Ser Leu Ser Ser Glu Asp Pro Ser Ser 115

165 170 175

Lys Ala Leu Val Arg Tyr Lys Arg Ser Gly Ser Ser Leu Thr Lys Pro

185
Arg Glu Arg Asp Asn Lys Ile Gln Lys Leu Asn His
200

- (2) INFORMATION FOR SEQ ID NO:945:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1071 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1071
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595760
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945: gttcttttcc acagcattgc aacatgaaga gacattcttg ttgttacaaa caaaagctga 60 120 gaaaaggtct ttggtctcct gaagaagatg agaaacttct caattacatt accaaacatg 180 gccatggttg ctggagttct gtccctaaac tcgggtctcg agagatgtgg aaagagctgt 240 agactcagat ggatcaatta cttaagacct gatttaaaga gaggagettt ctcttcagag 300 gaacagaatc tcattgtcga gcttcatgct gttcttggaa acagatggtc gcaaattgct 360 gcgaggcttc ccgggagaac cgacaacgag ataaagaact tgtggaattc gtgcattaag aagaagctga tgaagaaagg cattgaccct attacacata aacccctctc cgaggttggt 420 480 aaagaaacaa acagaagcga caataacaat tccacaagtt tttcctcaga aactaatcaa 540 gacttgtttg tcaagaaaac gtctgatttt gccgagtatt ctgcgtttca gaaagaagaa 600 tocaactotg tttcactcag aaattcgctc tcttccatga tcccaacgca attcaacatc 660 gacgatggtt ctgtctcaaa tgcgggtttt gatacacaag tatgcgtgaa accctcgatt attettette etectecaaa caacaettea ageaetgtet etggacagga teatgtaaae 720 gtgtcagagc ctaattggga atcaaacagt ggaaccacaa gccacctcaa caatcccggt 780 840 atggaagaaa tgaaatggtc cgaggagtac ctaaacgaat cgttattctc tacccaagtt tacgtgaaat cagagacgga tttcaactcc aacattgcct ttccttggag ccaaagccaa 900 960 gcttgtgacg tattccccaa ggatcttcag agaatggcct tctcttttgg tggtcagacc ctttagtttc tttttcttat cagatttaga catattgata cgtgtaatga atggatcaaa 1020 tgttctattt ggccatacgt taaaaaaata aaaaagcaca atcctttcct c
- (2) INFORMATION FOR SEQ ID NO:946:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..292
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595761
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946: Met Arg Asn Phe Ser Ile Thr Leu Pro Asn Met Ala Met Val Ala Gly 10 Val Leu Ser Leu Asn Ser Gly Leu Glu Arg Cys Gly Lys Ser Cys Arg 25 Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe 40 Ser Ser Glu Glu Gln Asn Leu Ile Val Glu Leu His Ala Val Leu Gly 55 Asn Arg Trp Ser Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn 75 70 Glu Ile Lys Asn Leu Trp Asn Ser Cys Ile Lys Lys Lys Leu Met Lys 90 85 Lys Gly Ile Asp Pro Ile Thr His Lys Pro Leu Ser Glu Val Gly Lys 105 Glu Thr Asn Arg Ser Asp Asn Asn Asn Ser Thr Ser Phe Ser Ser Glu 120 Thr Asn Gln Asp Leu Phe Val Lys Lys Thr Ser Asp Phe Ala Glu Tyr 135 140 Ser Ala Phe Gln Lys Glu Glu Ser Asn Ser Val Ser Leu Arg Asn Ser 155 150 Leu Ser Ser Met Ile Pro Thr Gln Phe Asn Ile Asp Asp Gly Ser Val 170 165 Ser Asn Ala Gly Phe Asp Thr Gln Val Cys Val Lys Pro Ser Ile Ile 185 Leu Leu Pro Pro Pro Asn Asn Thr Ser Ser Thr Val Ser Gly Gln Asp

```
His Val Asn Val Ser Glu Pro Asn Trp Glu Ser Asn Ser Gly Thr Thr
                     215
Ser His Leu Asn Asn Pro Gly Met Glu Glu Met Lys Trp Ser Glu Glu
                                    235
        230
```

Tyr Leu Asn Glu Ser Leu Phe Ser Thr Gln Val Tyr Val Lys Ser Glu 250 245

Thr Asp Phe Asn Ser Asn Ile Ala Phe Pro Trp Ser Gln Ser Gln Ala 265 260

Cys Asp Val Phe Pro Lys Asp Leu Gln Arg Met Ala Phe Ser Phe Gly 280 275

Gly Gln Thr Leu

290

- (2) INFORMATION FOR SEQ ID NO:947:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..282
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595762
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947: Met Ala Met Val Ala Gly Val Leu Ser Leu Asn Ser Gly Leu Glu Arg 10 5 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp 25

Leu Lys Arg Gly Ala Phe Ser Ser Glu Glu Gln Asn Leu Ile Val Glu

Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ala Arg Leu 60 55 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Cys Ile

75 Lys Lys Lys Leu Met Lys Lys Gly Ile Asp Pro Ile Thr His Lys Pro 90 85

Leu Ser Glu Val Gly Lys Glu Thr Asn Arg Ser Asp Asn Asn Asn Ser 100 110 105

Thr Ser Phe Ser Ser Glu Thr Asn Gln Asp Leu Phe Val Lys Lys Thr 120 125

Ser Asp Phe Ala Glu Tyr Ser Ala Phe Gln Lys Glu Glu Ser Asn Ser 130 135 140

Val Ser Leu Arg Asn Ser Leu Ser Ser Met Ile Pro Thr Gln Phe Asn 150 155

Ile Asp Asp Gly Ser Val Ser Asn Ala Gly Phe Asp Thr Gln Val Cys 165 170 Val Lys Pro Ser Ile Ile Leu Leu Pro Pro Pro Asn Asn Thr Ser Ser

185 190 180 Thr Val Ser Gly Gln Asp His Val Asn Val Ser Glu Pro Asn Trp Glu

200 205 Ser Asn Ser Gly Thr Thr Ser His Leu Asn Asn Pro Gly Met Glu Glu

220 215 Met Lys Trp Ser Glu Glu Tyr Leu Asn Glu Ser Leu Phe Ser Thr Gln

235 230 Val Tyr Val Lys Ser Glu Thr Asp Phe Asn Ser Asn Ile Ala Phe Pro

250 245 Trp Ser Gln Ser Gln Ala Cys Asp Val Phe Pro Lys Asp Leu Gln Arg 270 265

Met Ala Phe Ser Phe Gly Gly Gln Thr Leu 280

(2) INFORMATION FOR SEQ ID NO:948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..280
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595763
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

Met Val Ala Gly Val Leu Ser Leu Asn Ser Gly Leu Glu Arg Cys Gly
1 10 15

Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys 20 25 30

Arg Gly Ala Phe Ser Ser Glu Glu Gln Asn Leu Ile Val Glu Leu His 35 40 45

Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ala Arg Leu Pro Gly 50 55 60

Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Cys Ile Lys Lys 65 70 75 80

Lys Leu Met Lys Lys Gly Ile Asp Pro Ile Thr His Lys Pro Leu Ser 85 90 95

Glu Val Gly Lys Glu Thr Asn Arg Ser Asp Asn Asn Asn Ser Thr Ser 100 105 110

Phe Ser Ser Glu Thr Asn Gln Asp Leu Phe Val Lys Lys Thr Ser Asp 115 120 125

Phe Ala Glu Tyr Ser Ala Phe Gln Lys Glu Glu Ser Asn Ser Val Ser 130 135 140

Leu Arg Asn Ser Leu Ser Ser Met Ile Pro Thr Gln Phe Asn Ile Asp 145 150 155 160

Asp Gly Ser Val Ser Asn Ala Gly Phe Asp Thr Gln Val Cys Val Lys 165 170 175

Pro Ser Ile Ile Leu Leu Pro Pro Pro Asn Asn Thr Ser Ser Thr Val 180 185 190

Ser Gly Gln Asp His Val Asn Val Ser Glu Pro Asn Trp Glu Ser Asn 195 200 205

Ser Gly Thr Thr Ser His Leu Asn Asn Pro Gly Met Glu Glu Met Lys 210 215 220

Trp Ser Glu Glu Tyr Leu Asn Glu Ser Leu Phe Ser Thr Gln Val Tyr 225 230 235 240

Val Lys Ser Glu Thr Asp Phe Asn Ser Asn Ile Ala Phe Pro Trp Ser 245 250 255

Gln Ser Gln Ala Cys Asp Val Phe Pro Lys Asp Leu Gln Arg Met Ala 260 265 270

Phe Ser Phe Gly Gly Gln Thr Leu 275 280

- (2) INFORMATION FOR SEQ ID NO:949:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..614
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595764

attgagaget atggeactae gateagtaag caggaggete gggageagaa ttttgaatea 180 acgttccttt gttgcttcgc ttcactctca tgccacaagt ttcgggtttc aagaagtaaa 240 300 ggaagaagag aaaagcaaat tggttggtaa tgtattcacc aatgtagctt cgagttatga tattatgaat gatgtgatga gtggtggttt gcataggcta tggaaggaaa gactcgttgg 360 gaagctaagt ccatttgcag ggatgaagca tcttgatgtg gccggaggaa caggtgatgt 420 480 tgcctttagg atctatgatg ctgtttacag tgtcaaacga agagcattgc agaaagttga tgaggettet ettgaggaaa etcagatata egtatgtgae attaateeta acatgttaaa 540 cgttgggaaa caacgagctg ctgagagagg tctaagagat aacaagtcac tcgtatgggt 600 cqaaqqagat gcag

- (2) INFORMATION FOR SEQ ID NO:950:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595765
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

Met Ala Leu Arg Ser Val Ser Arg Arg Leu Gly Ser Arg Ile Leu Asn 1 5 10 15

Gln Arg Ser Phe Val Ala Ser Leu His Ser His Ala Thr Ser Phe Gly 20 25 30

Phe Gln Glu Val Lys Glu Glu Glu Lys Ser Lys Leu Val Gly Asn Val 35 40 45

Phe Thr Asn Val Ala Ser Ser Tyr Asp Ile Met Asn Asp Val Met Ser 50 55 60

Gly Gly Leu His Arg Leu Trp Lys Glu Arg Leu Val Gly Lys Leu Ser 65 70 75 80

Pro Phe Ala Gly Met Lys His Leu Asp Val Ala Gly Gly Thr Gly Asp 85 90 95

Val Ala Phe Arg Ile Tyr Asp Ala Val Tyr Ser Val Lys Arg Arg Ala 100 105 110

Leu Gln Lys Val Asp Glu Ala Ser Leu Glu Glu Thr Gln Ile Tyr Val

Cys Asp Ile Asn Pro Asn Met Leu Asn Val Gly Lys Gln Arg Ala Ala 130 135 140

Glu Arg Gly Leu Arg Asp Asn Lys Ser Leu Val Trp Val Glu Gly Asp 145 150 155 160

Ala

- (2) INFORMATION FOR SEQ ID NO:951:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595766
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Met Asn Asp Val Met Ser Gly Gly Leu His Arg Leu Trp Lys Glu Arg

Leu Val Gly Lys Leu Ser Pro Phe Ala Gly Met Lys His Leu Asp Val

Ala Gly Gly Thr Gly Asp Val Ala Phe Arg Ile Tyr Asp Ala Val Tyr

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Ser Val Lys Arg Arg Ala Leu Gln Lys Val Asp Glu Ala Ser Leu Glu
50 55 60
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Glu Thr Gln Ile Tyr Val Cys Asp Ile Asn Pro Asn Met Leu Asn Val 65 70 75 80

Gly Lys Gln Arg Ala Ala Glu Arg Gly Leu Arg Asp Asn Lys Ser Leu 85 90 95

Val Trp Val Glu Gly Asp Ala 100

- (2) INFORMATION FOR SEQ ID NO:952:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595767
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952: Met Ser Gly Gly Leu His Arg Leu Trp Lys Glu Arg Leu Val Gly Lys 10 5 Leu Ser Pro Phe Ala Gly Met Lys His Leu Asp Val Ala Gly Gly Thr 25 30 20 Gly Asp Val Ala Phe Arg Ile Tyr Asp Ala Val Tyr Ser Val Lys Arg 40 Arg Ala Leu Gln Lys Val Asp Glu Ala Ser Leu Glu Glu Thr Gln Ile 55 Tyr Val Cys Asp Ile Asn Pro Asn Met Leu Asn Val Gly Lys Gln Arg 75 70 Ala Ala Glu Arg Gly Leu Arg Asp Asn Lys Ser Leu Val Trp Val Glu
- (2) INFORMATION FOR SEQ ID NO:953:

85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 823 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

Gly Asp Ala

- (A) NAME/KEY: -
- (B) LOCATION: 1..823
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595783
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

60 gtatcgagat cgaatcggca atggctgctt caagctccgt tttcacagta tccccgtcgc gaaatettge agetatteet etteateagt eestatetee aeegttgett agateeaget 120 ccgtcgcgtt tcgtcccaaa cgaagatcca gctcactcgt cttatgctca actgatgaaa 180 caaagagcac cgcagagaaa gagatcccaa tcgaactaag gtatgaggcg tttccgacag 240 tgatggacat caataagata caagagattt tgcctcacag attcccattt ctgttagttg 300 atagagtgat agagtacaca gctggtgtat ctgcggtagc tattaaaaac gttaccatta 360 atgacaattt ctttcctggg catttccctg agagacctat aatgcctgga gttctcatgg 420 ttgaggcaat ggctcaagtg ggaggtatag tgatgctaca accagaagtt ggcggatcta 480 gaagcaactt cttctttgct ggaatcgaca aagtcagatt caggaagcca gtgattgcag 540 600 gtgatacgct ggtgatgagg atgacacttg tgaagttgca gaagcggttt gggatagcga 660 aaatggaagg gaaagcatat gtagggaact ctgtggtatg tgaaggagag ttcttgatgg 720 ctatgggaaa agaagagtga tcacgccttt gtttctttct tcttcatacg ggccttgtgg 780 ctgctaatta gttgtcacat cctaagttga gtctcatttc tatcttcaat ttatgatgtt tgtttgcaca ttatgattat attaaaaaag caacttcagt ttt

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..225 (D) OTHER INFORMATION: / Ceres Seq. ID 1595784 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954: Ile Glu Ile Glu Ser Ala Met Ala Ala Ser Ser Ser Val Phe Thr Val 10 5 Ser Pro Ser Arg Asn Leu Ala Ala Ile Pro Leu His Gln Ser Leu Ser 20 25 Pro Pro Leu Leu Arg Ser Ser Ser Val Ala Phe Arg Pro Lys Arg Arg 40 Ser Ser Ser Leu Val Leu Cys Ser Thr Asp Glu Thr Lys Ser Thr Ala 60 55 Glu Lys Glu Ile Pro Ile Glu Leu Arg Tyr Glu Ala Phe Pro Thr Val 75 70 Met Asp Ile Asn Lys Ile Gln Glu Ile Leu Pro His Arg Phe Pro Phe 90 85 Leu Leu Val Asp Arg Val Ile Glu Tyr Thr Ala Gly Val Ser Ala Val 100 105 110 Ala Ile Lys Asn Val Thr Ile Asn Asp Asn Phe Phe Pro Gly His Phe 115 120 125 Pro Glu Arg Pro Ile Met Pro Gly Val Leu Met Val Glu Ala Met Ala 130 135 140 Gln Val Gly Gly Ile Val Met Leu Gln Pro Glu Val Gly Gly Ser Arg 155 150 Ser Asn Phe Phe Phe Ala Gly Ile Asp Lys Val Arg Phe Arg Lys Pro 170 175 165 Val Ile Ala Gly Asp Thr Leu Val Met Arg Met Thr Leu Val Lys Leu 185 Gln Lys Arg Phe Gly Ile Ala Lys Met Glu Gly Lys Ala Tyr Val Gly 200 205 Asn Ser Val Val Cys Glu Gly Glu Phe Leu Met Ala Met Gly Lys Glu 21.5 Glu 225 (2) INFORMATION FOR SEQ ID NO:955: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 219 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..219 (D) OTHER INFORMATION: / Ceres Seq. ID 1595785 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:955: Met Ala Ala Ser Ser Ser Val Phe Thr Val Ser Pro Ser Arg Asn Leu 10 5 Ala Ala Ile Pro Leu His Gln Ser Leu Ser Pro Pro Leu Leu Arg Ser 25 20 Ser Ser Val Ala Phe Arg Pro Lys Arg Arg Ser Ser Ser Leu Val Leu 40 45 Cys Ser Thr Asp Glu Thr Lys Ser Thr Ala Glu Lys Glu Ile Pro Ile

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Glu Leu Arg Tyr Glu Ala Phe Pro Thr Val Met Asp Ile Asn Lys Ile
                                    75
                  70
Gln Glu Ile Leu Pro His Arg Phe Pro Phe Leu Leu Val Asp Arg Val
                                90
              85
Ile Glu Tyr Thr Ala Gly Val Ser Ala Val Ala Ile Lys Asn Val Thr
                            105
Ile Asn Asp Asn Phe Phe Pro Gly His Phe Pro Glu Arg Pro Ile Met
                                           125
           120
Pro Gly Val Leu Met Val Glu Ala Met Ala Gln Val Gly Gly Ile Val
                                       140
                  135
Met Leu Gln Pro Glu Val Gly Gly Ser Arg Ser Asn Phe Phe Phe Ala
                                   155
                 150
Gly Ile Asp Lys Val Arg Phe Arg Lys Pro Val Ile Ala Gly Asp Thr
                                170
            165
Leu Val Met Arg Met Thr Leu Val Lys Leu Gln Lys Arg Phe Gly Ile
        180
                            185
Ala Lys Met Glu Gly Lys Ala Tyr Val Gly Asn Ser Val Val Cys Glu
                                            205
      195 200
Gly Glu Phe Leu Met Ala Met Gly Lys Glu Glu
           215
   210
```

- (2) INFORMATION FOR SEQ ID NO:956:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..145
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595786
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:956: Met Asp Ile Asn Lys Ile Gln Glu Ile Leu Pro His Arg Phe Pro Phe 10 5 Leu Leu Val Asp Arg Val Ile Glu Tyr Thr Ala Gly Val Ser Ala Val 25 2.0 Ala Ile Lys Asn Val Thr Ile Asn Asp Asn Phe Phe Pro Gly His Phe 40 Pro Glu Arg Pro Ile Met Pro Gly Val Leu Met Val Glu Ala Met Ala 60 55 Gln Val Gly Gly Ile Val Met Leu Gln Pro Glu Val Gly Gly Ser Arg 75 70 Ser Asn Phe Phe Phe Ala Gly Ile Asp Lys Val Arg Phe Arg Lys Pro 90 85

Val Ile Ala Gly Asp Thr Leu Val Met Arg Met Thr Leu Val Lys Leu
100 105 110

Gln Lys Arg Phe Gly Ile Ala Lys Met Glu Gly Lys Ala Tyr Val Gly
115 120 125

Asn Ser Val Val Cys Glu Gly Glu Phe Leu Met Ala Met Gly Lys Glu

Glu

- (2) INFORMATION FOR SEQ ID NO:957:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

- (B) LOCATION: 1..1130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595787
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957: atcaaccgta aacttattgc tttcttcctt ctggtagttc cccaaaactc aaagtactct 60 ttttgtgtgt aaacaaaaaa aaaaatcaac ggtactcttt ctcttctaag tttttgttcc 120 atggagaaga gtttccagaa atcagctctc cttgtgacat tgactctctt cttctgcatt 180 240 ccagtttcaa tctcggttcc attcattctg tttcatggga ttagagatca atgctccaat 300 ggtggagtaa gcagcttcgt acagctcctt agcaacctct ctagctccca tggatcttgc 360 ttagaaatag gagatggaga gcaagattcg gtgactatgc cgcttacgca acaagcgagt 420 gtagcgtgtg agaaagttaa acagctgaag gatttgagtc aaggctacaa cattgttgca cagteteaag gaaacttggt agetagaggt etaategagt tttgtgacaa tgeteeteeg 480 gtcttcaact atatatcttt aggaggtcct catgctggca tatccgacat tTcccaagtg 540 600 taattctaca cttttgcgag ttgctgaaaa cagcggtcta caccgacttc gtacaagatc 660 atattgctcc aagtggttat atcaagattc ctacagatat aaaagattac ctggaacact 720 ccaagtatct gccaaagatc aacaacgaga gacctaacga aaggaacacc acttttaaag 780 accggttcac tagcttgcac aacttggtcc ttgtcatgtt tgagggtgat gcagtagtga 840 ttcctaaaga aagttcttgg ttcggatatt acccggatgg agcttcctca cctcttttgt 900 ccagaaaagt taagtttgtc agtgtccctg gcgagcacct aagaatagcg caagacgacg 960 1020 ttgtaaaaca cgtcgtgcct tacctcaaga accagcctgc gtctatgagt gaagatttgg agatactgca tctatgattg agacttcatt gttatgctct cttagaatca aatttaaaag 1080 tgaagaactt tagaggctcc tttttcttaa tcataaatcc aaataatttc
- (2) INFORMATION FOR SEQ ID NO:958:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595788
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

Met Glu Lys Ser Phe Gln Lys Ser Ala Leu Leu Val Thr Leu Thr Leu 1 Phe Phe Cys Ile Pro Val Ser Ile Ser Val Pro Phe Ile Leu Phe His

20 25 30

Gly Ile Arg Asp Gln Cys Ser Asn Gly Gly Val Ser Ser Phe Val Gln

35 40 45
Leu Leu Ser Asn Leu Ser Ser Ser His Gly Ser Cys Leu Glu Ile Gly

50 55 60
Asp Gly Glu Gln Asp Ser Val Thr Met Pro Leu Thr Gln Gln Ala Ser
70 75 80

70 75 80

Val Ala Cys Glu Lys Val Lys Gln Leu Lys Asp Leu Ser Gln Gly Tyr
85 90 95

Asn Ile Val Ala Gln Ser Gln Gly Asn Leu Val Ala Arg Gly Leu Ile 100 105 110

Glu Phe Cys Asp Asn Ala Pro Pro Val Phe Asn Tyr Ile Ser Leu Gly 115 120 125

- Gly Pro His Ala Gly Ile Ser Asp Ile Ser Gln Val 130 135 140
- (2) INFORMATION FOR SEQ ID NO:959:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

Met Phe Glu Gly Asp Ala Val Val Ile Pro Lys Glu Ser Ser Trp Phe

Gly Tyr Tyr Pro Asp Gly Ala Ser Ser Pro Leu Leu Ser Pro Gln Gln 20 25 30

Thr Lys Leu Tyr Thr Glu Asp Trp Ile Gly Leu Lys Thr Leu Asp Ala 35 40 45

Ala Arg Lys Val Lys Phe Val Ser Val Pro Gly Glu His Leu Arg Ile 50 55 60

Ala Gln Asp Asp Val Val Lys His Val Val Pro Tyr Leu Lys Asn Gln 65 70 75 80

Pro Ala Ser Met Ser Glu Asp Leu Glu Ile Leu His Leu 85 90

- (2) INFORMATION FOR SEQ ID NO:960:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1219
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595790
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:960: aaatggcgat ggagatcgga gaagatgaat ggaaggtttg ctgtggaagc tccgaattcg cgaaGcagat gtctacgtct ggaccgttaa cttctcaaga agcaatatat actgcaagag 120 acatctggtt caaccaagtt aatgtgacag attggcttga agctttctct gctcatcctc 180 agattgggaa tactccttca ccttctatca actccgattt tgctcgtcgg agcgtatcag 240 300 aacagtcaac cgcctttgcc acaacttctg cttctgcttt acaggagctt gccgaatgga 360 atgtacttta caaaaagaag tttggcttta tcttcattat ttgcgcttct ggcaggactc 420 acgctgagat gctccatgcg ttaaaggtca acttttgcat ttccaaatca gtttttgttg 480 agtgtgagtg aatgagaaag ttacatattc atcaaatcgt ctcttttca ggaaaggtat aaaaataggc caatagtgga gcttgagatt gctgctatgg aacaaatgaa aataacagag 540 ctacgaatgg caaagctgtt ctccgataag gctaaagtta tatcagaaac tgacagctct 600 660 agctctcctg tttcaacaaa acctcaagat cgtcagagaa tcattggagg gcatttgaat 720 gttgcagctg aagcaaaagc tcccaagaga agtaggccac cgatcacgac tcatgtbtta 780 gacgtctcac gtggtgctcc agctgcaggt gttgaagtgc acttagaagt gtggagtggt 840 actaccggtc cttcctttgt tcatggaggt ggtggggtct ggtccagtgt gggcacatca 900 gctactgata gagatgggcg cagtgggcca ctgatggatt tggttgacgc tttgaatcca 960 gggacatata ggattagett egacaetgea aagtatteee eaggetgett ettteeetat gtttccattg tatttcaggt tacagaatca cagaaatggg agcatttcca tgtcccactg 1020 1080 ttgcttgcac ctttttcttt ctccacatac cgtgggagct agagctatgc tactgctgtc tgcggcacca actttccaac acattttgtt ttggttgtac cactacggga acatgtatca 1140 aaattgctat gaaatgaagt ctttattcga catgtataaa aattgctatg aaataatgtc 1200 tattcgagta tttatttgg
- (2) INFORMATION FOR SEQ ID NO:961:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 181 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..181
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595791
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met Glu Gln Met Lys Ile Thr Glu Leu Arg Met Ala Lys Leu Phe Ser

Asp Lys Ala Lys Val Ile Ser Glu Thr Asp Ser Ser Ser Pro Val 25 Ser Thr Lys Pro Gln Asp Arg Gln Arg Ile Ile Gly Gly His Leu Asn Val Ala Ala Glu Ala Lys Ala Pro Lys Arg Ser Arg Pro Pro Ile Thr 55 Thr His Xaa Leu Asp Val Ser Arg Gly Ala Pro Ala Ala Gly Val Glu 75 70 Val His Leu Glu Val Trp Ser Gly Thr Thr Gly Pro Ser Phe Val His 90 8.5 Gly Gly Gly Val Trp Ser Ser Val Gly Thr Ser Ala Thr Asp Arg 105 Asp Gly Arg Ser Gly Pro Leu Met Asp Leu Val Asp Ala Leu Asn Pro 125 120 Gly Thr Tyr Arg Ile Ser Phe Asp Thr Ala Lys Tyr Ser Pro Gly Cys 135 140 Phe Phe Pro Tyr Val Ser Ile Val Phe Gln Val Thr Glu Ser Gln Lys 150 155 Trp Glu His Phe His Val Pro Leu Leu Leu Ala Pro Phe Ser Phe Ser 170 165 Thr Tyr Arg Gly Ser 180

- (2) INFORMATION FOR SEQ ID NO:962:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..178
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595792
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

Met Lys Ile Thr Glu Leu Arg Met Ala Lys Leu Phe Ser Asp Lys Ala 1 5 10 15 Lys Val Ile Ser Glu Thr Asp Ser Ser Ser Ser Pro Val Ser Thr Lys

Lys Val Ile Ser Glu Thr Asp Ser Ser Ser Ser Pro Val Ser Thr Lys
20 25 30

Pro Gln Asp Arg Gln Arg Ile Ile Gly Gly His Leu Asn Val Ala Ala 35 40 45

Glu Ala Lys Ala Pro Lys Arg Ser Arg Pro Pro Ile Thr Thr His Xaa 50 55 60

Leu Asp Val Ser Arg Gly Ala Pro Ala Ala Gly Val Glu Val His Leu 65 70 75 80 80 Glu Val Trp Ser Gly Thr Thr Gly Pro Ser Phe Val His Gly Gly Gly

85 90 95

Gly Val Trp Ser Ser Val Gly Thr Ser Ala Thr Asp Arg Asp Gly Arg

100 105 110

Ser Gly Pro Leu Met Asp Leu Val Asp Ala Leu Asn Pro Gly Thr Tyr
115 120 125

Arg Ile Ser Phe Asp Thr Ala Lys Tyr Ser Pro Gly Cys Phe Phe Pro 130 135 140

Tyr Val Ser Ile Val Phe Gln Val Thr Glu Ser Gln Lys Trp Glu His 145 150 155 160

Phe His Val Pro Leu Leu Leu Ala Pro Phe Ser Phe Ser Thr Tyr Arg
165 170 175

Gly Ser

- (2) INFORMATION FOR SEQ ID NO:963:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..171
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595793
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

Met Ala Lys Leu Phe Ser Asp Lys Ala Lys Val Ile Ser Glu Thr Asp

Ser Ser Ser Ser Pro Val Ser Thr Lys Pro Gln Asp Arg Gln Arg Ile 20 25 30

Ile Gly Gly His Leu Asn Val Ala Ala Glu Ala Lys Ala Pro Lys Arg 35 40 45

Ser Arg Pro Pro Ile Thr Thr His Xaa Leu Asp Val Ser Arg Gly Ala 50 55 60

Pro Ala Ala Gly Val Glu Val His Leu Glu Val Trp Ser Gly Thr Thr 65 70 75 80

Gly Pro Ser Phe Val His Gly Gly Gly Gly Val Trp Ser Ser Val Gly 85 90 95

Thr Ser Ala Thr Asp Arg Asp Gly Arg Ser Gly Pro Leu Met Asp Leu
100 105 110

Val Asp Ala Leu Asn Pro Gly Thr Tyr Arg Ile Ser Phe Asp Thr Ala 115 120 125

Lys Tyr Ser Pro Gly Cys Phe Phe Pro Tyr Val Ser Ile Val Phe Gln 130 135 140

Val Thr Glu Ser Gln Lys Trp Glu His Phe His Val Pro Leu Leu Leu 145 150 150

Ala Pro Phe Ser Phe Ser Thr Tyr Arg Gly Ser 165 170

- (2) INFORMATION FOR SEQ ID NO:964:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..597
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595794
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

gattcgtgaa atggcgactg gtaaaaccgt gaaagatgtt tctcctcacg atttcgtgaa 60 ggcttacgct tctcacctca agcgatctgg aaagattgag cttcctctat ggacagacat 120 tgtgaagact ggtcgtttga aggagcttgc tccatatgac cctgattggt actacattag 180 agctgcttct atggccagaa agatttactt gagaggaggt cttggtgttg gtgctttcag 240 aagaatttat ggaggtagca aaagaaatgg aagtcgacca ccacatttct gtaagagcag 300 tggtggtatt gctcgccata ttctccaaca gttggagaca atgagcattg tcgagcttga 360 cactaaagga gggagaagaa tcacttcgag cggtcaacgg gatttggatc aggttgctgg 420 gcgtattgca gctgaatcat gaagagctgt tgttctcctt atgcttgctt tggaggagcc 480 tcaagaatgt tatagatett tttagetttt gtgattttag atetetaete tettetgete 540 tgttcatttt gacgaactaa tttgatattt gatgaagcta ttaaagtttt gttcttt

- (2) INFORMATION FOR SEQ ID NO:965:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595795

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965: Ile Arg Glu Met Ala Thr Gly Lys Thr Val Lys Asp Val Ser Pro His
- Asp Phe Val Lys Ala Tyr Ala Ser His Leu Lys Arg Ser Gly Lys Ile 20 25 30
- Glu Leu Pro Leu Trp Thr Asp Ile Val Lys Thr Gly Arg Leu Lys Glu 35 40
- Leu Ala Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser Met 50 55 60
- Ala Arg Lys Ile Tyr Leu Arg Gly Gly Leu Gly Val Gly Ala Phe Arg 65 70 75 80
- Arg Ile Tyr Gly Gly Ser Lys Arg Asn Gly Ser Arg Pro Pro His Phe 85 90 95
- Cys Lys Ser Ser Gly Gly Ile Ala Arg His Ile Leu Gln Gln Leu Glu 100 105 110
- Thr Met Ser Ile Val Glu Leu Asp Thr Lys Gly Gly Arg Arg Ile Thr 115 120 125
- Ser Ser Gly Gln Arg Asp Leu Asp Gln Val Ala Gly Arg Ile Ala Ala 130 135 140

Glu Ser

- (2) INFORMATION FOR SEQ ID NO:966:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:
- Met Ala Thr Gly Lys Thr Val Lys Asp Val Ser Pro His Asp Phe Val

 10
 15
- Lys Ala Tyr Ala Ser His Leu Lys Arg Ser Gly Lys Ile Glu Leu Pro
 20 25 30
- Leu Trp Thr Asp Ile Val Lys Thr Gly Arg Leu Lys Glu Leu Ala Pro 35 40 45
- Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser Met Ala Arg Lys 50 55 60
- Ile Tyr Leu Arg Gly Gly Leu Gly Val Gly Ala Phe Arg Arg Ile Tyr65707580Gly Gly Ser Lys Arg Asn Gly Ser Arg Pro Pro His Phe Cys Lys Ser
- 85 90 95 Ser Gly Gly Ile Ala Arg His Ile Leu Gln Gln Leu Glu Thr Met Ser 100 105 110
- Ile Val Glu Leu Asp Thr Lys Gly Gly Arg Arg Ile Thr Ser Ser Gly
 115 120 125
- Gln Arg Asp Leu Asp Gln Val Ala Gly Arg Ile Ala Ala Glu Ser 130 135 140
- (2) INFORMATION FOR SEQ ID NO:967:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..83
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595797
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

Met Ala Arg Lys Ile Tyr Leu Arg Gly Gly Leu Gly Val Gly Ala Phe 1 $$ 5 $$ 10 $$ 15

Arg Arg Ile Tyr Gly Gly Ser Lys Arg Asn Gly Ser Arg Pro Pro His 20 25 30

Phe Cys Lys Ser Ser Gly Gly Ile Ala Arg His Ile Leu Gln Gln Leu 35 40 45

Glu Thr Met Ser Ile Val Glu Leu Asp Thr Lys Gly Gly Arg Arg Ile 50 55 60

Thr Ser Ser Gly Gln Arg Asp Leu Asp Gln Val Ala Gly Arg Ile Ala 65 70 75 80

Ala Glu Ser

- (2) INFORMATION FOR SEQ ID NO: 968:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..571
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595802
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968: 60 atcqtcaaaq caaccaaaca cataaaagag agatttaata caaaagaaag agaaaaaaga 120 aagatatggc aggactcatc aacaagatcg gagacgcact ccacattgga ggaggcaaca aggaaggtga gcacaagaag gaagaggaac acaagaaaca cgttgacgag cacaagagtg 180 gtgagcacaa agaaggtatt gttgacaaga tcaaagacaa gatccacggt ggtgaaggta 240 aaagccacga cggagaaggc aaaagccacg acggtgagaa gaaaaagaat aaggacaaga 300 aggagaagaa acatcatgat gatggtcacc acagcagcag cagtgacagc gacaGcgaGt 360 taaggtgagg aagtgaggag gatcgcttga ataaaacaga tctggttctg gctattatta 420 attaatgttg ctgtatgttc ttatcatctt agagagaggt taaagacagg agaaccgtgc 480 atctatcttt gtttgttatg tttctgtttt cttgtcatga aaattatgct catgtatctt 540 atctaaatca aaaataataa tttgatgaat c
- (2) INFORMATION FOR SEQ ID NO:969:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

Ile Val Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn Thr Lys Glu
1 10 15

Arg Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg Ser Glu Thr

His Ser Thr Leu Glu Glu Ala Thr Arg Lys Val Ser Thr Arg Arg Lys 35 40 45

Arg Asn Thr Arg Asn Thr Leu Thr Ser Thr Arg Val Val Ser Thr Lys 50 55 60

Lys Val Leu Leu Thr Arg Ser Lys Thr Arg Ser Thr Val Val Lys Val

960

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80
                                        75
                   70
Lys Ala Thr Thr Glu Lys Ala Lys Ala Thr Thr Val Arg Arg Lys Arg
                                90
Ile Arg Thr Arg Arg Arg Asn Ile Met Met Wal Thr Thr Ala
           100 105
Ala Ala Val Thr Ala Thr Ala Ser
        115
(2) INFORMATION FOR SEQ ID NO: 970:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 100 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..100
          (D) OTHER INFORMATION: / Ceres Seq. ID 1595804
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:
Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Ile Gly Gly
                                   10
               5
Gly Asn Lys Glu Gly Glu His Lys Lys Glu Glu Glu His Lys Lys His
                               25
          20
Val Asp Glu His Lys Ser Gly Glu His Lys Glu Gly Ile Val Asp Lys
                            40
Ile Lys Asp Lys Ile His Gly Gly Glu Gly Lys Ser His Asp Gly Glu
                        55
Gly Lys Ser His Asp Gly Glu Lys Lys Lys Asn Lys Asp Lys Lys Glu
                  70
                                       75
Lys Lys His His Asp Asp Gly His His Ser Ser Ser Ser Asp Ser Asp
                                    90
                85
Ser Glu Leu Arg
            100
(2) INFORMATION FOR SEQ ID NO:971:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1090 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
          (A) NAME/KEY: -
           (B) LOCATION: 1..1090
           (D) OTHER INFORMATION: / Ceres Seq. ID 1595805
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:
tttttttttt tccctcctcc tagatccacc acttccacct ctctctcctc ctcctctttc
                                                                       120
 egececttet ectetectee gtecatgtet teegeegeeg etgeegeegt ggaateegte
gtctccgacg agactctttc ctcgaatcct ctcttgcagg acttcgattt ccctccgttt
                                                                       180
 gattccgttg atgccagtca tgttcgtcct gggattcgtg ctctattgca gcatctcgaa
                                                                       240
 gctgaattgg aggagctaga gaaatctgtg gagccaacat ggccaaaact ggtggaacca
                                                                       300
 ttagagaaaa tcgttgatcg gttaactgtt gtttggggaa tgatcaatca ccttaaggct
                                                                       360
 gtcaaggaca cacctgagct acgtgctgcc atcgaagacg ttcagccaga gaaagtgaag
                                                                       420
 ttccagctca ggttggggca aagcaagcct atttacaatg cctttaaagc tattcgtgaa
                                                                       480
 tctcctgatt ggtcatcgct cagtgaagct cgtcaacgct tagtagaagc tcaaaAtaaa
                                                                       540
 ggaggcggtt ctcattggta ttgctcttga tgatgaaaag agagaagagt ttaataaaat
                                                                       600
 tgaacaggaa ctcgaaaaac tttcccataa gttttctgag aatgttttgg atgcaacaaa
                                                                       660
 gaaatttgaa aagttgataa cagacaagaa agagatcgag ggattgcctc catctgctct
                                                                       720
 tgggctattc gcacaagcag ctgtctccaa gggccatgaa aatgcaactg ctgagaatgg
                                                                       780
                                                                       840
 accatggatc attacactgg atgetectag ttatetteet gteatgeaac atgetaaaaa
 ccgtgctctg cgtgaggaag tctaccgtgc ttacctatct cgtgcctctt ctggcgattt
                                                                       900
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ggataatacg gcaattattg accagatttt gaagcttcgc ttggaaaaag ctaagcttct

tggttacaac aattacgctg aggtaagcat ggctatgaaa atggctactg ttgagaaagc 1020 agcagagctt ttagagaagc ttcgtagtgc atcctgggat gcggctgttc aagacatgga 1080 agacctcaag

- (2) INFORMATION FOR SEQ ID NO:972:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..189
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

Phe Phe Phe Leu Pro Pro Pro Arg Ser Thr Thr Ser Thr Ser Leu Ser 1 5 10 15

Ser Ser Ser Phe Arg Pro Phe Ser Ser Pro Pro Ser Met Ser Ser Ala 20 25 30

Ala Ala Ala Val Glu Ser Val Val Ser Asp Glu Thr Leu Ser Ser 40 45

Asn Pro Leu Leu Gln Asp Phe Asp Phe Pro Pro Phe Asp Ser Val Asp 50 55 60

Ala Ser His Val Arg Pro Gly Ile Arg Ala Leu Leu Gln His Leu Glu 65 70 75 80

Ala Glu Leu Glu Glu Leu Glu Lys Ser Val Glu Pro Thr Trp Pro Lys 85 90 95

Leu Val Glu Pro Leu Glu Lys Ile Val Asp Arg Leu Thr Val Val Trp
100 105 110

Gly Met Ile Asn His Leu Lys Ala Val Lys Asp Thr Pro Glu Leu Arg 115 120 125

Ala Ala Ile Glu Asp Val Gln Pro Glu Lys Val Lys Phe Gln Leu Arg 130 135 140

Leu Gly Gln Ser Lys Pro Ile Tyr Asn Ala Phe Lys Ala Ile Arg Glu 145 150 155 160

Ser Pro Asp Trp Ser Ser Leu Ser Glu Ala Arg Gln Arg Leu Val Glu 165 170 175

Ala Gl
n Asn Lys Gly Gly Ser His Trp Tyr Cys Ser $$180\$

- (2) INFORMATION FOR SEQ ID NO:973:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

Met Ser Ser Ala Ala Ala Ala Val Glu Ser Val Val Ser Asp Glu 1 5 10 15

Thr Leu Ser Ser Asn Pro Leu Leu Gln Asp Phe Asp Phe Pro Pro Phe 20 25 30

Asp Ser Val Asp Ala Ser His Val Arg Pro Gly Ile Arg Ala Leu Leu

Gln His Leu Glu Ala Glu Leu Glu Glu Leu Glu Lys Ser Val Glu Pro
50 55 60

Thr Trp Pro Lys Leu Val Glu Pro Leu Glu Lys Ile Val Asp Arg Leu 65 70 75 80

Thr Val Val Trp Gly Met Ile Asn His Leu Lys Ala Val Lys Asp Thr 90 85 Pro Glu Leu Arg Ala Ala Ile Glu Asp Val Gln Pro Glu Lys Val Lys 110 100 105 Phe Gln Leu Arg Leu Gly Gln Ser Lys Pro Ile Tyr Asn Ala Phe Lys 125 120 Ala Ile Arg Glu Ser Pro Asp Trp Ser Ser Leu Ser Glu Ala Arg Gln 140 135 Arg Leu Val Glu Ala Gln Asn Lys Gly Gly Ser His Trp Tyr Cys 145 150 155 Ser

- (2) INFORMATION FOR SEQ ID NO: 974:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..648
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595812
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974: aaaggtttgg aaacgtgaga tcagagggaa gcgtacggcg cactctttgg tccaaacttt 60 120 gctaaagcaa gaatcagcgg tcacggcttt ggtcacgagc cacatggcag tgtatagtgg ttcaagcgac ggagctgtga atttttggga gatgggagag aagaaaatct tgaagcattg 180 tgaagttttc aagaagcata gacttgctgt cctttgtatc geggctgccg gaaaattgtt 240 300 360 gtgtgtctct gtgttaaccg gtcataccgg accagttaag tgtttggcgg tggtggagcc atcgggaggt gaagaagaag acggaggaga tgggaggttg gttttgtata gtggaagtct 420 tgacaaatcg gtcaaagtgt ggagggtacc acgtcattaa atgtaggatt ttattcggtg 480 540 tottaaqaga tittgggatgt atgtaggtaa gtaagaacaa aaacccaagt caaatgatga 600 attatqaqqt tcgtaatata tgatatttat tagtaattta atatatcttt gatacatgta taattgaact agggttatcg tttacggtga atatcaaata tcaatatt
- (2) INFORMATION FOR SEQ ID NO: 975:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595813
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:
- Lys Val Trp Lys Arg Glu Ile Arg Gly Lys Arg Thr Ala His Ser Leu
 1 5 10 15
- Val Gln Thr Leu Leu Lys Gln Glu Ser Ala Val Thr Ala Leu Val Thr 20 25 30
- Ser His Met Ala Val Tyr Ser Gly Ser Ser Asp Gly Ala Val Asn Phe 35 40 45
- Trp Glu Met Gly Glu Lys Lys Ile Leu Lys His Cys Glu Val Phe Lys 50 55 60
- Lys His Arg Leu Ala Val Leu Cys Ile Ala Ala Ala Gly Lys Leu Leu 65 70 75 80
- Phe Ser Gly Gly Ala Asp Lys Ile Cys Val Trp Arg Arg Glu Gly
 85 90 95
- Lys Val His Thr Cys Val Ser Val Leu Thr Gly His Thr Gly Pro Val

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
Lys Cys Leu Ala Val Val Glu Pro Ser Gly Gly Glu Glu Glu Asp Gly
                           120
Gly Asp Gly Arg Leu Val Leu Tyr Ser Gly Ser Leu Asp Lys Ser Val
            135
Lys Val Trp Arg Val Pro Arg His
                  150
(2) INFORMATION FOR SEQ ID NO:976:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 118 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..118
          (D) OTHER INFORMATION: / Ceres Seq. ID 1595814
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:
Met Ala Val Tyr Ser Gly Ser Ser Asp Gly Ala Val Asn Phe Trp Glu
                                   10
Met Gly Glu Lys Lys Ile Leu Lys His Cys Glu Val Phe Lys Lys His
                                25
           20
Arg Leu Ala Val Leu Cys Ile Ala Ala Ala Gly Lys Leu Leu Phe Ser
                           40
Gly Gly Ala Asp Lys Lys Ile Cys Val Trp Arg Arg Glu Gly Lys Val
                        55
His Thr Cys Val Ser Val Leu Thr Gly His Thr Gly Pro Val Lys Cys
                                        75
                    70
Leu Ala Val Val Glu Pro Ser Gly Gly Glu Glu Asp Gly Gly Asp
                                   90
               85
Gly Arg Leu Val Leu Tyr Ser Gly Ser Leu Asp Lys Ser Val Lys Val
          100
                                105
Trp Arg Val Pro Arg His
        115
(2) INFORMATION FOR SEQ ID NO:977:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 102 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595815
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

Met Gly Glu Lys Lys Ile Leu Lys His Cys Glu Val Phe Lys Lys His

Arg Leu Ala Val Leu Cys Ile Ala Ala Ala Gly Lys Leu Leu Phe Ser 20 25 30

Gly Gly Ala Asp Lys Lys Ile Cys Val Trp Arg Arg Glu Gly Lys Val
35 40 45

His Thr Cys Val Ser Val Leu Thr Gly His Thr Gly Pro Val Lys Cys

Leu Ala Val Val Glu Pro Ser Gly Gly Glu Glu Glu Asp Gly Gly Asp 65 70 75 80

Gly Arg Leu Val Leu Tyr Ser Gly Ser Leu Asp Lys Ser Val Lys Val 85 90 95

Trp Arg Val Pro Arg His

100

(2) INFORMATION FOR SEQ ID NO:978:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..625
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595820
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

60 acaaatatca gaggaaataa atctaagaaa aaagaaagag tccagagttt gctccacttt tacctttgaa attttgtttc ctttttaatt tttgcgaaat ttcaggagtg tttctggtta 120 atgtgagaaa gtagattcgc aagaaaccaa aattaaaaaa gtgagcgatt cgtgttcgat 180 tgattttgtg gatgatccat tatctttctc caatattttt gatttgagcg agagttttgc 240 ttcattcgga atcttaagat gtcaggtccc gttcatcgat tcgcaatacc atgttttgag 300 360 ggaatattga gcagtgatga gaaaaaggaa agaaagtctg attttgagaa ctcagaagat gagaggagaa caagaatcgg ttctttgaag aagaaagcaa tcaatgcatc taccaagttc 420 aagcattctc aagaaaaaga gaagaaaaag tgatgtccgg gtcagttctg tctccattga 480 ggatgttcgt gatgttgagg agcttcaagc ggttgatgag tttagacaag cattggtaat 540 ggaggagttg cttccccata aacacgatga ctatcatatg atgttgaggt tcttgaaggc 600 taggaaattc gacattgaga aagct

- (2) INFORMATION FOR SEQ ID NO:979:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595821
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

Met Ser Gly Pro Val His Arg Phe Ala Ile Pro Cys Phe Glu Gly Ile
1 5 10 15

Leu Ser Ser Asp Glu Lys Lys Glu Arg Lys Ser Asp Phe Glu Asn Ser 20 25 30

Glu Asp Glu Arg Arg Thr Arg Ile Gly Ser Leu Lys Lys Lys Ala Ile
35 40 45

Asn Ala Ser Thr Lys Phe Lys His Ser Gln Glu Lys Glu Lys Lys 50 55 60

- (2) INFORMATION FOR SEQ ID NO:980:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..74
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595822
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

Met His Leu Pro Ser Ser Ser Ile Leu Lys Lys Arg Arg Lys Ser 10 15

Asp Val Arg Val Ser Ser Val Ser Ile Glu Asp Val Arg Asp Val Glu 20 25 30

Glu Leu Gln Ala Val Asp Glu Phe Arg Gln Ala Leu Val Met Glu Glu

Leu Leu Pro His Lys His Asp Asp Tyr His Met Met Leu Arg Phe Leu 50 55 60

Lys Ala Arg Lys Phe Asp Ile Glu Lys Ala 65 70

- (2) INFORMATION FOR SEQ ID NO:981:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..782
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595829
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981: aaaagaaaag atgttgtgta gaatggtggt ggtgactggc cggaaaaaga aacccggttc 60 ggttccggtt tatctgaatg tatacgatct cacacccatc aatggctacg cttactggtt 120 aggacttggg atctatcact ctggtgttga agttcatgga gttgaatatg gtttcggagc 180 tcacgatcat tcgactaccg ggatattcga ggtaaccgaa gcaatgtccg ggtttcacat 240 ttaggaagtc tatattgatt ggaagaactg atttagatcc tgaaaacgtt cgtgtcttta 300 tggagaaact tgcggaagaa tatagtggaa acagttatca tttgattact aagaattgca 360 atcacttttg caatgatgtt tgtgtgcaac tgactcgaag atcgatccct agttgggtta 420 acceptcttgc tcgctttggt ttgttttgca actgtgttct gccggcggag ttgaatgaga 480 ctaaggtgag gcaggtgaga tcaaaggaag agaagattcc ggaagtagag aagaagaaac 540 ttcggagtag atcaagtagg tttccacctg gtccttcgct ttcttcgtcg ggttctttaa 600 accgaagcag aagaggagaa aggagaagac aatgtettee tecateacca actgtgagtg 660 720 tttagctcta gtcctagtaa aattatacct ttttgtttcg caatttgatt ctgtagtaat gtttaagcta caagatatgg attgaacaaa cattttcttg atagtaatgg tataagattt 780
- (2) INFORMATION FOR SEQ ID NO:982:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595830
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Lys Glu Lys Met Leu Cys Arg Met Val Val Val Thr Gly Arg Lys Lys 1 5 10 15

Lys Pro Gly Ser Val Pro Val Tyr Leu Asn Val Tyr Asp Leu Thr Pro 20 25 30

Ile Asn Gly Tyr Ala Tyr Trp Leu Gly Leu Gly Ile Tyr His Ser Gly 35 40 45

Val Glu Val His Gly Val Glu Tyr Gly Phe Gly Ala His Asp His Ser 50 60

Thr Thr Gly Ile Phe Glu Val Thr Glu Ala Met Ser Gly Phe His Ile 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:983:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

60

- (ii) MOLECULE TYPE: peptide (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595831
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

Met Leu Cys Arg Met Val Val Val Thr Gly Arg Lys Lys Pro Gly 10

Ser Val Pro Val Tyr Leu Asn Val Tyr Asp Leu Thr Pro Ile Asn Gly 30 25 2.0

Tyr Ala Tyr Trp Leu Gly Leu Gly Ile Tyr His Ser Gly Val Glu Val 45 40

His Gly Val Glu Tyr Gly Phe Gly Ala His Asp His Ser Thr Thr Gly 55

- Ile Phe Glu Val Thr Glu Ala Met Ser Gly Phe His Ile 70
- (2) INFORMATION FOR SEQ ID NO:984:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..121
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595832
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

Met Glu Lys Leu Ala Glu Glu Tyr Ser Gly Asn Ser Tyr His Leu Ile 10

Thr Lys Asn Cys Asn His Phe Cys Asn Asp Val Cys Val Gln Leu Thr 30 20 25

Arg Arg Ser Ile Pro Ser Trp Val Asn Arg Leu Ala Arg Phe Gly Leu 40

Phe Cys Asn Cys Val Leu Pro Ala Glu Leu Asn Glu Thr Lys Val Arg 55

Gln Val Arg Ser Lys Glu Glu Lys Ile Pro Glu Val Glu Lys Lys 75 70

Leu Arg Ser Arg Ser Ser Arg Phe Pro Pro Gly Pro Ser Leu Ser Ser 85 90 Ser Gly Ser Leu Asn Arg Ser Arg Arg Gly Glu Arg Arg Arg Gln Cys

105 100 Leu Pro Pro Ser Pro Thr Val Ser Val

- (2) INFORMATION FOR SEQ ID NO:985:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

115

- (A) NAME/KEY: -
- (B) LOCATION: 1..1579
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595837
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

agctctgttg tggaacatcg gaaatcagaa ctgaaacaga aacagaaacc atggagaaga gagaagacga acaacaaaag cgcgacgatt ctagattcaa tcaaacactc aagaacgtcc 120 ctcctccata cccaatctct ccaacatatc aacggagctt atctgagaat gacgccggaa 240 gaaatgagct attcgaaagt cctgttgagg tggaggatca caattcaagc aagaaacatg 300

360 ataatacata tgctggtaag ctacgatcaa actctagtgc tgaaaggagt gtgaaagaag ttcaaaactt gaagataggt gttcgatcaa gtgactctgc tagagttatg aagttcaaca 420 480 aagtgctttc agaaacaact gtcatattag agaaactgcg cgagctagca tggaatggtg 540 taccacacta tatgcggcct gatgtctggc ggcttctctt gggatatgca ccacctaatt 600 cagatagaag ggaggctgtt ctgagaagaa aacgtcttga atatctggaa tctgttggcc 660 aattttatga ccttccagat tccgaacgtt ctgatgatga gatcaatatg cttcgccaga ttgctgttga ctgtccgagg actgtaccag atgtcagttt ctttcagcaa gaacaggtgc 720 780 agaaatcact ggagcgtatt ctttacacgt gggccattag acatccagca agcggatatg ttcagggaat aaatgacctg gtcacgccct tcctagtgat tttcttgtaa gaatatctag 840 900 atggcggtgt agacagttgg tcaatggatg atctatctgc tgaaaaagtc tcagatgtag 960 aagcggattg ctactggtgc ttaacaaagc tccttgacgg tatgcaagat cattacacgt ttgctcaacc tggaatccag agacttgtgt ttaagctgaa ggaactggtc aggcgtatcg 1020 atgaacctgt ttcaagacac atggaagagc atgggctaga gtttcttcaa tttgctttcc 1080 ggtggtataa ttgtcttctg attcgtgaga tcccattcaa tctcatcaat cgactatggg 1140 acacttatct tgctgaagga gatgcgttgc cagacttcct ggkgtatata tgctagcttt 1200 ctcttgacgt ggtctgatga gctgaagaag ctagattttc aagaaatggt aatgttcctg 1260 caacaccttc cgacacataa ctggtcagac caagagctcg aaatggtttt gtcaagagct 1320 1380 tacatgtggc atagtatgtt caataattcc ccaaaccatt tggctagctg aaatgacttt tectecatgg tgettgetge tgttttteee tttgttatat tatettette ttettgttgt 1440 ctaaatcagc tttcgttttg ttttgggtta tggtaaatgc taacattctt gtcttgttaa 1500 ttgttattag tttatgtatg gtttcacttg ttgaatctgt caccagtttg tgtgtttgta 1560 atatttgtag ctttcactg

- (2) INFORMATION FOR SEQ ID NO:986:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..275
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595838
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

Leu Cys Cys Gly Thr Ser Glu Ile Arg Thr Glu Thr Glu Thr Glu Thr 10 5 Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe 25 Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile 40 Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Pro Tyr Pro 60 55 Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg 75 70 Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser 90 85 Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser 110 105 Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg 125 120 Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu 135 140 Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val 160 155 150 Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Gly Tyr Ala 175 170 Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu 185 180 Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu

200 Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys

215 210 Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Glu Glu Val Gln 235 230 Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala 250 245 Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val 265 Ile Phe Leu 275 (2) INFORMATION FOR SEQ ID NO:987: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 259 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..259 (D) OTHER INFORMATION: / Ceres Seq. ID 1595839 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe 5 10 Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile 20 25 Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Pro Tyr Pro 40 Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg 55 Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser 70 75 Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser 90 85 Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg 100 105 Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu 115 120 125 Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val 135 140 Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Gly Tyr Ala 155 150 Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu 170 175 165 Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu 180 185 190

Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys

Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Gln Val Gln

Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala 225 230 235 240 Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val

215 220

250

200 205

(2) INFORMATION FOR SEQ ID NO:988:

Ile Phe Leu

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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Client Docket No. 80146.003
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..140
          (D) OTHER INFORMATION: / Ceres Seq. ID 1595840
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:
Met Lys Phe Asn Lys Val Leu Ser Glu Thr Thr Val Ile Leu Glu Lys
                                    10
Leu Arg Glu Leu Ala Trp Asn Gly Val Pro His Tyr Met Arg Pro Asp
                                25
            20
Val Trp Arg Leu Leu Gly Tyr Ala Pro Pro Asn Ser Asp Arg Arg
                            40
Glu Ala Val Leu Arg Arg Lys Arg Leu Glu Tyr Leu Glu Ser Val Gly
                        55
Gln Phe Tyr Asp Leu Pro Asp Ser Glu Arg Ser Asp Asp Glu Ile Asn
                    70
                                        75
Met Leu Arg Gln Ile Ala Val Asp Cys Pro Arg Thr Val Pro Asp Val
                                    90
Ser Phe Phe Gln Gln Glu Gln Val Gln Lys Ser Leu Glu Arg Ile Leu
                                105
Tyr Thr Trp Ala Ile Arg His Pro Ala Ser Gly Tyr Val Gln Gly Ile
                           120
                                                 125
Asn Asp Leu Val Thr Pro Phe Leu Val Ile Phe Leu
                                            140
                        135
    130
(2) INFORMATION FOR SEQ ID NO:989:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 764 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..764
          (D) OTHER INFORMATION: / Ceres Seq. ID 1595841
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:
acacggaaca agtaataaga acgaataact ttttttttt tgtttgacta gcaatgttac
                                                                        60
aatagagaat attatttett gagagaaett tgggaagatt acagagaaaa attgatggca
                                                                       1.20
acttcgaagc ttcaagctct ttggaatcat ccagctggac ctaagacaat tcatttttgg
                                                                       180
gegeegaegt teaagtgggg tataageatt geeaatateg eagaetttea aaaaceteea
                                                                       240
gagacacttt cataccctca acaaattgtg atcacaggta ctggacttgt ttggtcacgt
                                                                       300
tacagcactg taattactcc gaaaaactgg aatctcttta gcgtgagtct tggtatggct
                                                                       360
gtgtctctgg aatatttatt ggaagaccag tggtttttgc actagctgct gaaggagaag
                                                                       420
ccggagtcaa aaaggtgctt caaatgttgc gtgatgagtt cgagctaacc atggcactaa
                                                                       480
                                                                       540
gtgggtgccg gtcactcagt gaaatcaccc gtaaccacat tgtcacggaa tgggacactc
cacgccattt gcccaggtta tagagaagaa aaaaaaacag agaacagaaa caacacggca
                                                                       600
ccaaaacgta ttcatattct gattgatcac tttgcttcta ctctgctata tttatatctc
                                                                        660
gaaaaacttg tttctcccta tatcggatca caaaaacgtg cgtagagatt ctctgtaatg
                                                                       720
ctatttggct acattttacc tttccgttta ttcttattgc ttgt
 (2) INFORMATION FOR SEQ ID NO:990:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 96 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
```

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide(B) LOCATION: 1..96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

(D) OTHER INFORMATION: / Ceres Seq. ID 1595842

(ix) FEATURE:

Met Ala Thr Ser Lys Leu Gln Ala Leu Trp Asn His Pro Ala Gly Pro 10 Lys Thr Ile His Phe Trp Ala Pro Thr Phe Lys Trp Gly Ile Ser Ile 30 25 20 Ala Asn Ile Ala Asp Phe Gln Lys Pro Pro Glu Thr Leu Ser Tyr Pro 4.0 Gln Gln Ile Val Ile Thr Gly Thr Gly Leu Val Trp Ser Arg Tyr Ser 60 Thr Val Ile Thr Pro Lys Asn Trp Asn Leu Phe Ser Val Ser Leu Gly 70 75 Met Ala Val Ser Leu Glu Tyr Leu Leu Glu Asp Gln Trp Phe Leu His 85 90

(2) INFORMATION FOR SEQ ID NO:991:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 741 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..741
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595847
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:991: acatcaacac gccctaaaac cgctctcgag agacgaatcg ctctcagctt cttctagaac 60 cttctccttc tccttcgacg catcgtcgcc ttcaagatca cactacctcg cacaacaatg 120 gagttctggg gtgttgaagt taagaatggc aaaccacttc acctagatcc tgggctagac 180 aggctcgtgc acatctctca ggttgctttg ggagagagta agaacaatgt aaccgaacca 240 atccagcttt acgtgactgt tggatcggat aagcttctca ttggaacgct atctcatgag 300 aagtttcctc agctgtctac ggagattgtc ttggaaagga actttgcgct gtctcatact 360 tggaagaatg ggagcgtttt cttctctggt tacaaagttg atgcatctga tcccgagcct 420 gaggatttga ttgatgatca acttgaggct gctggtttca aagctgctcc gaaatctgct 480 gcgaaacagg tgaactttca gttgccaaat gaagatgtca aagccaagca agatgatgac 540 gctgacggta gtgaagaaga ttcttcagat gatgatgata gtgaaaactc tggagacgag 600 gaggaagaga aggttactgc tgaatctgac agtgaggaag atgactcatc agacgacgaa 660 720 qaaqatgact cctcagaaga ggaaacccca aagaagcctg aagaacccaa gaagaggtct gcagaaccca actectecaa q
- (2) INFORMATION FOR SEQ ID NO:992:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..208
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595848
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992: Met Glu Phe Trp Gly Val Glu Val Lys Asn Gly Lys Pro Leu His Leu 10 Asp Pro Gly Leu Asp Arg Leu Val His Ile Ser Gln Val Ala Leu Gly 2.5
- Glu Ser Lys Asn Asn Val Thr Glu Pro Ile Gln Leu Tyr Val Thr Val 45
- Gly Ser Asp Lys Leu Leu Ile Gly Thr Leu Ser His Glu Lys Phe Pro 55
- Gln Leu Ser Thr Glu Ile Val Leu Glu Arg Asn Phe Ala Leu Ser His 75 70

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Thr Trp Lys Asn Gly Ser Val Phe Phe Ser Gly Tyr Lys Val Asp Ala
                                   90
                8.5
Ser Asp Pro Glu Pro Glu Asp Leu Ile Asp Asp Gln Leu Glu Ala Ala
                               105
                                                   110
            100
Gly Phe Lys Ala Ala Pro Lys Ser Ala Ala Lys Gln Val Asn Phe Gln
                           120
       115
Leu Pro Asn Glu Asp Val Lys Ala Lys Gln Asp Asp Asp Ala Asp Gly
                                           140
                       135
Ser Glu Glu Asp Ser Ser Asp Asp Asp Ser Glu Asn Ser Gly Asp
                                       155
                   150
Glu Glu Glu Lys Val Thr Ala Glu Ser Asp Ser Glu Glu Asp Asp
                                   170
               165
Ser Ser Asp Asp Glu Glu Asp Asp Ser Ser Glu Glu Glu Thr Pro Lys
                               185
            180
Lys Pro Glu Glu Pro Lys Lys Arg Ser Ala Glu Pro Asn Ser Ser Lys
                           200
```

- (2) INFORMATION FOR SEQ ID NO:993:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595853
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:993: 60 gattggatcg gggaatttgg gaaaagtatg gagaagaaga cgaaagtgct aattgtggga ggtactggat acttgggtca gcatcttctt caagctttcg ccggcaacta agcggtgaat 120 gtgagctata cgacgtcgct ttcactcacc attcttctcc acttcccgct cgtttgctcg acgetttece teattecece gegttteetg tegatettaa ateeggteta gggeteaatt 240 ccatatccca ggactttcgt cagcctgatg tggtcgtgaa ttgtgctgct ctgtctgtcc cacgagettg egageaagat ecagatteeg ecatgteeat caaegtaeet acttetettg 360 taaactggtt atcaagtttt gagactaaca aaaccttgtt gattcatctc tctactgatc 420 aagtttatca aggtgtcaag totttctaca aggaagaaga tgagactgtt gcagtcaacg 480 tttatgggaa atcaaaagtt gcagcagagc ttctcatcaa ggataagtgt caaagctttg 540 600 caatattgag aagtagtatc atctttggtc ctcaaactgt atcacctctc cccaagactc 660 toccaattoa gtggattgat agotoottaa agaaagggga cacggtagac ttottocatg 720 acgagtttcg ttgccccatt tacgttaagg atcttgtgaa tatcactttc aaattaatag 780 acagatgggt ctctgatgat aaacagatgc ggctagttct gaatgctggt ggacccgaga 840 ggctatctcg tgttcaaatg gctcaaatgg ttgcagaagt cagaggatac gacctgtcct tgattaaaca tgtgtctgca tcatcgattg atcgtggcgt agtgtcacca gcagatatat 900 ctatggacat aactaaactg attcatacac ttgagctctc tccaacttct ttcaaggaag 960 gtgttaggtt aacgettgae tetgaatete atteteatat geteecatga tagtatteee 1020 ttatgtgctc ttctttacca ctctgcttct ttctatggag aaaaatctcg gtttgagaaa 1080 accaatgtaa aacggttgat atggtttcgg aattaaggtt tggttttc
- (2) INFORMATION FOR SEQ ID NO:994:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..335
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595854
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

Leu Asp Arg Gly Ile Trp Glu Lys Tyr Gly Glu Glu Asp Glu Ser Ala 10 Asn Cys Gly Arg Tyr Trp Ile Leu Gly Ser Ala Ser Ser Ser Phe Arg Arg Gln Leu Ser Gly Glu Cys Glu Leu Tyr Asp Val Ala Phe Thr 40 His His Ser Ser Pro Leu Pro Ala Arg Leu Leu Asp Ala Phe Pro His 55 Ser Pro Ala Phe Pro Val Asp Leu Lys Ser Gly Leu Gly Leu Asn Ser 7.0 Ile Ser Gln Asp Phe Arg Gln Pro Asp Val Val Val Asn Cys Ala Ala 90 85 Leu Ser Val Pro Arg Ala Cys Glu Gln Asp Pro Asp Ser Ala Met Ser 105 100 Ile Asn Val Pro Thr Ser Leu Val Asn Trp Leu Ser Ser Phe Glu Thr 120 Asn Lys Thr Leu Leu Ile His Leu Ser Thr Asp Gln Val Tyr Gln Gly 140 135 Val Lys Ser Phe Tyr Lys Glu Glu Asp Glu Thr Val Ala Val Asn Val 150 155 Tyr Gly Lys Ser Lys Val Ala Ala Glu Leu Leu Ile Lys Asp Lys Cys 165 170 Gln Ser Phe Ala Ile Leu Arg Ser Ser Ile Ile Phe Gly Pro Gln Thr 180 185 Val Ser Pro Leu Pro Lys Thr Leu Pro Ile Gln Trp Ile Asp Ser Ser 200 Leu Lys Lys Gly Asp Thr Val Asp Phe Phe His Asp Glu Phe Arg Cys 220 215 Pro Ile Tyr Val Lys Asp Leu Val Asn Ile Thr Phe Lys Leu Ile Asp 235 230 Arg Trp Val Ser Asp Asp Lys Gln Met Arg Leu Val Leu Asn Ala Gly 250 245 Gly Pro Glu Arg Leu Ser Arg Val Gln Met Ala Gln Met Val Ala Glu 265 260 Val Arg Gly Tyr Asp Leu Ser Leu Ile Lys His Val Ser Ala Ser Ser 285 280 Ile Asp Arg Gly Val Val Ser Pro Ala Asp Ile Ser Met Asp Ile Thr 290 295 300 Lys Leu Ile His Thr Leu Glu Leu Ser Pro Thr Ser Phe Lys Glu Gly 305 310 315 320 Val Arg Leu Thr Leu Asp Ser Glu Ser His Ser His Met Leu Pro

- 325
 (2) INFORMATION FOR SEQ ID NO:995:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..225
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595855

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:
- Met Ser Ile Asn Val Pro Thr Ser Leu Val Asn Trp Leu Ser Ser Phe 1 5 10 15
- Glu Thr Asn Lys Thr Leu Leu Ile His Leu Ser Thr Asp Gln Val Tyr 20 25 30
- Gln Gly Val Lys Ser Phe Tyr Lys Glu Glu Asp Glu Thr Val Ala Val
- Asn Val Tyr Gly Lys Ser Lys Val Ala Ala Glu Leu Leu Ile Lys Asp

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55
                                             60
    50
Lys Cys Gln Ser Phe Ala Ile Leu Arg Ser Ser Ile Ile Phe Gly Pro
                                        75
                    70
Gln Thr Val Ser Pro Leu Pro Lys Thr Leu Pro Ile Gln Trp Ile Asp
                                    90
                85
Ser Ser Leu Lys Lys Gly Asp Thr Val Asp Phe Phe His Asp Glu Phe
                                                    110
                                105
            100
Arg Cys Pro Ile Tyr Val Lys Asp Leu Val Asn Ile Thr Phe Lys Leu
                                                125
                            120
Ile Asp Arg Trp Val Ser Asp Asp Lys Gln Met Arg Leu Val Leu Asn
                        135
Ala Gly Gly Pro Glu Arg Leu Ser Arg Val Gln Met Ala Gln Met Val
                                        155
                    150
Ala Glu Val Arg Gly Tyr Asp Leu Ser Leu Ile Lys His Val Ser Ala
                                                         175
                                    170
                165
Ser Ser Ile Asp Arg Gly Val Val Ser Pro Ala Asp Ile Ser Met Asp
                                185
            180
Ile Thr Lys Leu Ile His Thr Leu Glu Leu Ser Pro Thr Ser Phe Lys
                                                 205
                             200
        195
Glu Gly Val Arg Leu Thr Leu Asp Ser Glu Ser His Ser His Met Leu
                        215
    210
Pro
225
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- (2) INFORMATION FOR SEQ ID NO:996:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..735
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595856
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996: 60 atgeettett eteatttete accaacteee tecaaaceea acaaaagtgt ttatattage aaagccgcca aagtgtaaac ghaagtttat aaatttcatt tctgtgatct tacgtaattg 120 gaggaagatc aaaattttca atccccattc ttcgattgct tcaattgaag tttctccgat 180 ggcgcaagtt agcagaatct gcaatggtgt gcagaaccca tctcttatct ccaatctctc 240 gaaatccagt caacgcaaat ctcccttatc ggtttctctg aagacgcage agcatccacg 300 360 agcttatccg atttcgtcgt cgtggggatt gaagaaAgag tgggatgGac gttaattggc tetgacette gteetettaa ggteatgtet tetgttteea eggeggagaa agegteggag 420 attgtacttc aacccattag agaaatctcc ggtcttatta agcttcctgg ctccaagtct 480 ctatcaaatc ggatcctgct tctcgctgct ctatctgagg gaacaactgt agtggacaac 540 ttgttgaata gcgatgacat caattacatg cttgatgcgt tgaagagatt gggacttaat 600 gtggaaactg acagtgaaaa taatcgtgct gwagttgaag gatgtggcgg gatattccca 660 gcttccatag attcaaagag tgatatcgaa ctttacctcg gtaatgcagg aacagcaatg 720 cgtccactta ccgct
- (2) INFORMATION FOR SEQ ID NO:997:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..117
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595857
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:
- Cys Leu Leu Leu Ile Ser His Gln Leu Pro Pro Asn Pro Thr Lys Val

10 Phe Ile Leu Ala Lys Pro Pro Lys Cys Lys Xaa Lys Phe Ile Asn Phe 25 Ile Ser Val Ile Leu Arg Asn Trp Arg Lys Ile Lys Ile Phe Asn Pro 40 His Ser Ser Ile Ala Ser Ile Glu Val Ser Pro Met Ala Gln Val Ser 55 Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser 70 75 Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln 85 90 Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys 100 105 Glu Trp Asp Gly Arg 115 (2) INFORMATION FOR SEQ ID NO:998: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..58 (D) OTHER INFORMATION: / Ceres Seq. ID 1595858 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:998: Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu 10 Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val 25 Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Glu Trp Asp Gly Arg 50 55 (2) INFORMATION FOR SEQ ID NO:999: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..117 (D) OTHER INFORMATION: / Ceres Seq. ID 1595859 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:999: Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln 10 Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser 25 20 Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr 40 Val Val Asp Asn Leu Leu Asn Ser Asp Asp Ile Asn Tyr Met Leu Asp 55 Ala Leu Lys Arg Leu Gly Leu Asn Val Glu Thr Asp Ser Glu Asn Asn 70 75 Arg Ala Xaa Val Glu Gly Cys Gly Gly Ile Phe Pro Ala Ser Ile Asp 90

Ser Lys Ser Asp Ile Glu Leu Tyr Leu Gly Asn Ala Gly Thr Ala Met 100 105 110

Arg Pro Leu Thr Ala 115

- (2) INFORMATION FOR SEQ ID NO:1000:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 985 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..985
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595906
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

tctaatattc aatagttaca agacacttga tgggagagga gctaatgttc acattgttgg 60 120 tggtggctgc atcactcttc aatatgtctc caatatcatc attcacaaca tccatatcca ccattgttac caatccggga atactaacgt gcggtcaagt ccaacgcact atgggttcag 180 aacgaaatcg gacggtgatg gtatctctat attcggatca aaggacattt ggatcgacca 240 ttgttctcta tcgagatgca aggacggtct gatagatgcg gtaatgggtt ccacaggaat 300 aactatatcg aacaacttct tctctcacca taatgaagtc atgcttcttg gtcacagega 360 ccactatgaa ccagacagtg gcatgcaggt aacaattgcg tttaatcact ttggagagaa 420 attgatacaa aggatgccga ggtgtcgacg tggatacatc catgtggtta ataacgattt 480 540 tactcaatgg gaaatgtatg ccattggcgg tagcggtaac ccgactatta acagtcaggg 600 taaccqctac accqccccaa ccaacccqtt tqccaaqqaq qtqacaaaqa qaqtqqaaac 660 accggatggt gattggaaag ggtggaattg gagatcggag ggggacattt tggtgaatgg 720 agcettette qtggcateeq qqgaagqtge gqaaatgagg tatgagaagg catatagegt cgagectaaa teegeeteat teateaceea aateacattt caetetggtg ttettggegt 780 tggtggcagg aataacaatc tggggatgtg gactactact ggatcggaag gtactagegg 840 900 tttagattct tataatgact ataccgatga aatgtctggc gctggttcaa ccaaccggtt atctttttca gttcttgttt tcttgctaag ttcgatatca tatttggtcg tgttcacttc 960 ttcaacccaa atgtttatgt tgtaa

- (2) INFORMATION FOR SEQ ID NO:1001:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..327
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595907
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:
- Leu Ile Phe Asn Ser Tyr Lys Thr Leu Asp Gly Arg Gly Ala Asn Val 1 5 10 15
- His Ile Val Gly Gly Gly Cys Ile Thr Leu Gln Tyr Val Ser Asn Ile 20 25 30
- Ile Ile His Asn Ile His Ile His His Cys Tyr Gln Ser Gly Asn Thr 35 40 45
- Asn Val Arg Ser Ser Pro Thr His Tyr Gly Phe Arg Thr Lys Ser Asp 50 55 60
- Gly Asp Gly Ile Ser Ile Phe Gly Ser Lys Asp Ile Trp Ile Asp His 65 70 75 80
- Cys Ser Leu Ser Arg Cys Lys Asp Gly Leu Ile Asp Ala Val Met Gly
 85 90 95
- Ser Thr Gly Ile Thr Ile Ser Asn Asn Phe Phe Ser His His Asn Glu 100 105 110
- Val Met Leu Gly His Ser Asp His Tyr Glu Pro Asp Ser Gly Met 115 120 125
- Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Lys Leu Ile Gln Arg 130 135 140

Met Pro Arg Cys Arg Arg Gly Tyr Ile His Val Val Asn Asn Asp Phe 150 155 Thr Gln Trp Glu Met Tyr Ala Ile Gly Gly Ser Gly Asn Pro Thr Ile 170 165 Asn Ser Gln Gly Asn Arg Tyr Thr Ala Pro Thr Asn Pro Phe Ala Lys 180 185 Glu Val Thr Lys Arg Val Glu Thr Pro Asp Gly Asp Trp Lys Gly Trp 200 Asn Trp Arg Ser Glu Gly Asp Ile Leu Val Asn Gly Ala Phe Phe Val 215 220 Ala Ser Gly Glu Gly Ala Glu Met Arg Tyr Glu Lys Ala Tyr Ser Val 230 235 Glu Pro Lys Ser Ala Ser Phe Ile Thr Gln Ile Thr Phe His Ser Gly 245 250 Val Leu Gly Val Gly Gly Arg Asn Asn Leu Gly Met Trp Thr Thr 260 265 Thr Gly Ser Glu Gly Thr Ser Gly Leu Asp Ser Tyr Asn Asp Tyr Thr 280 Asp Glu Met Ser Gly Ala Gly Ser Thr Asn Arg Leu Ser Phe Ser Val 295 300 Leu Val Phe Leu Leu Ser Ser Ile Ser Tyr Leu Val Val Phe Thr Ser 315 310 Ser Thr Gln Met Phe Met Leu

325
(2) INFORMATION FOR SEQ ID NO:1002:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..233
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595908
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002: Met Gly Ser Thr Gly Ile Thr Ile Ser Asn Asn Phe Phe Ser His His

1 5 10 15 Asn Glu Val Met Leu Leu Gly His Ser Asp His Tyr Glu Pro Asp Ser 20 25 30

Gly Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Lys Leu Ile 35 40 45

Gln Arg Met Pro Arg Cys Arg Arg Gly Tyr Ile His Val Val Asn Asn
50
55
60

Asp Phe Thr Gln Trp Glu Met Tyr Ala Ile Gly Gly Ser Gly Asn Pro 65 70 75 80

Thr Ile Asn Ser Gln Gly Asn Arg Tyr Thr Ala Pro Thr Asn Pro Phe 85 90 95

Ala Lys Glu Val Thr Lys Arg Val Glu Thr Pro Asp Gly Asp Trp Lys 100 105 110

Gly Trp Asn Trp Arg Ser Glu Gly Asp Ile Leu Val Asn Gly Ala Phe 115 120 125

Phe Val Ala Ser Gly Glu Gly Ala Glu Met Arg Tyr Glu Lys Ala Tyr 130 135 140

Ser Val Glu Pro Lys Ser Ala Ser Phe Ile Thr Gln Ile Thr Phe His

145 150 155 160 Ser Gly Val Leu Gly Val Gly Gly Arg Asn Asn Leu Gly Met Trp

165 170 175

Thr Thr Thr Gly Ser Glu Gly Thr Ser Gly Leu Asp Ser Tyr Asn Asp 180 185 190 Tyr Thr Asp Glu Met Ser Gly Ala Gly Ser Thr Asn Arg Leu Ser Phe

60 120

180

240

```
200
       195
                                              205
Ser Val Leu Val Phe Leu Leu Ser Ser Ile Ser Tyr Leu Val Val Phe
                215 220
Thr Ser Ser Thr Gln Met Phe Met Leu
225
                  230
(2) INFORMATION FOR SEQ ID NO:1003:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 214 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..214
         (D) OTHER INFORMATION: / Ceres Seq. ID 1595909
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:
Met Leu Leu Gly His Ser Asp His Tyr Glu Pro Asp Ser Gly Met Gln
                                  10
Val Thr Ile Ala Phe Asn His Phe Gly Glu Lys Leu Ile Gln Arg Met
                               25
Pro Arg Cys Arg Arg Gly Tyr Ile His Val Val Asn Asn Asp Phe Thr
                          40
Gln Trp Glu Met Tyr Ala Ile Gly Gly Ser Gly Asn Pro Thr Ile Asn
Ser Gln Gly Asn Arg Tyr Thr Ala Pro Thr Asn Pro Phe Ala Lys Glu
                   70
                                      75
Val Thr Lys Arg Val Glu Thr Pro Asp Gly Asp Trp Lys Gly Trp Asn
               85
                                  90
Trp Arg Ser Glu Gly Asp Ile Leu Val Asn Gly Ala Phe Phe Val Ala
                                                 110
           100
                              105
Ser Gly Glu Gly Ala Glu Met Arg Tyr Glu Lys Ala Tyr Ser Val Glu
       115
                          120
                                              125
Pro Lys Ser Ala Ser Phe Ile Thr Gln Ile Thr Phe His Ser Gly Val
                      135
                                          140
Leu Gly Val Gly Gly Arg Asn Asn Leu Gly Met Trp Thr Thr Thr
                   150 155
Gly Ser Glu Gly Thr Ser Gly Leu Asp Ser Tyr Asn Asp Tyr Thr Asp
                                 170 175
               165
Glu Met Ser Gly Ala Gly Ser Thr Asn Arg Leu Ser Phe Ser Val Leu
                              185
          180
Val Phe Leu Leu Ser Ser Ile Ser Tyr Leu Val Val Phe Thr Ser Ser
       195
                          200
Thr Gln Met Phe Met Leu
   210
(2) INFORMATION FOR SEQ ID NO:1004:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 561 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..561
         (D) OTHER INFORMATION: / Ceres Seq. ID 1595931
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:
atggctgaca aatgttggtg gtacctcaga cctatgttga aatccgggcc tcatggaaga
aacatagtct accgaccgga tgtcctgaaa gatgcaaata ttttcagcat gtgcgacgat
cccgatgact tctacgcggc tggccacgat ccaaatgaca tcaactctga atgtcgctat
```

agaccettet teaaacggtg ettagagget gagegaattg teeetaggta egeegetgea

accettgeet gegeaattet ttacatatgt gtegttaatg etcacatggg tggtgtetae 300 ttteggetet teggaageaa ecattatget ttagaategg aggatacaeg tgacatttgt 360 gaggaggtge tagaagaata aaagaaatat ggtaataett taaaatatae atacgetaaa 420 agettttegt accetgaatg tggtgacatt egtactettg attgegegat gatgtgttae 480 atgagategg gaetetteaa taatetttge aaegaatgtt acatetggtg gtgtgeeaaa 540 eggattagee agattetgta g

- (2) INFORMATION FOR SEQ ID NO:1005:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..186
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595932
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

Met Ala Asp Lys Cys Trp Trp Tyr Leu Arg Pro Met Leu Lys Ser Gly
1 5 10 15

Pro His Gly Arg Asn Ile Val Tyr Arg Pro Asp Val Leu Lys Asp Ala 20 25 30

Asn Ile Phe Ser Met Cys Asp Asp Pro Asp Asp Phe Tyr Ala Ala Gly $35 \hspace{1cm} 40 \hspace{1cm} 45$

His Asp Pro Asn Asp Ile Asn Ser Glu Cys Arg Tyr Arg Pro Phe Phe 50 55 60

Lys Arg Cys Leu Glu Ala Glu Arg Ile Val Pro Arg Tyr Ala Ala Ala 65 70 75 80

Thr Leu Ala Cys Ala Ile Leu Tyr Ile Cys Val Val Asn Ala His Met 85 90 95

Gly Gly Val Tyr Phe Arg Leu Phe Gly Ser Asn His Tyr Ala Leu Glu 100 105 110

Ser Glu Asp Thr Arg Asp Ile Cys Glu Glu Val Leu Glu Glu Ile Lys 115 120 125

Lys Tyr Gly Asn Thr Leu Lys Tyr Thr Tyr Ala Lys Ser Phe Ser Tyr 130 135 140

Pro Glu Cys Gly Asp Ile Arg Thr Leu Asp Cys Ala Met Met Cys Tyr 145 150 155 160

Met Arg Ser Gly Leu Phe Asn Asn Leu Cys Asn Glu Cys Tyr Ile Trp 165 170 175

Trp Cys Ala Lys Arg Ile Ser Gln Ile Leu 180 185

- (2) INFORMATION FOR SEQ ID NO:1006:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..175
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595934
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

Met Leu Lys Ser Gly Pro His Gly Arg Asn Ile Val Tyr Arg Pro Asp 1 10 15

Val Leu Lys Asp Ala Asn Ile Phe Ser Met Cys Asp Asp Pro Asp Asp 20 25 30

Phe Tyr Ala Ala Gly His Asp Pro Asn Asp Ile Asn Ser Glu Cys Arg 35 40 45

Tyr Arg Pro Phe Phe Lys Arg Cys Leu Glu Ala Glu Arg Ile Val Pro

```
50
                  5.5
Arg Tyr Ala Ala Ala Thr Leu Ala Cys Ala Ile Leu Tyr Ile Cys Val
              70 75
Val Asn Ala His Met Gly Gly Val Tyr Phe Arg Leu Phe Gly Ser Asn
                           90
            8.5
His Tyr Ala Leu Glu Ser Glu Asp Thr Arg Asp Ile Cys Glu Glu Val
        100
                        105
                                       110
Leu Glu Glu Ile Lys Lys Tyr Gly Asn Thr Leu Lys Tyr Thr Tyr Ala
                    120 125
     115
Lys Ser Phe Ser Tyr Pro Glu Cys Gly Asp Ile Arg Thr Leu Asp Cys
               135
Ala Met Met Cys Tyr Met Arg Ser Gly Leu Phe Asn Asn Leu Cys Asn
              150 155
Glu Cys Tyr Ile Trp Trp Cys Ala Lys Arg Ile Ser Gln Ile Leu
            165 170
```

- (2) INFORMATION FOR SEQ ID NO:1007:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1305
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595943
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007: 60 atggcgaagc cttcaacatc tcagaagaaa tctcatagtg aagatgataa aaagcaaaga 120 qtatccaaca tttacataga ggccaagaaa catctgtctg agatgttaaa caatggagat cttgattcga agtcaacgag cagacaggtt caaagaagcc tagggagaat teteteettt 180 240 cctqaqtact tqtctcctct aaacagccca ggaagaagat gggaaaagag ctcaatagct 300 cacaagaagt ctgcttcagc ggatttcata aatcttgtga acatcaagaa agaaactcat 360 qeqaqccaac cagaggaaaa tgctgatatt caggtctgca atctaagcaa agaacctgat 420 gattctatcc aaccaatcgc aagtgaacct actgagaaaa gtgttgacat tgaagatgaa actgctaacg aagataaaat gtcttctgca ggttctgcag atgatgtgat gattcccaat 480 540 gagetagatg aaacctetet tgaagagage caaccaccac tgtcctcctc tgtggcctca 600 ccatcccact gqttnqctca aactqaqqaq tqcaaatcaq ctattactga tttcccggag tggtcaagcc caatatcagt tcttgagcca ctcttcgttg aagatgatat aagcccagca 660 aaaatgcgat ctcagtctgg tgaagcagag gtgcaaccgt ggtgtatcca cttcgatgaa 720 aaaqatcctg cacctacata ccgagagaat tctgtgacaa gtgacaaaga attggtgttt 780 aagtatgtaa aagctgtctt ggacgcagta gactcagaca tcgaagagct ctatctaaag 840 900 gegeaattet etgaeeaget tettgaaeea geaettatea geaatataee attetgteea 960 aaccagettt gteetgaeca tgageteete tttgaetgea teaatgaage teteatggag ttatqctqtt qcccaccttq qqcttcqttt qttacaccaa gaaccagagt cttctctacc 1020 qtcaaaaqcq tcatccatqa qqttcaaqaa qcqqtttact qgcatctctt gccattgcca 1080 ctccctcacg ccttggatca gatagttaga aaagatatgg ctagagctgg aaactggtta 1140 qacatcaqat qtqacattqa ctqcattqqc ttcqaaacta qtqaactqat tctcaacqaq 1200 ttactcqaaq agctcactct caactctctc aacaacactg agcactctct ggtttcacct 1260 qaqttgaaga cggatgggag catccttatt ctagaaaggt cttga
- (2) INFORMATION FOR SEQ ID NO:1008:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..434
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595944
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

Met Ala Lys Pro Ser Thr Ser Gln Lys Lys Ser His Ser Glu Asp Asp 10 Lys Lys Gln Arg Val Ser Asn Ile Tyr Ile Glu Ala Lys Lys His Leu 25 20 Ser Glu Met Leu Asn Asn Gly Asp Leu Asp Ser Lys Ser Thr Ser Arg 40 Gln Val Gln Arg Ser Leu Gly Arg Ile Leu Ser Phe Pro Glu Tyr Leu 55 Ser Pro Leu Asn Ser Pro Gly Arg Arg Trp Glu Lys Ser Ser Ile Ala 75 70 His Lys Lys Ser Ala Ser Ala Asp Phe Ile Asn Leu Val Asn Ile Lys 90 Lys Glu Thr His Ala Ser Gln Pro Glu Glu Asn Ala Asp Ile Gln Val 100 105 Cys Asn Leu Ser Lys Glu Pro Asp Asp Ser Ile Gln Pro Ile Ala Ser 120 125 115 Glu Pro Thr Glu Lys Ser Val Asp Ile Glu Asp Glu Thr Ala Asn Glu 135 140 Asp Lys Met Ser Ser Ala Gly Ser Ala Asp Asp Val Met Ile Pro Asn 150 155 Glu Leu Asp Glu Thr Ser Leu Glu Glu Ser Gln Pro Pro Leu Ser Ser 165 170 Ser Val Ala Ser Pro Ser His Trp Xaa Ala Gln Thr Glu Glu Cys Lys 190 180 185 Ser Ala Ile Thr Asp Phe Pro Glu Trp Ser Ser Pro Ile Ser Val Leu 200 195 Glu Pro Leu Phe Val Glu Asp Asp Ile Ser Pro Ala Lys Met Arg Ser 215 220 Gln Ser Gly Glu Ala Glu Val Gln Pro Trp Cys Ile His Phe Asp Glu 230 235 Lys Asp Pro Ala Pro Thr Tyr Arg Glu Asn Ser Val Thr Ser Asp Lys 250 Glu Leu Val Phe Lys Tyr Val Lys Ala Val Leu Asp Ala Val Asp Ser 265 Asp Ile Glu Glu Leu Tyr Leu Lys Ala Gln Phe Ser Asp Gln Leu Leu 280 Glu Pro Ala Leu Ile Ser Asn Ile Pro Phe Cys Pro Asn Gln Leu Cys 295 Pro Asp His Glu Leu Leu Phe Asp Cys Ile Asn Glu Ala Leu Met Glu 310 315 Leu Cys Cys Cys Pro Pro Trp Ala Ser Phe Val Thr Pro Arg Thr Arg 330 Val Phe Ser Thr Val Lys Ser Val Ile His Glu Val Gln Glu Ala Val 345 Tyr Trp His Leu Leu Pro Leu Pro Leu Pro His Ala Leu Asp Gln Ile 360 Val Arg Lys Asp Met Ala Arg Ala Gly Asn Trp Leu Asp Ile Arg Cys 375 380 Asp Ile Asp Cys Ile Gly Phe Glu Thr Ser Glu Leu Ile Leu Asn Glu 395 390 Leu Leu Glu Glu Leu Thr Leu Asn Ser Leu Asn Asn Thr Glu His Ser 405 410 Leu Val Ser Pro Glu Leu Lys Thr Asp Gly Ser Ile Leu Ile Leu Glu 420 425 Arg Ser

- (2) INFORMATION FOR SEQ ID NO:1009:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

- (B) LOCATION: 1..400
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595946
- Met Leu Asn Asn Gly Asp Leu Asp Ser Lys Ser Thr Ser Arg Gln Val 5 10 Gln Arg Ser Leu Gly Arg Ile Leu Ser Phe Pro Glu Tyr Leu Ser Pro 25 Leu Asn Ser Pro Gly Arg Arg Trp Glu Lys Ser Ser Ile Ala His Lys 35 40 45 Lys Ser Ala Ser Ala Asp Phe Ile Asn Leu Val Asn Ile Lys Lys Glu 55 Thr His Ala Ser Gln Pro Glu Glu Asn Ala Asp Ile Gln Val Cys Asn 70 75 Leu Ser Lys Glu Pro Asp Ser Ile Gln Pro Ile Ala Ser Glu Pro 90 Thr Glu Lys Ser Val Asp Ile Glu Asp Glu Thr Ala Asn Glu Asp Lys 100 105 Met Ser Ser Ala Gly Ser Ala Asp Asp Val Met Ile Pro Asn Glu Leu 120 125 Asp Glu Thr Ser Leu Glu Glu Ser Gln Pro Pro Leu Ser Ser Val 135 140 Ala Ser Pro Ser His Trp Xaa Ala Gln Thr Glu Glu Cys Lys Ser Ala 145 150 155 160 Ile Thr Asp Phe Pro Glu Trp Ser Ser Pro Ile Ser Val Leu Glu Pro 170 175 165 Leu Phe Val Glu Asp Asp Ile Ser Pro Ala Lys Met Arg Ser Gln Ser 185 180 190 Gly Glu Ala Glu Val Gln Pro Trp Cys Ile His Phe Asp Glu Lys Asp 195 200 205 Pro Ala Pro Thr Tyr Arg Glu Asn Ser Val Thr Ser Asp Lys Glu Leu 215 220 Val Phe Lys Tyr Val Lys Ala Val Leu Asp Ala Val Asp Ser Asp Ile 235 240 230 Glu Glu Leu Tyr Leu Lys Ala Gln Phe Ser Asp Gln Leu Leu Glu Pro 245 250 255 Ala Leu Ile Ser Asn Ile Pro Phe Cys Pro Asn Gln Leu Cys Pro Asp 260 265 270

Lys Asp Met Ala Arg Ala Gly Asn Trp Leu Asp Ile Arg Cys Asp Ile 340 345 350

Asp Cys Ile Gly Phe Glu Thr Ser Glu Leu Ile Leu Asn Glu Leu Leu 355 360 365

His Glu Leu Leu Phe Asp Cys Ile Asn Glu Ala Leu Met Glu Leu Cys 275 280 285 Cys Cys Pro Pro Trp Ala Ser Phe Val Thr Pro Arg Thr Arg Val Phe

Ser Thr Val Lys Ser Val Ile His Glu Val Gln Glu Ala Val Tyr Trp

His Leu Leu Pro Leu Pro Leu Pro His Ala Leu Asp Gln Ile Val Arg

310 315

330

290 295 300

- 355 360 365
 Glu Glu Leu Thr Leu Asn Ser Leu Asn Asn Thr Glu His Ser Leu Val
- Glu Glu Leu Thr Leu Asn Ser Leu Asn Asn Thr Glu His Ser Leu Va.

 370

 375

 380

 Ser Pro Glu Leu Lys Thr Asn Gly Ser Ile Leu Ile Leu Glu Arg Ser
- Ser Pro Glu Leu Lys Thr Asp Gly Ser Ile Leu Ile Leu Glu Arg Ser 385 390 395 400
- (2) INFORMATION FOR SEQ ID NO:1010:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..447
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

tttgggctag caagaacgtc gaatgagaca gagataatga ctgagtatgt tgtgacgaga 60 tggtaccgtg cacctgaatt gcttctcaac agctctgaat acacaggagc tattgacatt 120 tggtctgttg gttgcatttt catggagata cttagaagag agacgctttt ccctggataa cttagaagag agacgctttt ccctggataa ctcgactctt tgagaagcga taatgcgcgg aagtacgtaa aacaactccc acatgttcaa aacaactact tcagagaaaa gtttccaaac atttccccaa tggctctaga tcttgctgaa 360 aagatgctag ttttcgatcc ttcaaagcgc atcacaggtg cttatcacgt tgtttacta 420 ctttgttatg ctataaatgg aatgtga

- (2) INFORMATION FOR SEQ ID NO:1011:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595993
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

Phe Gly Leu Ala Arg Thr Ser Asn Glu Thr Glu Ile Met Thr Glu Tyr
1 10 15

Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Ser 20 25 30

Glu Tyr Thr Gly Ala Ile Asp Ile Trp Ser Val Gly Cys Ile Phe Met 35 40 45

Glu Ile Leu Arg Arg Glu Thr Leu Phe Pro Gly Lys Asp Tyr Val Gln 50 55 60

Gln Leu Lys Leu Ile Thr Glu Leu Leu Gly Ser Pro Asp Asp Ser Asp 65 70 75 80
Leu Asp Phe Leu Arg Ser Asp Asn Ala Arg Lys Tyr Val Lys Gln Leu

Pro His Val Gln Lys Gln Ser Phe Arg Glu Lys Phe Pro Asn Ile Ser

Pro Met Ala Leu Asp Leu Ala Glu Lys Met Leu Val Phe Asp Pro Ser

Lys Arg Ile Thr Gly Ala Tyr His Val Val Leu Leu Cys Tyr Ala 130 135 140

Ile Asn Gly Met

145

- (2) INFORMATION FOR SEQ ID NO:1012:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1595994

240

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:
Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
                                   10
                                                        15
                5
Leu Asn Ser Ser Glu Tyr Thr Gly Ala Ile Asp Ile Trp Ser Val Gly
Cys Ile Phe Met Glu Ile Leu Arg Arg Glu Thr Leu Phe Pro Gly Lys
                            40
Asp Tyr Val Gln Gln Leu Lys Leu Ile Thr Glu Leu Leu Gly Ser Pro
                        55
Asp Asp Ser Asp Leu Asp Phe Leu Arg Ser Asp Asn Ala Arg Lys Tyr
                    70
Val Lys Gln Leu Pro His Val Gln Lys Gln Ser Phe Arg Glu Lys Phe
                85
Pro Asn Ile Ser Pro Met Ala Leu Asp Leu Ala Glu Lys Met Leu Val
                                105
           100
Phe Asp Pro Ser Lys Arg Ile Thr Gly Ala Tyr His Val Val Leu Leu
                            120
        115
Leu Cys Tyr Ala Ile Asn Gly Met
    130
                       135
(2) INFORMATION FOR SEQ ID NO:1013:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 101 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
          (A) NAME/KEY: peptide
           (B) LOCATION: 1..101
           (D) OTHER INFORMATION: / Ceres Seq. ID 1595995
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:
Met Glu Ile Leu Arg Arg Glu Thr Leu Phe Pro Gly Lys Asp Tyr Val
                                     10
Gln Gln Leu Lys Leu Ile Thr Glu Leu Leu Gly Ser Pro Asp Asp Ser
                                 25
Asp Leu Asp Phe Leu Arg Ser Asp Asn Ala Arg Lys Tyr Val Lys Gln
                            40
Leu Pro His Val Gln Lys Gln Ser Phe Arg Glu Lys Phe Pro Asn Ile
                         55
 Ser Pro Met Ala Leu Asp Leu Ala Glu Lys Met Leu Val Phe Asp Pro
                                         75
                    70
 Ser Lys Arg Ile Thr Gly Ala Tyr His Val Val Leu Leu Cys Tyr
                                     90
                85
 Ala Ile Asn Gly Met
            100
 (2) INFORMATION FOR SEQ ID NO:1014:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 699 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..699
           (D) OTHER INFORMATION: / Ceres Seq. ID 1596012
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:
 tctccgacgg aagctctttt ccttctcaac ggcaaatgga tcctcgccta cacatcgttc
 gtgaatttgt tcccgttgct atcacgagga atcgtaccgt taataaaagt cgatgagatc
```

totcaaacca ttgattcaga taacttcacc gtccagaact ctgttcgttt cgctggtcct ttaggtacaa actcgattag caccaacgct aaattcgaaa tccgaagccc taaacgcgtc

cagattaagt ttgagcaagg cgtaattggg acgcctcagc taacggattc tattgagata 360 ccggaatatg tagaggttct tggtcaaaag attgatctta acccgatcag agggttactt accteggtge aagacacage etegtetgtg getagaacca tatcaageca accacegttg 420 aaattotott tgccggcgga caatgcgcag tottggctac tcacgactta totagacaaa 480 540 gacattcgga tctctagagg agacggtgga agtttactgt acttgatgta ctcagtcatt ggaaatggtt ctattagcat gagacaatca gccaatcagt ttgttagagg gtttgatgca 600 gagagcatga aagcatttga agagcttaga atcagagcca aaactgaaag tggaggagac 660 gataataatg ataacaatga agaagaatct gtaaactga

- (2) INFORMATION FOR SEQ ID NO:1015:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..232
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596013
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

Ser Pro Thr Glu Ala Leu Phe Leu Leu Asn Gly Lys Trp Ile Leu Ala 10

Tyr Thr Ser Phe Val Asn Leu Phe Pro Leu Leu Ser Arg Gly Ile Val 25 20

Pro Leu Ile Lys Val Asp Glu Ile Ser Gln Thr Ile Asp Ser Asp Asn 40

Phe Thr Val Gln Asn Ser Val Arg Phe Ala Gly Pro Leu Gly Thr Asn 55

Ser Ile Ser Thr Asn Ala Lys Phe Glu Ile Arg Ser Pro Lys Arg Val 70 75

Gln Ile Lys Phe Glu Gln Gly Val Ile Gly Thr Pro Gln Leu Thr Asp 90

Ser Ile Glu Ile Pro Glu Tyr Val Glu Val Leu Gly Gln Lys Ile Asp 105 110 100

Leu Asn Pro Ile Arg Gly Leu Leu Thr Ser Val Gln Asp Thr Ala Ser 125 115 120 Ser Val Ala Arg Thr Ile Ser Ser Gln Pro Pro Leu Lys Phe Ser Leu

135 140

Pro Ala Asp Asn Ala Gln Ser Trp Leu Leu Thr Thr Tyr Leu Asp Lys 155 150

Asp Ile Arg Ile Ser Arg Gly Asp Gly Gly Ser Leu Leu Tyr Leu Met 170 165

Tyr Ser Val Ile Gly Asn Gly Ser Ile Ser Met Arg Gln Ser Ala Asn 185 190 180 Gln Phe Val Arg Gly Phe Asp Ala Glu Ser Met Lys Ala Phe Glu Glu

205 200 195 Leu Arg Ile Arg Ala Lys Thr Glu Ser Gly Gly Asp Asp Asn Asn Asp

220

Asn Asn Glu Glu Glu Ser Val Asn

230 225

- (2) INFORMATION FOR SEQ ID NO:1016:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1969 base pairs

215

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1969
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016: totaaagato gaggaggoto gggaatocao aaaaccaato cotgatoogg taatatotat 60 ctqccttqac qacaaaaaac ccqaqcqatq cqtqqaaatc ggcagagatc taggagaaga 120 attaacaget gaacteacca catteeteag agaaaacgte aatatatteg cetggteece 180 agaagatctg cccggagtaa gtgttgacat cgtatcacac gagctcaaca tcgacccgac 240 300 ttttaaatct gttaagcaga agaggaggaa attgggtcga gagcgagcag aagccgtgaa 360 aqccqaaqta qaaaaattac taaggatcga ctccatcacc gaggcaaaat atcttgattg gctcgcgaac ccaatcgtag taaaaaagaa aaacggcaaa tggaaagtct gcgtagattt 420 480 caccqaccat aacaaagect gcccgaaaga cagtttccca ttaccgcaca tcgatcgcct cgtagaatca acttctgaaa acaagttgtt gtcattcatg gacgctttcg ctggttacaa 540 600 ccaqatcatq atqaaccccq acqatcaaga aaaaaatgca ttcgacacag aacaaggcat 660 cttctqttac cqaqtqatqc cattcqqact caaaaacqct ggggcgactt atcaacqctt 720 cqtcaacaaa atcttcacat tacaqatcaq qaaqacaatq qaagtttaca tcgaagacat 780 gttagtgaaa tccatggcag aggaagaaca catatcccat ttgcgcgaat gtttccaaca 840 gettaacete tacaacgtca aactcaatee agetaagtge egettegggg taagateegg 900 agagtteete gggtatetag teaegeacea eggeategag gtgaateega ageaaatega 960 cgcattgttg ggaatgacat cacctcagaa caagcgagaa gtgcagcgcc taacaggaag 1020 agttacggcc cttaactgtt tcatctctcg ctcaaccgac aaatgcttga ccttttacga tgtgcttcgg ggaaacaaga agttcgaatg gacgatccgg tgcgaagaag cttttcagga 1080 actcaagaaa tatctggcaa caccacccat cctcgcaaaa cccataatcg aagaaccact 1140 1200 atacttqtat gttgtcatat gggatactgc agtcagtgga gtgttagttc gagaagacaa 1260 aggtgaacag aaaccgattt tttacgtatc gcagactttc accagtgcgg aatcttgcta 1320 cccqcaaatq qaqaaactcq ctttqqcaqc cataatqtcq gctcqqaaac tqcqacccta 1380 ctttcaatcc aatttcatca tagtaatggg atccatgccg ctccgcgcta tcttacacag 1440 tecaagegaa teaggatgee tagetaaatg ggegategag eteagegaat atgaeateaa 1500 gtatoggaac aaaacatacg gotogtoato aaaacaaggo togggtgtag goatoogoot 1560 cacttegeea acageagagg teetegagea ateatttaga ttaaaettea aggetaceaa 1620 caatqtqqcc qaatacgaag cgctcgtagc aggacttaat ctggatcggg ggctaaagat agagaaaatc cgagctttta gcgaccccca acttgtcgca aatcagttca acagagaata 1680 1740 catagctcgg gacgaaagaa tggaagccta tctaactcat gtacaaaatc tgacgaagaa tttcgacgag ttcgagttaa caaggatccc tcgaggagaa aatacatcgg ctgacgccct 1800 agctgctcta gcctcgacat ctgacccgcg cctgagaaga gtcatcccag tagagttcat 1860 cgaaaagcca aatattgagc tcaacgaaga agaacatgtc ctccccatac aaatcggcac 1920 ggatcacaac gacgctccgg acgacagccc ggacgaattc aactcatag

- (2) INFORMATION FOR SEQ ID NO:1017:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..655
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596023
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

Leu Lys Ile Glu Glu Ala Arg Glu Ser Thr Lys Pro Ile Pro Asp Pro 1 5 10 15

Val Ile Ser Ile Cys Leu Asp Asp Lys Lys Pro Glu Arg Cys Val Glu
20 25 30

Ile Gly Arg Asp Leu Gly Glu Glu Leu Thr Ala Glu Leu Thr Thr Phe
35 40 45

Leu Arg Glu Asn Val Asn Ile Phe Ala Trp Ser Pro Glu Asp Leu Pro 50 55 60

Gly Val Ser Val Asp Ile Val Ser His Glu Leu Asn Ile Asp Pro Thr
65 70 75 80

Pho Luc Ser Val Luc Cla Luc Arg Arg Luc Leu Gly Arg Glu Arg Ala

Phe Lys Ser Val Lys Gln Lys Arg Arg Lys Leu Gly Arg Glu Arg Ala 85 90 95

Glu Ala Val Lys Ala Glu Val Glu Lys Leu Leu Arg Ile Asp Ser Ile 100 105 110 Thr Glu Ala Lys Tyr Leu Asp Trp Leu Ala Asn Pro Ile Val Val Lys

		115					120					125			
Lys	Lys 130		Gly	Lys	Trp	Lys 135		Cys	Val	Asp	Phe 140		Asp	His	Asn
Lys 145		Cys	Pro	Lys	Asp 150		Phe	Pro	Leu	Pro 155	His	Ile	Asp	Arg	Leu 160
Val	Glu	Ser	Thr	Ser 165	Glu	Asn	Lys	Leu	Leu 170	Ser	Phe	Met	Asp	Ala 175	Phe
Ala	Gly	Tyr	Asn 180	Gln	Ile	Met	Met	Asn 185	Pro	Asp	Asp	Gln	Glu 190	Lys	Asn
Ala	Phe	Asp 195	Thr	Glu	Gln	Gly	Ile 200	Phe	Cys	Tyr	Arg	Val 205	Met	Pro	Phe
Gly	Leu 210	Lys	Asn	Ala	Gly	Ala 215	Thr	Tyr	Gln	Arg	Phe 220	Val	Asn	Lys	Ile
Phe 225	Thr	Leu	Gln	Ile	Arg 230	Lys	Thr	Met	Glu	Val 235	Tyr	Ile	Glu	Asp	Met 240
Leu	Val	Lys	Ser	Met 245	Ala	Glu	Glu	Glu	His 250	Ile	Ser	His	Leu	Arg 255	Glu
			260					265					Pro 270		
-		275					280					285	Leu		
	290					295					300		Leu		
305					310	_	_			315	_		Thr	_	320
				325	-				330				Lys	335	
			340					345					Trp 350		
_	_	355					360					365	Ala -		
	370			_		375					380	_	Leu		
385					390					395			Glu		400
				405					410				Thr	415	
			420					425					Ala 430		
		435	_				440					445	Ile		
	450					455					460		Ser		
$46\bar{5}$	_			-	470					475		_	Asp		480
_				485					490				Ser	495	
_		_	500					505					Gln 510		
_		515		_			520					525	Glu		
	530					535					540		Lys		
545			-		550					555			Arg		560
		_	_	565					570				Val	575	
		_	580		_			585					Pro 590		
Glu	Asn	Thr 595	Ser	Ala	Asp	Ala	Leu 600	Ala	Ala	Leu	Ala	Ser 605	Thr	Ser	Asp

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Pro Arg Leu Arg Arg Val Ile Pro Val Glu Phe Ile Glu Lys Pro Asn
                                           620
                      615
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Ile Glu Leu Asn Glu Glu Glu His Val Leu Pro Ile Gln Ile Gly Thr 630 635

Asp His Asn Asp Ala Pro Asp Asp Ser Pro Asp Glu Phe Asn Ser 650 645

- (2) INFORMATION FOR SEQ ID NO:1018:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..483
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596024
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018: Met Asp Ala Phe Ala Gly Tyr Asn Gln Ile Met Met Asn Pro Asp Asp 10 Gln Glu Lys Asn Ala Phe Asp Thr Glu Gln Gly Ile Phe Cys Tyr Arg 25 Val Met Pro Phe Gly Leu Lys Asn Ala Gly Ala Thr Tyr Gln Arg Phe 40 Val Asn Lys Ile Phe Thr Leu Gln Ile Arg Lys Thr Met Glu Val Tyr 5.5 Ile Glu Asp Met Leu Val Lys Ser Met Ala Glu Glu Glu His Ile Ser 75 70 His Leu Arg Glu Cys Phe Gln Gln Leu Asn Leu Tyr Asn Val Lys Leu 90 85 Asn Pro Ala Lys Cys Arg Phe Gly Val Arg Ser Gly Glu Phe Leu Gly 105 100 Tyr Leu Val Thr His His Gly Ile Glu Val Asn Pro Lys Gln Ile Asp 120 Ala Leu Leu Gly Met Thr Ser Pro Gln Asn Lys Arg Glu Val Gln Arg 135 140 Leu Thr Gly Arg Val Thr Ala Leu Asn Cys Phe Ile Ser Arg Ser Thr 155 150 Asp Lys Cys Leu Thr Phe Tyr Asp Val Leu Arg Gly Asn Lys Lys Phe 170 165 Glu Trp Thr Ile Arg Cys Glu Glu Ala Phe Gln Glu Leu Lys Lys Tyr 185 Leu Ala Thr Pro Pro Ile Leu Ala Lys Pro Ile Ile Glu Glu Pro Leu 205 195 200 Tyr Leu Tyr Val Val Ile Trp Asp Thr Ala Val Ser Gly Val Leu Val 215 220 Arg Glu Asp Lys Gly Glu Gln Lys Pro Ile Phe Tyr Val Ser Gln Thr 230 235 Phe Thr Ser Ala Glu Ser Cys Tyr Pro Gln Met Glu Lys Leu Ala Leu 245 250 Ala Ala Ile Met Ser Ala Arg Lys Leu Arg Pro Tyr Phe Gln Ser Asn 260 265 Phe Ile Ile Val Met Gly Ser Met Pro Leu Arg Ala Ile Leu His Ser 280 285 Pro Ser Glu Ser Gly Cys Leu Ala Lys Trp Ala Ile Glu Leu Ser Glu 300 295 Tyr Asp Ile Lys Tyr Arg Asn Lys Thr Tyr Gly Ser Ser Ser Lys Gln 315 310 Gly Ser Gly Val Gly Ile Arg Leu Thr Ser Pro Thr Ala Glu Val Leu 330 325

Glu Gln Ser Phe Arg Leu Asn Phe Lys Ala Thr Asn Asn Val Ala Glu

345 353 340 Tyr Glu Ala Leu Val Ala Gly Leu Asn Leu Asp Arg Gly Leu Lys The 355 360 365 Glu Lys Ile Arg Ala Phe Ser Asp Pro Gln Leu Val Ala Asn Gln Phe 375 Asn Arg Glu Tyr Ile Ala Arg Asp Glu Arg Met Glu Ala Tyr Leu Thr 395 400 390 His Val Gln Asn Leu Thr Lys Asn Phe Asp Glu Phe Glu Leu Thr Arg 410 415 Ile Pro Arg Gly Glu Asn Thr Ser Ala Asp Ala Leu Ala Ala Leu Ala 425 420 Ser Thr Ser Asp Pro Arg Leu Arg Arg Val Ile Pro Val Glu Phe Ile 440 435 Glu Lys Pro Asn Ile Glu Ieu Asn Glu Glu Glu His Val Leu Pro Ile 450 455 Gln Ile Gly Thr Asp His Asn Asp Ala Pro Asp Asp Ser Pro Asp Glu 470 475

- (2) INFORMATION FOR SEQ ID NO:1019:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

Phe Asn Ser

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596025
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:
- Met Met Asn Pro Asp Asp Gln Glu Lys Asn Ala Phe Asp Thr Glu Gln 1 5 10
- Gly Ile Phe Cys Tyr Arg Val Met Pro Phe Gly Leu Lys Asn Ala Gly 20 25
- Ala Thr Tyr Gln Arg Phe Val Asn Lys Ile Phe Thr Leu Gln Ile Arg 4.0
- Lys Thr Met Glu Val Tyr Ile Glu Asp Met Leu Val Lys Ser Met Ala 60 55
- Glu Glu Glu His Ile Ser His Leu Arg Glu Cys Phe Gln Gln Leu Asn 75 70
- Leu Tyr Asn Val Lys Leu Asn Pro Ala Lys Cys Arg Phe Gly Val Arg 85 90
- Ser Gly Glu Phe Leu Gly Tyr Leu Val Thr His His Gly Ile Glu Val 105 100
- Asn Pro Lys Gln Ile Asp Ala Leu Leu Gly Met Thr Ser Pro Gln Asn 125 115 120
- Lys Arg Glu Val Gln Arg Leu Thr Gly Arg Val Thr Ala Leu Asn Cys 135 140
- Phe Ile Ser Arg Ser Thr Asp Lys Cys Leu Thr Phe Tyr Asp Val Leu 150 155
- Arg Gly Asn Lys Lys Phe Glu Trp Thr Ile Arg Cys Glu Glu Ala Phe 170 165
- Gln Glu Leu Lys Lys Tyr Leu Ala Thr Pro Pro Ile Leu Ala Lys Pro 180 185
- Ile Ile Glu Glu Pro Leu Tyr Leu Tyr Val Val Ile Trp Asp Thr Ala 205 195 200
- Val Ser Gly Val Leu Val Arg Glu Asp Lys Gly Glu Gln Lys Pro Ile 210 215 220
- Phe Tyr Val Ser Gln Thr Phe Thr Ser Ala Glu Ser Cys Tyr Pro Gln 230 235

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Met Glu Lys Leu Ala Leu Ala Ala Ile Met Ser Ala Arg Lys Leu Arg
                                   250
Pro Tyr Phe Gln Ser Asn Phe Ile Ile Val Met Gly Ser Met Pro Leu
                                                   270
                              265
Arg Ala Ile Leu His Ser Pro Ser Glu Ser Gly Cys Leu Ala Lys Trp
                          280
                                               285
Ala Ile Glu Leu Ser Glu Tyr Asp Ile Lys Tyr Arg Asn Lys Thr Tyr
                                         300
                       295
Gly Ser Ser Ser Lys Gln Gly Ser Gly Val Gly Ile Arg Leu Thr Ser
                                       315
                   310
Pro Thr Ala Glu Val Leu Glu Gln Ser Phe Arg Leu Asn Phe Lys Ala
                                   330
                                                      335
               325
Thr Asn Asn Val Ala Glu Tyr Glu Ala Leu Val Ala Gly Leu Asn Leu
           340
                               345
Asp Arg Gly Leu Lys Ile Glu Lys Ile Arg Ala Phe Ser Asp Pro Gln
                                               365
                           360
Leu Val Ala Asn Gln Phe Asn Arg Glu Tyr Ile Ala Arg Asp Glu Arg
                                           380
                       375
Met Glu Ala Tyr Leu Thr His Val Gln Asn Leu Thr Lys Asn Phe Asp
                   390
                                       395
Glu Phe Glu Leu Thr Arg Ile Pro Arg Gly Glu Asn Thr Ser Ala Asp
                                   410
               405
Ala Leu Ala Ala Leu Ala Ser Thr Ser Asp Pro Arg Leu Arg Arg Val
                               425
            420
Ile Pro Val Glu Phe Ile Glu Lys Pro Asn Ile Glu Leu Asn Glu Glu
                                               445
                           440
       435
Glu His Val Leu Pro Ile Gln Ile Gly Thr Asp His Asn Asp Ala Pro
                                           460
                       455
Asp Asp Ser Pro Asp Glu Phe Asn Ser
                   470
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- (2) INFORMATION FOR SEQ ID NO:1020:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..969
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596038
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020: tottcacttt ottcatcaca acaatactto togogtootg caacgcatco gcaaaggcca aaacgcaacc ngctgttccc agcgattcta atctttggtg attcaacagt cgacacaggc 120 aacaataact accettcaca aacaatette agagetaaac atgttettae gtttgtteet cccttcttac aaccaaatct caccgaccaa gaaattgtaa ccggagtctg ttttgcatca 240 gcaggtgccg gttacgatga ccaaaccagt ctcacgacac aagcgattcg tgtctcggaa 300 caaccaaata tgttcaagag ttacattgct cgtcttaaga gtatcgtagg agacaagaaa 420 gccatgaaga tcataaacaa tgctttggtg gttgtgagtg cagggcctaa tgatttcatc ttgaattatt acgaggttcc cacatggcgt cgcatgtatc ctagcatttc tgattaccaa 540 gattttgttc ttaataagct taacaatttc gtgatggagc tttacagcct aggttgccgg 600 aaaattttgg tcggaggttt accgccaatg ggatgtttac cgattcaaat gactgctcaa ttccgcaacg tcctaaggtt ttgcttggaa caagagaaca gagactctgt tttatacaat 720 caqaaacttc agaagctctt acctcagaca caagcatctc ttacaggaag caagatcctt 780 tactctgatg tctatgaccc tatgatggag atgctccaaa accctagcaa atacgggttt 840 aaagagacga cgagaggatg ttgtggaaca gggttcttgg agacgagctt catgtgtaat gcttattctt ccatgtgtga gaatcgctcg gagtttctgt tctttgactc gattcatcca 900 tctgaagcta cctacaatta cattggtaat gttctggata ctaagattcg tgggtggctt 960 aaggcttaa
- (2) INFORMATION FOR SEQ ID NO:1021:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..322
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596039
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:
- Ser Ser Leu Ser Ser Ser Gln Gln Tyr Phe Ser Arg Pro Ala Thr His
- Pro Gln Arg Pro Lys Arg Asn Xaa Leu Phe Pro Ala Ile Leu Ile Phe 20 25 30
- Gly Asp Ser Thr Val Asp Thr Gly Asn Asn Asn Tyr Pro Ser Gln Thr 35 40 45
- Ile Phe Arg Ala Lys His Val Leu Thr Phe Val Pro Pro Phe Leu Gln 50 60
- Pro Asn Leu Thr Asp Gln Glu Ile Val Thr Gly Val Cys Phe Ala Ser
- Ala Gly Ala Gly Tyr Asp Asp Gln Thr Ser Leu Thr Thr Gln Ala Ile

 85
 90
 95
- 85 90 95
 Arg Val Ser Glu Gln Pro Asn Met Phe Lys Ser Tyr Ile Ala Arg Leu
 100 105 110
- Lys Ser Ile Val Gly Asp Lys Lys Ala Met Lys Ile Ile Asn Asn Ala 115 120 125
- Leu Val Val Val Ser Ala Gly Pro Asn Asp Phe Ile Leu Asn Tyr Tyr 130 135 140
- Glu Val Pro Thr Trp Arg Arg Met Tyr Pro Ser Ile Ser Asp Tyr Gln
 145 150 155 160
- Asp Phe Val Leu Asn Lys Leu Asn Asn Phe Val Met Glu Leu Tyr Ser 165 170 175
- Leu Gly Cys Arg Lys Ile Leu Val Gly Gly Leu Pro Pro Met Gly Cys
 180 185 190
- Leu Pro Ile Gln Met Thr Ala Gln Phe Arg Asn Val Leu Arg Phe Cys 195 200 205

 Leu Glu Gln Glu Asn Arg Asp Ser Val Leu Tyr Asn Gln Lys Leu Gln
- 210 215 220 Lys Leu Leu Pro Gln Thr Gln Ala Ser Leu Thr Gly Ser Lys Ile Leu
- 225 230 235 240

 Tyr Ser Asp Val Tyr Asp Pro Met Met Glu Met Leu Gln Asn Pro Ser
- 245 250 255
- Lys Tyr Gly Phe Lys Glu Thr Thr Arg Gly Cys Cys Gly Thr Gly Phe
 260 265 270
- Leu Glu Thr Ser Phe Met Cys Asn Ala Tyr Ser Ser Met Cys Glu Asn 275 280 285
- Arg Ser Glu Phe Leu Phe Phe Asp Ser Ile His Pro Ser Glu Ala Thr 290 295 300
- Tyr Asn Tyr Ile Gly Asn Val Leu Asp Thr Lys Ile Arg Gly Trp Leu 305 310 315 320
- Lys Ala
- (2) INFORMATION FOR SEQ ID NO:1022:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1596040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

Met Phe Lys Ser Tyr Ile Ala Arg Leu Lys Ser Ile Val Gly Asp Lys

1 5 10 15

Lys Ala Met Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly

Lys Ala Met Lys lie lie Ash Ash Ala Leu val val val Sel Ala Gly
20 25 30

Pro Asn Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg 35 40 45

Met Tyr Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu 50 55 60

Asn Asn Phe Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu 65 70 75 80

Val Gly Gly Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala 85 90 95

Gln Phe Arg Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp
100 105 110

Ser Val Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln
115 120 125

Ala Ser Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro 130 135 140

Met Met Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr 145 150 155 160

Thr Arg Gly Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys 165 170 175

Asn Ala Tyr Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe 180 185 190

Asp Ser Ile His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val 195 200 205

Leu Asp Thr Lys Ile Arg Gly Trp Leu Lys Ala 210 215

- (2) INFORMATION FOR SEQ ID NO:1023:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..201
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

Met Lys Ile Ile Asn Asn Ala Leu Val Val Ser Ala Gly Pro Asn 1 5 10 15

Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg Met Tyr 20 25 30

Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu Asn Asn 35 40 45

Phe Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu Val Gly 50 55 60

Gly Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala Gln Phe 65 70 75 80

Arg Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp Ser Val 85 90 95

Leu Tyr Asn Gln Lys Leu Gln Lys Leu Pro Gln Thr Gln Ala Ser

Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro Met Met
115 120 125

Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr Thr Arg

- (2) INFORMATION FOR SEQ ID NO:1024:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2196
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596062
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024: atggagaagc tagagaagac catctctaat ttccttaaaa acgaggtctt tacacatatc 60 ctcgctgacg ttcatcatct ccgggccgat accagtgtgc gtttggatcg ggttgacatg 120 agectegaca gggtgattea geaagtgggt teeatgaaaa ttgggggagg tggettgata 180 240 tcagaggcca tgaagagagc cgaggctatg gagattgaga ccaacgacga ttcggagaaa tttggggttg gattggaatt gggaaaggtt aaggttaaga agatgatgtt cgaatctcaa 300 360 ggaggggttt ttgggatcag tggaatgggc ggtgttggta aaaccactct tgccaaagaa cttcaacggg accatgaagt ccaatgtcac tttgagaacc ggattttgtt tctgactgta 420 tcacaatctc cgcttcttga ggagctgagg gaacttatat ggggtttctt atctggttgt 480 540 qaagctggaa atcctgttcc tgactgtaat tttccgtttg atggcgcgcg taagctcgtg 600 attcttgatg atgtttggac cacacagget etggaceget tgacetegtt taagttteet ggttgcacaa ctcttgtggt ctcacgatcc aaactcactg agcctaaatt cacttatgat 660 gtcgaagtac tgagtgaaga tgaagcaatc tctctcttct gtctctgtgc tttcggtcag 720 780 aaatctatcc ctcttggttt ctgcaaagat ctggttaagc aggttgctaa tgaatgtaaa 840 gggcttcctt tagctctcaa agtcacgggt gcttcattaa atggcaaacc tgaaatgtac 900 tggaagggcg tattgcagag gttatcaaaa ggtgaacctg ctgataactc tcacgagagt 960 agattgcttc gtcaaatgga agctagtcta gacaatctcg accagacgac caaagattgt 1020 ttcttggatc ttggcgcctt ccctgaagac aggaagattc ctcttgatgt tctcatcaac atttggattg agttacatga tatagatgaa ggaaatgctt ttgccatcct tgttgatttg 1080 tcacacaaga atctccttac tcttgggaag gatccacggc ttggctcttt gtacgcaagc 1140 cactatgata tatttgtgac acagcatgat gttctgcgag acctagcact tcatttaagc 1200 aatgcaggga aagtaaacag aagaaagcgg ttgctgatgc cgaaaagaga gttaaagctt 1260 ccaggagatt gggaaaggaa caatgatgag cattacattg cccagattgt ctctattcat 1320 actggcaaga gcttttctac actgcaaata ttcttggttc tctcatggga aatgaatgac 1380 atgcaatggt ttgacatgga gttccccaag gcagagattc taatattgaa cttctcttca 1440 gacaagtatg ttcttccgcc ttttatcagt aagatgagcc ggcttaaggt cctagtgatt 1500 atcaacaacg gcatgtctca tgcggttctc catgactttt caatatttgc tcatttgtcg 1560 aaactaagaa gtctctggct agagagggtt cacgtccctc aactctccaa ctcaaccacc 1620 cccttgaaaa atctccacaa gatgtctttg attctgtgca agatcaataa aagttttgat 1680 caaaccggac ttgacgtggc agatatcttc ccaaaattgg gcgatctgac gatagatcac 1740 tgtgatgatc tcgtggcact acctccaagc atttgcggac tgacctccct tagctgctta 1800 1860 agcataacaa attgtccacg cctcggtgaa ttgcccaaga acctcagtaa gctacaggct 1920 ctcgaaatct taaggctata tgcttgccct gagctaaaga cattacctgg agaaatatgt gagetteetg ggettaagta tetegacate teacaatgtg teageetgag ttgtetteea 1980 gaggaaatag gaaagctaaa gaagcttgag aagatcgaca tgagagaatg ttgcttctcg 2040 gatagaccga gctctgctgt ttcactgaag tctctgcgcc atgtaatatg tgataccgac 2100 gttgcattta tgtgggaaga agttgagaag gctgttccag gattaaagat cgaagctgct 2160 gagaaatgct tcagcctaga ctggcttgac gagtaa
- (2) INFORMATION FOR SEQ ID NO:1025:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 731 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..731
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025: Met Glu Lys Leu Glu Lys Thr Ile Ser Asn Phe Leu Lys Asn Glu Val 10 5 Phe Thr His Ile Leu Ala Asp Val His His Leu Arg Ala Asp Thr Ser 25 20 Val Arg Leu Asp Arg Val Asp Met Ser Leu Asp Arg Val Ile Gln Gln 4.0 Val Gly Ser Met Lys Ile Gly Gly Gly Gly Leu Ile Ser Glu Ala Met 55 Lys Arg Ala Glu Ala Met Glu Ile Glu Thr Asn Asp Asp Ser Glu Lys 7.0 Phe Gly Val Gly Leu Glu Leu Gly Lys Val Lys Val Lys Met Met 90 8.5 Phe Glu Ser Gln Gly Gly Val Phe Gly Ile Ser Gly Met Gly Gly Val 105 100 Gly Lys Thr Thr Leu Ala Lys Glu Leu Gln Arg Asp His Glu Val Gln 120 115 cys His Phe Glu Asn Arg Ile Leu Phe Leu Thr Val Ser Gln Ser Pro 135 1.40 Leu Leu Glu Glu Leu Arg Glu Leu Ile Trp Gly Phe Leu Ser Gly Cys 155 150 Glu Ala Gly Asn Pro Val Pro Asp Cys Asn Phe Pro Phe Asp Gly Ala 170 165 Arg Lys Leu Val Ile Leu Asp Asp Val Trp Thr Thr Gln Ala Leu Asp 185 1.80 Arg Leu Thr Ser Phe Lys Phe Pro Gly Cys Thr Thr Leu Val Val Ser 205 200 195 Arg Ser Lys Leu Thr Glu Pro Lys Phe Thr Tyr Asp Val Glu Val Leu 220 215 Ser Glu Asp Glu Ala Ile Ser Leu Phe Cys Leu Cys Ala Phe Gly Gln 230 235 Lys Ser Ile Pro Leu Gly Phe Cys Lys Asp Leu Val Lys Gln Val Ala 250 Asn Glu Cys Lys Gly Leu Pro Leu Ala Leu Lys Val Thr Gly Ala Ser 265 260 Leu Asn Gly Lys Pro Glu Met Tyr Trp Lys Gly Val Leu Gln Arg Leu 285 280 Ser Lys Gly Glu Pro Ala Asp Asn Ser His Glu Ser Arg Leu Leu Arg 295 300 Gln Met Glu Ala Ser Leu Asp Asn Leu Asp Gln Thr Thr Lys Asp Cys 310 315 Phe Leu Asp Leu Gly Ala Phe Pro Glu Asp Arg Lys Ile Pro Leu Asp 325 330 Val Leu Ile Asn Ile Trp Ile Glu Leu His Asp Ile Asp Glu Gly Asn 340 345 Ala Phe Ala Ile Leu Val Asp Leu Ser His Lys Asn Leu Leu Thr Leu 360 365 Gly Lys Asp Pro Arg Leu Gly Ser Leu Tyr Ala Ser His Tyr Asp Ile 380 375 Phe Val Thr Gln His Asp Val Leu Arg Asp Leu Ala Leu His Leu Ser 390 395 Asn Ala Gly Lys Val Asn Arg Arg Lys Arg Leu Leu Met Pro Lys Arg 405 410 415

Glu Leu Lys Leu Pro Gly Asp Trp Glu Arg Asn Asn Asp Glu His Tyr

430 425 420 Ile Ala Gln Ile Val Ser Ile His Thr Gly Lys Ser Phe Ser Thr Leu 435 440 445 Gln Ile Phe Leu Val Leu Ser Trp Glu Met Asn Asp Met Gln Trp Phe 450 455 460 Asp Met Glu Phe Pro Lys Ala Glu Ile Leu Ile Leu Asn Phe Ser Ser 465 470 475 480 Asp Lys Tyr Val Leu Pro Pro Phe Ile Ser Lys Met Ser Arg Leu Lys 485 490 495 Val Leu Val Ile Ile Asn Asn Gly Met Ser His Ala Val Leu His Asp 500 505 510 Phe Ser Ile Phe Ala His Leu Ser Lys Leu Arg Ser Leu Trp Leu Glu 515 520 525 Arg Val His Val Pro Gln Leu Ser Asn Ser Thr Thr Pro Leu Lys Asn 530 535 540 Leu His Lys Met Ser Leu Ile Leu Cys Lys Ile Asn Lys Ser Phe Asp 555 560 550 Gln Thr Gly Leu Asp Val Ala Asp Ile Phe Pro Lys Leu Gly Asp Leu 565 570 Thr Ile Asp His Cys Asp Asp Leu Val Ala Leu Pro Pro Ser Ile Cys 585 590 580 Gly Leu Thr Ser Leu Ser Cys Leu Ser Ile Thr Asn Cys Pro Arg Leu 595 600 605 Gly Glu Leu Pro Lys Asn Leu Ser Lys Leu Gln Ala Leu Glu Ile Leu 610 615 620 Arg Leu Tyr Ala Cys Pro Glu Leu Lys Thr Leu Pro Gly Glu Ile Cys 630 635 Glu Leu Pro Gly Leu Lys Tyr Leu Asp Ile Ser Gln Cys Val Ser Leu 650 645 Ser Cys Leu Pro Glu Glu Ile Gly Lys Leu Lys Lys Leu Glu Lys Ile 665 670 660 Asp Met Arg Glu Cys Cys Phe Ser Asp Arg Pro Ser Ser Ala Val Ser 675 680 685 Leu Lys Ser Leu Arg His Val Ile Cys Asp Thr Asp Val Ala Phe Met 690 695 700 Trp Glu Glu Val Glu Lys Ala Val Pro Gly Leu Lys Ile Glu Ala Ala 705 710 715 Glu Lys Cys Phe Ser Leu Asp Trp Leu Asp Glu 725 730

- (2) INFORMATION FOR SEQ ID NO:1026:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 692 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..692
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596065
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:
- Met Ser Leu Asp Arg Val Ile Gln Gln Val Gly Ser Met Lys Ile Gly
 1 5 10 15
- Gly Gly Leu Ile Ser Glu Ala Met Lys Arg Ala Glu Ala Met Glu 20 25 30
- Ile Glu Thr Asn Asp Asp Ser Glu Lys Phe Gly Val Gly Leu Glu Leu 35 40 45
- Gly Lys Val Lys Val Lys Met Met Phe Glu Ser Gln Gly Gly Val
 50 55 60
- Phe Gly Ile Ser Gly Met Gly Gly Val Gly Lys Thr Thr Leu Ala Lys 65 70 75 80

Glu	Leu	Gln	Arg	Asp 85	His	Glu	Val	Gln	Cys 90	His	Phe	Glu	Asn	Arg 95	Ile
			Thr 100					105					110		
		115	Gly				120					125			
	130		Phe			135					140				
145			Thr		150					155					160
			Thr	165					170					175	
_			Tyr 180					185					190		
		195	Leu				200					205			
	210		Leu			215					220				
225			Lys		230					235					240
			Gly	245					250					255	
			Glu 260					265					270		
		275	Gln				280					285			
	290	_	Arg			295					300				
305			Asp		310					315					320
			Lys	325					330					335	
			Ala 340					345					350		
		355	Leu				360					365			
_	370		Leu			375					380				
385			Asn		390					395					400
			. Lys	405					410					415	
_			420					425					430		Ala
		435)				440					445			Pro
	450					455	i				460				Asn
465					470					475					Leu 480
				485	i				490)				495	
			500)				505	·				510		Ile
		515	5				520)				525)		Ala
	530)				535	5				540)			Asp
545)				550)				555	5				Cys 560
Lev	ı Ser	: I16	e Thi	: Asr	т СУЗ	s Pro	Arg	у тег	r GTZ	A GT	и пег	r ETC	, пув	, A31	Leu

	Attorney Docket No. 2750-1237P																
	Client Docket No. 80146.003														,		
					565					570					575		
				580			Glu		585					590			
			595				Glu	600					605				
		610					Val 615					620					
	Gly 625	Lys	Leu	Lys	Lys	Leu 630	Glu	Lys	Ile	Asp	Met 635	Arg	Glu	Cys	Cys	Phe 640	
	Ser	Asp	Arg	Pro	Ser 645	Ser	Ala	Val	Ser	Leu 650	Lys	Ser	Leu	Arg	His 655	Val	
	Ile	Cys	Asp	Thr 660	Asp	Val	Ala	Phe	Met 665	Trp	Glu	Glu	Val	Glu 670	Lys	Ala	
	Val	Pro	Gly 675	Leu	Lys	Ile	Glu	Ala 680	Ala	Glu	Lys	Cys	Phe 685	Ser	Leu	Asp	
	Trp	Leu 690	Asp	Glu													
	(2)	INF					ID 1										
		(i	-				CTER										
(A) LENGTH: 411 base pairs																	
	(B) TYPE: nucleic acid																
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: DNA (genomic)																
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			()		AME/												
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- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596069
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027: ggatctaaga tacagattac cattagaaag cattatattg gcaagtttaa catgtcacta 60 aagggtattc tttacaatgg cagacatatt aggtcaagtg aaaaagtatt tagtgcttta 120 aaaagtgtaa agcatgacga gaagacagtg gttctgatat gctatgctaa aatcaataat 180 tttaaagctt tacacattgc aagcaattct gttttccata aaagaacgaa gcatattgag 240 300 cqtqattgtc acaaggttag ggaatgtatt gaagctggga ttctcaaaac catgtttgtt cgttctgata atcagcttgc ggatatgcta actaaacctc tttatccggc gctctttcga 360 gctaacaaca ccaagcttgg agttctcaac atatatgaag ctcaagcttg a
- (2) INFORMATION FOR SEQ ID NO:1028:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596070
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

Gly Ser Lys Ile Gln Ile Thr Ile Arg Lys His Tyr Ile Gly Lys Phe 5 10 1

Asn Met Ser Leu Lys Gly Ile Leu Tyr Asn Gly Arg His Ile Arg Ser 30 25 20

Ser Glu Lys Val Phe Ser Ala Leu Lys Ser Val Lys His Asp Glu Lys 45 40 35

Thr Val Val Leu Ile Cys Tyr Ala Lys Ile Asn Asn Phe Lys Ala Leu 55

His Ile Ala Ser Asn Ser Val Phe His Lys Arg Thr Lys His Ile Glu 75 70 Arg Asp Cys His Lys Val Arg Glu Cys Ile Glu Ala Gly Ile Leu Lys

90 85 Thr Met Phe Val Arg Ser Asp Asn Gln Leu Ala Asp Met Leu Thr Lys

900

960

110 105 100 Pro Leu Tyr Pro Ala Leu Phe Arg Ala Asn Asn Thr Lys Leu Gly Val 120 115 Leu Asn Ile Tyr Glu Ala Gln Ala 130 135 (2) INFORMATION FOR SEQ ID NO:1029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..119 (D) OTHER INFORMATION: / Ceres Seq. ID 1596071 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029: Met Ser Leu Lys Gly Ile Leu Tyr Asn Gly Arg His Ile Arg Ser Ser 10 Glu Lys Val Phe Ser Ala Leu Lys Ser Val Lys His Asp Glu Lys Thr 25 20 Val Val Leu Ile Cys Tyr Ala Lys Ile Asn Asn Phe Lys Ala Leu His 40 Ile Ala Ser Asn Ser Val Phe His Lys Arg Thr Lys His Ile Glu Arg 55 Asp Cys His Lys Val Arg Glu Cys Ile Glu Ala Gly Ile Leu Lys Thr 75 70 Met Phe Val Arg Ser Asp Asn Gln Leu Ala Asp Met Leu Thr Lys Pro 90 85 Leu Tyr Pro Ala Leu Phe Arg Ala Asn Asn Thr Lys Leu Gly Val Leu 1.10 105 100 Asn Ile Tyr Glu Ala Gln Ala 115 (2) INFORMATION FOR SEQ ID NO:1030: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..1224 (D) OTHER INFORMATION: / Ceres Seq. ID 1596072 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030: atgtctcaaa acgggaagat aatcccaaat ctggaccaaa acagtacgag gctcctcaat ctcacagttc tccagcggat cgatccatac atcgaggaaa tcctcatcac agccgctcat 120 gtcactttct atgaattcaa cattgagctc agccaatgga gtcgtaagga cgttgaagga 180 tetttgtttg ttgtcaaaag aagtacacaa eetegattte agtttattgt gatgaategt 240 cgtaatacag ataatctggt ggagaatctc ctgggagatt ttgagtatga agtacaaggt 300 ccatatttac tttaccgtaa tgcatctcaa gaagtaaatg gcatttggtt ctacaataaa 360 cgtgaatgcg aggaggtagc aactcttttc aacagaatac tcagtgcata ttccaaggtt 420 aaccagaagc caaaggcctc atcttcaaag agtgagtttg aggaattgga agctaagcct 480 acaatggcag ttatggatgg tcctcttgaa ccatcatcaa ctgctaggga tgcccctgat 540 gatectgett ttgtcaactt etttagetea aegatgaate ttgggaacae tgegagtggg 600 660 tcagcaagtg gaccttacca atcatcagcg attcctcacc aacctcacca gcctcaccaa 720 cctcaccaac ccaccattgc tcctcctgta gcggcagcag cacctccaca gatacnatca ccaccgcctn tacnatcctc ctctcctctg atgactctct ttgacaacaa ccctgaagtt 780 atcagcagca actecaacat tcacacagat ttggtgacgc cgtctttctt tggcccccca 840

cgaatgatgg cacagccaca ceteatteet ggtgtateta tgeecagtge teeteetee

aatcctaata atgcgagtca ccagcagcgg tcatatggta ctccggtgct ccagcctttc

aaccagttcc tctcaaagct ttaa

ccaccccaa ctccaccac atcactcgct cctgcaccca ctggtccggt tatcagcaga 1020 gacaaagtga aggaagccct tttatccctg ttgcagctgg aggagtcggg aagtgagcga 1080 gctcagttcc gatgctatcg aagaagagac ccgtcaggct cttcccattt atcgcntgga atgctcgacg gagctagcca tccgatcagc ccaaatccta ccacgttcaa atctctcctc 1200

- (2) INFORMATION FOR SEQ ID NO:1031:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..407
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596073 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031: Met Ser Gln Asn Gly Lys Ile Ile Pro Asn Leu Asp Gln Asn Ser Thr 10 Arg Leu Leu Asn Leu Thr Val Leu Gln Arg Ile Asp Pro Tyr Ile Glu 30 25 20 Glu Ile Leu Ile Thr Ala Ala His Val Thr Phe Tyr Glu Phe Asn Ile 40 Glu Leu Ser Gln Trp Ser Arg Lys Asp Val Glu Gly Ser Leu Phe Val 55 Val Lys Arg Ser Thr Gln Pro Arg Phe Gln Phe Ile Val Met Asn Arg 75 70 Arg Asn Thr Asp Asn Leu Val Glu Asn Leu Leu Gly Asp Phe Glu Tyr 90 85 Glu Val Gln Gly Pro Tyr Leu Leu Tyr Arg Asn Ala Ser Gln Glu Val 105 110 Asn Gly Ile Trp Phe Tyr Asn Lys Arg Glu Cys Glu Glu Val Ala Thr 120 Leu Phe Asn Arg Ile Leu Ser Ala Tyr Ser Lys Val Asn Gln Lys Pro 140 135 Lys Ala Ser Ser Ser Lys Ser Glu Phe Glu Glu Leu Glu Ala Lys Pro 150 155 Thr Met Ala Val Met Asp Gly Pro Leu Glu Pro Ser Ser Thr Ala Arg 170 165 Asp Ala Pro Asp Asp Pro Ala Phe Val Asn Phe Phe Ser Ser Thr Met 180 185 Asn Leu Gly Asn Thr Ala Ser Gly Ser Ala Ser Gly Pro Tyr Gln Ser 200 Ser Ala Ile Pro His Gln Pro His Gln Pro His Gln Pro 220 215 Thr Ile Ala Pro Pro Val Ala Ala Ala Pro Pro Gln Ile Xaa Ser

Pro Pro Pro Xaa Xaa Ser Ser Ser Pro Leu Met Thr Leu Phe Asp Asn

Asn Pro Glu Val Ile Ser Ser Asn Ser Asn Ile His Thr Asp Leu Val

Thr Pro Ser Phe Phe Gly Pro Pro Arg Met Met Ala Gln Pro His Leu 275 280 285

Ile Pro Gly Val Ser Met Pro Ser Ala Pro Pro Leu Asn Pro Asn Asn

Ala Ser His Gln Gln Arg Ser Tyr Gly Thr Pro Val Leu Gln Pro Phe

Pro Pro Pro Thr Pro Pro Pro Ser Leu Ala Pro Ala Pro Thr Gly Pro

Val Ile Ser Arg Asp Lys Val Lys Glu Ala Leu Leu Ser Leu Leu Gln

345

235

300

315

330

270

250

265

230

295

310

325

245

260

340

Leu Glu Glu Ser Gly Ser Glu Arg Ala Gln Phe Arg Cys Tyr Arg Arg 360

Arg Asp Pro Ser Gly Ser Ser His Leu Ser Xaa Gly Met Leu Asp Gly 370 375 380

Ala Ser His Pro Ile Ser Pro Asn Pro Thr Thr Phe Lys Ser Leu Leu 395 390

Asn Gln Phe Leu Ser Lys Leu 405

- (2) INFORMATION FOR SEQ ID NO:1032:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..330
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596075
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032: Met Asn Arg Arg Asn Thr Asp Asn Leu Val Glu Asn Leu Leu Gly Asp 10 5 Phe Glu Tyr Glu Val Gln Gly Pro Tyr Leu Leu Tyr Arg Asn Ala Ser 25 20 Gln Glu Val Asn Gly Ile Trp Phe Tyr Asn Lys Arg Glu Cys Glu Glu 4.0 Val Ala Thr Leu Phe Asn Arg Ile Leu Ser Ala Tyr Ser Lys Val Asn 55 Gln Lys Pro Lys Ala Ser Ser Ser Lys Ser Glu Phe Glu Glu Leu Glu 75 70 Ala Lys Pro Thr Met Ala Val Met Asp Gly Pro Leu Glu Pro Ser Ser 85 90 Thr Ala Arg Asp Ala Pro Asp Asp Pro Ala Phe Val Asn Phe Phe Ser 105 Ser Thr Met Asn Leu Gly Asn Thr Ala Ser Gly Ser Ala Ser Gly Pro 115 120 Tyr Gln Ser Ser Ala Ile Pro His Gln Pro His Gln Pro His Gln Pro 130 135 His Gln Pro Thr Ile Ala Pro Pro Val Ala Ala Ala Pro Pro Gln 150 155 Ile Xaa Ser Pro Pro Pro Xaa Xaa Ser Ser Pro Leu Met Thr Leu 165 170 Phe Asp Asn Asn Pro Glu Val Ile Ser Ser Asn Ser Asn Ile His Thr 185 190 180 Asp Leu Val Thr Pro Ser Phe Phe Gly Pro Pro Arg Met Met Ala Gln 205 200 Pro His Leu Ile Pro Gly Val Ser Met Pro Ser Ala Pro Pro Leu Asn 220 215 Pro Asn Asn Ala Ser His Gln Gln Arg Ser Tyr Gly Thr Pro Val Leu 235 230 Gln Pro Phe Pro Pro Pro Thr Pro Pro Pro Ser Leu Ala Pro Ala Pro 245 250 Thr Gly Pro Val Ile Ser Arg Asp Lys Val Lys Glu Ala Leu Leu Ser 260 265 Leu Leu Gln Leu Glu Glu Ser Gly Ser Glu Arg Ala Gln Phe Arg Cys 285 280 Tyr Arg Arg Arg Asp Pro Ser Gly Ser Ser His Leu Ser Xaa Gly Met 300 295 Leu Asp Gly Ala Ser His Pro Ile Ser Pro Asn Pro Thr Thr Phe Lys 305 310 315 Ser Leu Leu Asn Gln Phe Leu Ser Lys Leu

325 330

- (2) INFORMATION FOR SEQ ID NO:1033:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..636
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596076
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033: atgagtaagc ttcagagtga ggccgttcgt gaagccatca ctactatcac agggaaatcc 60 120 gaggcaaaga aacgtaactt tgtcgagact attgagctcc agatcggtct gaagaactat gaccctcaaa aggacaagcg tttcagtgga tctgtcaagt taccacatat cccccgtcct 180 240 aaaatgaaga tctgcatgct cggagatgcc cagcatgttg aagaggctga gaagatgggg ttggaaaaca tggatgttga gtctctaaaa aagcttaaca agaacaagaa actcgtcaag 300 aagettgeaa agaaataeea tgetttettg geetetgagt etgteattaa geagatteet 360 cgtcttcttg gtcctggaaa attcccaact cttgtgagcc accaggaatc cttggagtca 420 aaggtgaatg aaacaaaggc aacagtgaag ttccagctga agaaggttct gtgcatggga 480 540 gttgcagttg gtaacctttc aatggaagag aagcagatct ttcagaatgt gcagatgagc gtcaacttcc tcgtctcgct attgaagaag aactggcaaa atgtcaggtg tttgtacctc 600 aagagcacaa tgggaccacc acaaagaatc ttctga
- (2) INFORMATION FOR SEQ ID NO:1034:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..211
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596077
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:
- Met Ser Lys Leu Gln Ser Glu Ala Val Arg Glu Ala Ile Thr Thr Ile
 1 5 10 15
- Thr Gly Lys Ser Glu Ala Lys Lys Arg Asn Phe Val Glu Thr Ile Glu 20 25 30
- Leu Gln Ile Gly Leu Lys Asn Tyr Asp Pro Gln Lys Asp Lys Arg Phe 35 40 45
- Ser Gly Ser Val Lys Leu Pro His Ile Pro Arg Pro Lys Met Lys Ile 50 55 60
- Cys Met Leu Gly Asp Ala Gln His Val Glu Glu Ala Glu Lys Met Gly 65 70 75 80
- Leu Glu Asn Met Asp Val Glu Ser Leu Lys Lys Leu Asn Lys Asn Lys 85 90 95
 Lys Leu Val Lys Lys Leu Ala Lys Lys Tyr His Ala Phe Leu Ala Ser
- 100 105 110

 Glu Ser Val The Lvs Gln The Pro Arg Leu Leu Gly Pro Gly Lys Phe
- Glu Ser Val Ile Lys Gln Ile Pro Arg Leu Leu Gly Pro Gly Lys Phe 115 120 125
- Pro Thr Leu Val Ser His Gln Glu Ser Leu Glu Ser Lys Val Asn Glu 130 135 140
- Thr Lys Ala Thr Val Lys Phe Gln Leu Lys Lys Val Leu Cys Met Gly
 145 150 155 160
- Val Ala Val Gly Asn Leu Ser Met Glu Glu Lys Gln Ile Phe Gln Asn 165 170 175

205 200 195 Arg Ile Phe 210 (2) INFORMATION FOR SEQ ID NO:1035: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..150 (D) OTHER INFORMATION: / Ceres Seq. ID 1596079 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035: Met Lys Ile Cys Met Leu Gly Asp Ala Gln His Val Glu Glu Ala Glu 10 Lys Met Gly Leu Glu Asn Met Asp Val Glu Ser Leu Lys Lys Leu Asn 25 30 20 Lys Asn Lys Lys Leu Val Lys Lys Leu Ala Lys Lys Tyr His Ala Phe 40 Leu Ala Ser Glu Ser Val Ile Lys Gln Ile Pro Arg Leu Leu Gly Pro 55 Gly Lys Phe Pro Thr Leu Val Ser His Gln Glu Ser Leu Glu Ser Lys 75 70 Val Asn Glu Thr Lys Ala Thr Val Lys Phe Gln Leu Lys Lys Val Leu 85 90 Cys Met Gly Val Ala Val Gly Asn Leu Ser Met Glu Glu Lys Gln Ile 105 100 Phe Gln Asn Val Gln Met Ser Val Asn Phe Leu Val Ser Leu Leu Lys 125 120 115 Lys Asn Trp Gln Asn Val Arg Cys Leu Tyr Leu Lys Ser Thr Met Gly 140 130 135 Pro Pro Gln Arg Ile Phe (2) INFORMATION FOR SEQ ID NO:1036: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..2349 (D) OTHER INFORMATION: / Ceres Seq. ID 1596087 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036: 60 atgaaggcta agaagggaat cagattttct ggaaaaatct ttcactatct catgcagcag agagtgaaaa caaaaggatc aactctttgg tttagagttg attctcaacc tatccgtttc 120 teettgagag agttetatet cacaacagga atteaatgtg aacetgttea tagggaactt cgacgaaagg ggaaagatcc tgtaaaagaa ccatactttt gggctagtaa aggatcctat 240 actcttggtg atctcgaaga tcgattgttt ttaaaaccta aggaaggtga acctgctgtt 300 gaagatgaag aaaagttgtg tottgctgca gtagtgttga ttgaaggaat tottttgaca ccatatggaa aagagaagat acctttgcca agattgcagc atgcttctga ttttgagatg 420 tacacagece aaccaatgga egagaaaact tgggcaaaag agaaatatga tttgagagga 480 tttggactag cgctaacaat atgggtgttg agcgcagttc tagcatttgg tgcagcatat 540 ggagttaaag ataaggaatt ccaatctgaa tatccattga tattgaagtg gaaaagcact 600 actactccag agtttttcaa gatcgtaaac cttgtaaatg atgtttctga gatggaggtg aatacaatta ttggaaatcc agaagaattc aagtctttag ttcctgattt ccacacagac 720 gacacaaaat tccaacatat tttgggacta gttaatatgg gctacagatt gaagaaaact 780 gaatggaata caagatgcgt tgatgtttgt gctgcccttg aagaagtagg tcaaaacaaa 840 atcaataaca aaatatctga tagcgagaag cttgatagga ttttgacaat ccttgaagat 900 cttaacaaga gagtcgagct gattgagagg attttggaca ttagaatgga ggaaaagaat 960 aatcagagat ctgaggaaga tgaagaaaga aaacaagaag atgaaggagt agaaagacaa 1020 ccagaggctg aagaagaagg aggactagaa agaaaagcag agaatgacaa tgaatcattt 1080 gaagattcaa teegagagee aaacacacag tatgggaget ateegggtga tgatgaaaae 1140 acccaacgtg atgttggtga tgaattagtt gaagaatcat caaaagataa gtctcctact 1200 ccacgatect ctacaccaaa tttcaatatt ttgtctgaag aaagtctgga tgttcaaaag 1260 gataagaaga gagttagcag aggaagaaat gagaacaaga gagttaaacc aaatgtttat 1320 1380 gctgaggata atcttaaaac aagaaaacag gtgccgagaa agaggcataa acaagttgat attgctgatg ttcatgttcc aacaaggaaa gaggcacaga gtaagaaaag gaaaaatatt 1440 ggcaatgatg gtgataacgc tgataatgat ggcgacaatg atgattttca gcccgctccg 1500 caaagaaaga gtaagcgggg tacggtccct tccattcata cccaagcacc tttcacagct 1560 gagaagaaga agcatccaat tttgcatcca tttgcgaaag ttgatgccac aagacttgag 1620 aaattggctg tatggaagaa gtcaaggaaa aacaagccac tatcaatcgc gggaaataat 1680 1740 gtagatacaa agtggtttac aaccctagag acgccaggga aagcaatcac agcaacgcat gttgatgcag ctttggagtt gatgaaaacg aggaaggaaa gcaatccaga attattcaaa 1800 1860 aacaaatcag ttgtatttgt tggatcgtct ttcttaaatg tgattgatga gtcatacatg gagtttttgg ataacaaaga gggatttcag tttcagtctg aagaaatcag taagctgata 1920 1980 atagaggaag aaaccaagtg catattggct cctttctgta tcaaaggaaa atgttgggtt gccttgctca tccacttgga acagaagaca gtttgtatat gggaatgtgc agcttcttat 2040 2100 ttaacagaag aagtcaagaa aaaatatgtt gctgcctact ctatagctat gccatacatt gttcggaaca tcctcaaaaa agaagacatg gatgtctctc catttagcat caaagtcctg 2160 2220 accacttttc ctcaggctcc tagaaatgaa gagtctggta tctatatgct gaagtttatg 2280 gaatgctact caatgtatac cagccattca aacyttgaag ggaacataat tcaaaacgtt aggaataaat tggctgctga catcttcacc gaattagggt gctttgattt gaatggaaaa 2340 ggactttaa

- (2) INFORMATION FOR SEQ ID NO:1037:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 782 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..782
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596088 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:
- 1 5 10 15

 Leu Met Gln Gln Arg Val Lys Thr Lys Gly Ser Thr Leu Trp Phe Arg
 20 25 30

 Val Asp Ser Gln Pro Ile Arg Phe Ser Leu Arg Glu Phe Tyr Leu Thr

Met Lys Ala Lys Lys Gly Ile Arg Phe Ser Gly Lys Ile Phe His Tyr

- Val Asp Ser Gin Pro lie Arg Phe Ser Hed Arg Sid The Tyr Lod 1112 35 40 45 Thr Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly
- 50 55 60

 Lys Asp Pro Val Lys Glu Pro Tyr Phe Trp Ala Ser Lys Gly Ser Tyr
- 70 75 80

 Thr Leu Gly Asp Leu Glu Asp Arg Leu Phe Leu Lys Pro Lys Glu Gly
 85 90 95
- Glu Pro Ala Val Glu Asp Glu Glu Lys Leu Cys Leu Ala Ala Val Val

 100
 105
 110
- Leu Ile Glu Gly Ile Leu Leu Thr Pro Tyr Gly Lys Glu Lys Ile Pro 115 120 125
- Leu Pro Arg Leu Gln His Ala Ser Asp Phe Glu Met Tyr Thr Ala Gln
 130 135 140
- Pro Met Asp Glu Lys Thr Trp Ala Lys Glu Lys Tyr Asp Leu Arg Gly 145 150 155 160
- Phe Gly Leu Ala Leu Thr Ile Trp Val Leu Ser Ala Val Leu Ala Phe 165 170 175 175 Gly Ala Ala Tyr Gly Val Lys Asp Lys Glu Phe Gln Ser Glu Tyr Pro

								105					190		
Tan	Tle	T.011	180 Lys '	Tro '	Lvs	Ser	Thr	185 Thr	Thr	Pro	Glu	Phe	Phe :	Lys :	Ile
		195					200					205			
	210					215					220		Thr		
225					230					235			His		Z4U
Asp				245					250					255	
			260					265					Cys 270		
		275					280					285	Ser		
	290					295					300		Asn		
305					310					315			Glu		320
				325					330				Asp	335	
			340					345					Glu 350		
		355					360					365	Glu		
	370					375					380		Gln		
385					390					395			Ser		400
				405					410				Glu	415	
			420					425					Asn 430		
		435					440					445			
	450					455					460		Ala		
465					470					475			Lys		480
				485					490)			Asp	495	
			500					505)				Pro 510		
		515					520	l				525	•		Leu
	530)				535)				540)			Val
545					550					555)				Asn 560
				565					570)				5/5	
			580					585	5				590		Lys
		595					600)				603)		Gly
	610)				61!	5				620	J			. Asp
625	5				630)				63	5				Ile 640
				645	5				65	0				655	
Lys	з Су:	s Tr <u>r</u>	Val 660		a Leu	ı Le	u Il	e Hi 66	s ье 5	u Gl	u GL:	и ъў	670	. val	. Cys

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Ile Trp Glu Cys Ala Ala Ser Tyr Leu Thr Glu Glu Val Lys Lys Lys
675
Tyr Val Ala Ala Tyr Ser Ile Ala Met Pro Tyr Ile Val Arg Asn Ile
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690 695 700

Leu Lys Lys Glu Asp Met Asp Val Ser Pro Phe Ser Ile Lys Val Leu 705 710 715 720

Thr Thr Phe Pro Gln Ala Pro Arg Asn Glu Glu Ser Gly Ile Tyr Met 725 730 735

Leu Lys Phe Met Glu Cys Tyr Ser Met Tyr Thr Ser His Ser Asn Xaa 740 745 750

Glu Gly Asn Ile Ile Gln Asn Val Arg Asn Lys Leu Ala Ala Asp Ile
755
760
765
Phe Thr Glu Leu Gly Cys Phe Asp Leu Asn Gly Lys Gly Leu

Phe Thr Glu Leu Gly Cys Phe Asp Leu Asn Gly Lys Gly Leu 770 780

- (2) INFORMATION FOR SEQ ID NO:1038:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..765
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596090
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met Gln Gln Arg Val Lys Thr Lys Gly Ser Thr Leu Trp Phe Arg Val 1 5 10 15

Asp Ser Gln Pro Ile Arg Phe Ser Leu Arg Glu Phe Tyr Leu Thr Thr 20 25 30

Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly Lys 35 40 45

Asp Pro Val Lys Glu Pro Tyr Phe Trp Ala Ser Lys Gly Ser Tyr Thr
50 55 60

Leu Gly Asp Leu Glu Asp Arg Leu Phe Leu Lys Pro Lys Glu Gly Glu 65 70 75 80

Pro Ala Val Glu Asp Glu Glu Lys Leu Cys Leu Ala Ala Val Val Leu 85 90 95 Ile Glu Gly Ile Leu Leu Thr Pro Tyr Gly Lys Glu Lys Ile Pro Leu

\$100\$ \$105\$ \$110\$ Pro Arg Leu Gln His Ala Ser Asp Phe Glu Met Tyr Thr Ala Gln Pro

115 120 125 Met Asp Glu Lys Thr Trp Ala Lys Glu Lys Tyr Asp Leu Arg Gly Phe 130 135 140

Gly Leu Ala Leu Thr Ile Trp Val Leu Ser Ala Val Leu Ala Phe Gly

145 150 155 160
Ala Ala Tyr Gly Val Lys Asp Lys Glu Phe Gln Ser Glu Tyr Pro Leu

165 170 175

Ile Leu Lys Trp Lys Ser Thr Thr Thr Pro Glu Phe Phe Lys Ile Val

180 185 Lon Val. Agn. Agn. Val. Sor. Cly. Met. Cly. Val. Agn. Thr. Ile. Ile. Cly.

Asn Leu Val Asn Asp Val Ser Glu Met Glu Val Asn Thr Ile Ile Gly 195 200 205

Asn Pro Glu Glu Phe Lys Ser Leu Val Pro Asp Phe His Thr Asp Asp 210 215 220

Thr Lys Phe Gln His Ile Leu Gly Leu Val Asn Met Gly Tyr Arg Leu 225 230 235 240

Lys Lys Thr Glu Trp Asn Thr Arg Cys Val Asp Val Cys Ala Ala Leu 245 250 255

Glu Glu Val Gly Gln Asn Lys Ile Asn Asn Lys Ile Ser Asp Ser Glu 260 265 270 Lys Leu Asp Arg Ile Leu Thr Ile Leu Glu Asp Leu Asn Lys Arg Val

275 280 Glu Leu Ile Glu Arg Ile Leu Asp Ile Arg Met Glu Glu Lys Asn Asn 295 Gln Arg Ser Glu Glu Asp Glu Glu Arg Lys Gln Glu Asp Glu Gly Val 310 315 Glu Arg Gln Pro Glu Ala Glu Glu Glu Gly Gly Leu Glu Arg Lys Ala 325 330 Glu Asn Asp Asn Glu Ser Phe Glu Asp Ser Ile Arg Glu Pro Asn Thr 345 Gln Tyr Gly Ser Tyr Pro Gly Asp Asp Glu Asn Thr Gln Arg Asp Val 360 Gly Asp Glu Leu Val Glu Glu Ser Ser Lys Asp Lys Ser Pro Thr Pro 375 Arg Ser Ser Thr Pro Asn Phe Asn Ile Leu Ser Glu Glu Ser Leu Asp 390 395 Val Gln Lys Asp Lys Lys Arg Val Ser Arg Gly Arg Asn Glu Asn Lys 405 410 Arg Val Lys Pro Asn Val Tyr Ala Glu Asp Asn Leu Lys Thr Arg Lys 425 Gln Val Pro Arg Lys Arg His Lys Gln Val Asp Ile Ala Asp Val His 440 Val Pro Thr Arg Lys Glu Ala Gln Ser Lys Lys Arg Lys Asn Ile Gly 455 Asn Asp Gly Asp Asn Ala Asp Asn Asp Gly Asp Asn Asp Phe Gln 470 475 Pro Ala Pro Gln Arg Lys Ser Lys Arg Gly Thr Val Pro Ser Ile His 490 485 Thr Gln Ala Pro Phe Thr Ala Glu Lys Lys His Pro Ile Leu His 505 Pro Phe Ala Lys Val Asp Ala Thr Arg Leu Glu Lys Leu Ala Val Trp 520 Lys Lys Ser Arg Lys Asn Lys Pro Leu Ser Ile Ala Gly Asn Asn Val 530 535 540 Asp Thr Lys Trp Phe Thr Thr Leu Glu Thr Pro Gly Lys Ala Ile Thr 550 555 Ala Thr His Val Asp Ala Ala Leu Glu Leu Met Lys Thr Arg Lys Glu 570 565 Ser Asn Pro Glu Leu Phe Lys Asn Lys Ser Val Val Phe Val Gly Ser 585 Ser Phe Leu Asn Val Ile Asp Glu Ser Tyr Met Glu Phe Leu Asp Asn 595 600 605 Lys Glu Gly Phe Gln Phe Gln Ser Glu Glu Ile Ser Lys Leu Ile Ile 615 620 Glu Glu Glu Thr Lys Cys Ile Leu Ala Pro Phe Cys Ile Lys Gly Lys 630 635 Cys Trp Val Ala Leu Leu Ile His Leu Glu Gln Lys Thr Val Cys Ile 645 650 Trp Glu Cys Ala Ala Ser Tyr Leu Thr Glu Glu Val Lys Lys Tyr 665 Val Ala Ala Tyr Ser Ile Ala Met Pro Tyr Ile Val Arg Asn Ile Leu 680 685 Lys Lys Glu Asp Met Asp Val Ser Pro Phe Ser Ile Lys Val Leu Thr 695 700 Thr Phe Pro Gln Ala Pro Arg Asn Glu Glu Ser Gly Ile Tyr Met Leu 710 715 Lys Phe Met Glu Cys Tyr Ser Met Tyr Thr Ser His Ser Asn Xaa Glu 725 730 735 Gly Asn Ile Ile Gln Asn Val Arg Asn Lys Leu Ala Ala Asp Ile Phe 745 740 Thr Glu Leu Gly Cys Phe Asp Leu Asn Gly Lys Gly Leu 760

- (2) INFORMATION FOR SEQ ID NO:1039:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2268 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2268
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596095
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

60 atgaaggcta agaagggaat cagattttct ggaaaaatct ttcactatct catgcagcag agagtgaaaa caaaaggatc aactctttgg tttagagttg attctcaacc tatccgtttc 120 180 tccttqaqaq aqttctatct cacaacaqqa attcaatqtq aacctqttca tagqqaactt 240 cgacgaaagg ggaaagatcc tgaaggtgaa cctgctgttg aagatgaaga aaagttgtgt 300 cttgctgcag tagtgttgat tgaaggaatt cttttgacac catatggaaa agagaagata 360 cctttgccaa gattgcagca tgcttctgat tttgagatgt acacagccca accaatggac 420 gagaaaactt gggcaaaaga gaaatatgat ttgagaggat ttggactagc gctaacaata tgggtgttga gcgcagttct agcatttggt gcagcatatg gagttaaaga taaggaattc 480 caatctgaat atccattgat attgaagtgg aaaagcacta ctactccaga gtttttcaag 540 600 atogtaaacc ttgtaaatga tgtttctgag atggaggtga atacaattat tggaaatcca 660 gaagaattca agtctttagt tcctgatttc cacacagacg acacaaaatt ccaacatatt 720 ttgggactag ttaatatggg ctacagattg aagaaaactg aatggaatac aagatgcgtt qatqtttqtq ctgcccttga agaaqtaggt caaaacaaaa tcaataacaa aatatctgat 780 agegagaage ttgataggat tttgacaate cttgaagate ttaacaagag agtegagetg 840 900 attgagagga ttttggacat tagaatggag gaaaagaata atcagagatc tgaggaagat gaagaaagaa aacaagaaga tgaaggagta gaaagacaac cagaggctga agaagaagga 960 1020 ggactagaaa gaaaagcaga gaatgacaat gaatcatttg aagattcaat ccgagagcca aacacacagt atgggageta teegggtgat gatgaaaaca eecaaegtga tgttggtgat 1080 gaattagttg aagaatcatc aaaagataag totoctactc cacgatcctc tacaccaaat 1140 ttcaatattt tgtctgaaga aagtctggat gttcaaaagg ataagaagag agttagcaga 1200 ggaagaaatg agaacaagag agttaaacca aatgtttatg ctgaggataa tcttaaaaca 1260 agaaaacagg tgccgagaaa gaggcataaa caagttgata ttgctgatgt tcatgttcca 1320 acaaqqaaaq aqqcacaqaq taaqaaaaqq aaaaatattg gcaatgatgg tgataacgct gataatgatg gcgacaatga tgattttcag cccgctccgc aaagaaagag taagcggggt 1500 acqqtccctt ccattcatac ccaaqcacct ttcacaqctg agaagaagaa gcatccaatt 1560 ttgcatccat ttgcgaaagt tgatgccaca agacttgaga aattggctgt atggaagaag 1620 tcaaggaaaa acaagccact atcaatcgcg ggaaataatg tagatacaaa gtggtttaca accctagaga cgccagggaa agcaatcaca gcaacgcatg ttgatgcagc tttggagttg atgaaaacga ggaaggaaag caatccagaa ttattcaaaa acaaatcagt tgtatttgtt 1740 ggatcgtctt tcttaaatgt gattgatgag tcatacatgg agtttttgga taacaaagag qqatttcaqt ttcaqtctga agaaatcagt aagctgataa tagaggaaga aaccaagtgc atattqqctc ctttctqtat caaaqqaaaa tqttqqqttq ccttqctcat ccacttggaa cagaagacag tttgtatatg ggaatgtgca gcttcttatt taacagaaga agtcaagaaa aaatatgttq ctqcctactc tataqctatq ccatacattq ttcqqaacat cctcaaaaaa 2040 gaagacatgg atgtctctcc atttagcatc aaagtcctga ccacttttcc tcaggctcct 2100 agaaatgaag agtctggtat ctatatgctg aagtttatgg aatgctactc aatgtatacc 2160 agccattcaa acyttgaagg gaacataatt caaaacgtta ggaataaatt ggctgctgac 2220 atcttcaccq aattagggtg ctttgatttg aatggaaaag gactttaa

- (2) INFORMATION FOR SEQ ID NO:1040:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 755 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..755
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040: Met Lys Ala Lys Lys Gly Ile Arg Phe Ser Gly Lys Ile Phe His Tyr 1 5 10 Leu Met Gln Gln Arg Val Lys Thr Lys Gly Ser Thr Leu Trp Phe Arg 25 Val Asp Ser Gln Pro Ile Arg Phe Ser Leu Arg Glu Phe Tyr Leu Thr 35 40 Thr Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly 55 Lys Asp Pro Glu Gly Glu Pro Ala Val Glu Asp Glu Glu Lys Leu Cys 65 70 75 Leu Ala Ala Val Val Leu Ile Glu Gly Ile Leu Leu Thr Pro Tyr Gly 90 85 Lys Glu Lys Ile Pro Leu Pro Arg Leu Gln His Ala Ser Asp Phe Glu 100 105 110 Met Tyr Thr Ala Gln Pro Met Asp Glu Lys Thr Trp Ala Lys Glu Lys 115 120 Tyr Asp Leu Arg Gly Phe Gly Leu Ala Leu Thr Ile Trp Val Leu Ser 130 135 140 Ala Val Leu Ala Phe Gly Ala Ala Tyr Gly Val Lys Asp Lys Glu Phe 145 150 155 Gln Ser Glu Tyr Pro Leu Ile Leu Lys Trp Lys Ser Thr Thr Thr Pro 165 170 Glu Phe Phe Lys Ile Val Asn Leu Val Asn Asp Val Ser Glu Met Glu 180 185 190 Val Asn Thr Ile Ile Gly Asn Pro Glu Glu Phe Lys Ser Leu Val Pro 200 195 Asp Phe His Thr Asp Asp Thr Lys Phe Gln His Ile Leu Gly Leu Val 215 220 Asn Met Gly Tyr Arg Leu Lys Lys Thr Glu Trp Asn Thr Arg Cys Val 230 235 240 Asp Val Cys Ala Ala Leu Glu Glu Val Gly Gln Asn Lys Ile Asn Asn 250 255 245 Lys Ile Ser Asp Ser Glu Lys Leu Asp Arg Ile Leu Thr Ile Leu Glu 260 265 270 Asp Leu Asn Lys Arg Val Glu Leu Ile Glu Arg Ile Leu Asp Ile Arg 275 280 Met Glu Glu Lys Asn Asn Gln Arg Ser Glu Glu Asp Glu Glu Arg Lys 290 295 300 Gln Glu Asp Glu Gly Val Glu Arg Gln Pro Glu Ala Glu Glu Gly 310 315 Gly Leu Glu Arg Lys Ala Glu Asn Asp Asn Glu Ser Phe Glu Asp Ser 325 330 Ile Arg Glu Pro Asn Thr Gln Tyr Gly Ser Tyr Pro Gly Asp Asp Glu 340 345 Asn Thr Gln Arg Asp Val Gly Asp Glu Leu Val Glu Glu Ser Ser Lys 360 365 Asp Lys Ser Pro Thr Pro Arg Ser Ser Thr Pro Asn Phe Asn Ile Leu 370 375 380 Ser Glu Glu Ser Leu Asp Val Gln Lys Asp Lys Lys Arg Val Ser Arg 390 395 Gly Arg Asn Glu Asn Lys Arg Val Lys Pro Asn Val Tyr Ala Glu Asp 410 415 Asn Leu Lys Thr Arg Lys Gln Val Pro Arg Lys Arg His Lys Gln Val 425 430 Asp Ile Ala Asp Val His Val Pro Thr Arg Lys Glu Ala Gln Ser Lys 435 440 445 Lys Arg Lys Asn Ile Gly Asn Asp Gly Asp Asn Ala Asp Asn Asp Gly 450 455 460 Asp Asn Asp Asp Phe Gln Pro Ala Pro Gln Arg Lys Ser Lys Arg Gly 470 475

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Thr Val Pro Ser Ile His Thr Gln Ala Pro Phe Thr Ala Glu Lys Lys
                          490
           485
Lys His Pro Ile Leu His Pro Phe Ala Lys Val Asp Ala Thr Arg Leu
       500 505 510
Glu Lys Leu Ala Val Trp Lys Lys Ser Arg Lys Asn Lys Pro Leu Ser
     515 520 525
Ile Ala Gly Asn Asn Val Asp Thr Lys Trp Phe Thr Thr Leu Glu Thr
  530 535
                     540
Pro Gly Lys Ala Ile Thr Ala Thr His Val Asp Ala Ala Leu Glu Leu
   550 555 560
Met Lys Thr Arg Lys Glu Ser Asn Pro Glu Leu Phe Lys Asn Lys Ser
          565 570 575
Val Val Phe Val Gly Ser Ser Phe Leu Asn Val Ile Asp Glu Ser Tyr
      580 585 590
Met Glu Phe Leu Asp Asn Lys Glu Gly Phe Gln Phe Gln Ser Glu Glu
                   600
                           605
Ile Ser Lys Leu Ile Ile Glu Glu Glu Thr Lys Cys Ile Leu Ala Pro
                 615
Phe Cys Ile Lys Gly Lys Cys Trp Val Ala Leu Leu Ile His Leu Glu
              630
                     635
Gln Lys Thr Val Cys Ile Trp Glu Cys Ala Ala Ser Tyr Leu Thr Glu
                        650
Glu Val Lys Lys Lys Tyr Val Ala Ala Tyr Ser Ile Ala Met Pro Tyr
                       665
Ile Val Arg Asn Ile Leu Lys Lys Glu Asp Met Asp Val Ser Pro Phe
                   680
                         685
Ser Ile Lys Val Leu Thr Thr Phe Pro Gln Ala Pro Arg Asn Glu Glu
  690 695
                        700
Ser Gly Ile Tyr Met Leu Lys Phe Met Glu Cys Tyr Ser Met Tyr Thr
      710 715 720
Ser His Ser Asn Xaa Glu Gly Asn Ile Ile Gln Asn Val Arg Asn Lys
     725 730 735
Leu Ala Ala Asp Ile Phe Thr Glu Leu Gly Cys Phe Asp Leu Asn Gly
  740 745
```

Lys Gly Leu 755

(2) INFORMATION FOR SEQ ID NO:1041:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 738 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..738
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

Met Gln Gln Arg Val Lys Thr Lys Gly Ser Thr Leu Trp Phe Arg Val 1 5 5 10 10 15 Asp Ser Gln Pro Ile Arg Phe Ser Leu Arg Glu Phe Tyr Leu Thr Thr

20 25 30 Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly Lys

Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly Lys
35 40 45
Asp Pro Glu Gly Glu Pro Ala Val Glu Asp Glu Glu Lys Leu Cys Leu

50 55 60 Ala Ala Val Val Leu Ile Glu Gly Ile Leu Leu Thr Pro Tyr Gly Lys

65 $\,$ 70 $\,$ 75 $\,$ 80 Glu Lys Ile Pro Leu Pro Arg Leu Gln His Ala Ser Asp Phe Glu Met

85 90 95 Tyr Thr Ala Gln Pro Met Asp Glu Lys Thr Trp Ala Lys Glu Lys Tyr

100 105 Asp Leu Arg Gly Phe Gly Leu Ala Leu Thr Ile Trp Val Leu Ser Ala 120 125 Val Leu Ala Phe Gly Ala Ala Tyr Gly Val Lys Asp Lys Glu Phe Gln 130 135 140 Ser Glu Tyr Pro Leu Ile Leu Lys Trp Lys Ser Thr Thr Thr Pro Glu 150 155 160 Phe Phe Lys Ile Val Asn Leu Val Asn Asp Val Ser Glu Met Glu Val 165 170 Asn Thr Ile Ile Gly Asn Pro Glu Glu Phe Lys Ser Leu Val Pro Asp 180 185 190 Phe His Thr Asp Asp Thr Lys Phe Gln His Ile Leu Gly Leu Val Asn 195 200 Met Gly Tyr Arg Leu Lys Lys Thr Glu Trp Asn Thr Arg Cys Val Asp 220 210 215 Val Cys Ala Ala Leu Glu Glu Val Gly Gln Asn Lys Ile Asn Asn Lys 230 235 Ile Ser Asp Ser Glu Lys Leu Asp Arg Ile Leu Thr Ile Leu Glu Asp 245 250 Leu Asn Lys Arg Val Glu Leu Ile Glu Arg Ile Leu Asp Ile Arg Met 265 Glu Glu Lys Asn Asn Gln Arg Ser Glu Glu Asp Glu Glu Arg Lys Gln 280 Glu Asp Glu Gly Val Glu Arg Gln Pro Glu Ala Glu Glu Gly Gly 295 300 Leu Glu Arg Lys Ala Glu Asn Asp Asn Glu Ser Phe Glu Asp Ser Ile 310 315 Arg Glu Pro Asn Thr Gln Tyr Gly Ser Tyr Pro Gly Asp Asp Glu Asn 325 330 Thr Gln Arg Asp Val Gly Asp Glu Leu Val Glu Glu Ser Ser Lys Asp 345 340 Lys Ser Pro Thr Pro Arg Ser Ser Thr Pro Asn Phe Asn Ile Leu Ser 360 365 Glu Glu Ser Leu Asp Val Gln Lys Asp Lys Lys Arg Val Ser Arg Gly 375 380 Arg Asn Glu Asn Lys Arg Val Lys Pro Asn Val Tyr Ala Glu Asp Asn 390 395 Leu Lys Thr Arg Lys Gln Val Pro Arg Lys Arg His Lys Gln Val Asp 410 405 Ile Ala Asp Val His Val Pro Thr Arg Lys Glu Ala Gln Ser Lys Lys 425 420 Arg Lys Asn Ile Gly Asn Asp Gly Asp Asn Ala Asp Asn Asp Gly Asp 440 Asn Asp Asp Phe Gln Pro Ala Pro Gln Arg Lys Ser Lys Arg Gly Thr 450 455 460 Val Pro Ser Ile His Thr Gln Ala Pro Phe Thr Ala Glu Lys Lys 465 470 475 His Pro Ile Leu His Pro Phe Ala Lys Val Asp Ala Thr Arg Leu Glu 490 495 485 Lys Leu Ala Val Trp Lys Lys Ser Arg Lys Asn Lys Pro Leu Ser Ile 505 510 500 Ala Gly Asn Asn Val Asp Thr Lys Trp Phe Thr Thr Leu Glu Thr Pro 515 520 525 Gly Lys Ala Ile Thr Ala Thr His Val Asp Ala Ala Leu Glu Leu Met 530 535 540 Lys Thr Arg Lys Glu Ser Asn Pro Glu Leu Phe Lys Asn Lys Ser Val 550 555 560 Val Phe Val Gly Ser Ser Phe Leu Asn Val Ile Asp Glu Ser Tyr Met 565 570 575 Glu Phe Leu Asp Asn Lys Glu Gly Phe Gln Phe Gln Ser Glu Glu Ile 585

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Ser Lys Leu Ile Ile Glu Glu Glu Thr Lys Cys Ile Leu Ala Pro Phe
                            600
Cys Ile Lys Gly Lys Cys Trp Val Ala Leu Leu Ile His Leu Glu Gln
                        615
                                            620
Lys Thr Val Cys Ile Trp Glu Cys Ala Ala Ser Tyr Leu Thr Glu Glu
                    630
                                        635
Val Lys Lys Tyr Val Ala Ala Tyr Ser Ile Ala Met Pro Tyr Ile
                                    650
Val Arg Asn Ile Leu Lys Lys Glu Asp Met Asp Val Ser Pro Phe Ser
                                665
Ile Lys Val Leu Thr Thr Phe Pro Gln Ala Pro Arg Asn Glu Glu Ser
                            680
                                                685
Gly Ile Tyr Met Leu Lys Phe Met Glu Cys Tyr Ser Met Tyr Thr Ser
                                            700
    690
                       695
His Ser Asn Xaa Glu Gly Asn Ile Ile Gln Asn Val Arg Asn Lys Leu
                    710
                                       715
Ala Ala Asp Ile Phe Thr Glu Leu Gly Cys Phe Asp Leu Asn Gly Lys
                725
                                    730
Gly Leu
```

(2) INFORMATION FOR SEQ ID NO:1042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -

aagtccacac ctacaaagga ggcataa

- (B) LOCATION: 1..1707
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596099
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042: atggttgaat cggacaagtc atccgttgaa gagctgaaga agagggttag gaagagaagc 60 120 cqtqqgaaqa aqaatgagca gcaaaaggct gaagaaaaaa cccacactgt agaggaaaac qctqatqaaa cqcaqaaqaa gagtqaaaag aaggttaaga aagtgagagg caaaatcgag qaaqagqaaq aaaaqgtqga aqcaatgqaa gatggtgaag atgagaagaa tattgtgatt 240 qtcqqqaaaq qqataatqac taatqtqact tttqattccc tcqacttatc tgaqcaaact tctataqcta tcaaqqatat qqqctttcaq tacatqacqc aaattcaaqc tggatcaatt 420 cagccccttt tggaggggaa ggatgttctt ggtgctgcca gaactggttc tggtaaaact cttgcttttc tcattccggc tgttgagttg ctgtttaaag agcgtttctc tcctcgcaac 480 gggactggtg tgattgttat ttgccccaca agggaacttg ctatccagac taaaaatgtg gcggaggagt tactcaagca tcattcacag acagtcagca tggttattgg tggcaataac 600 660 agaaggtcgg aagcacaacg cattgccagt ggttcaaact tggtgatagc aactcctggt cgtcttcttg accatcttca gaatacaaag gctttcattt ataaacactt gaagtgcctt 720 gtgatcgatg aagctgatag gatactggaa gagaattttg aggaagacat gaataagatt 780 ctaaagattt taccaaagac taggcaaact gcgttattct ctgccaccca gacctctaag 840 gttaaagatc ttgctcgggt gtcattgaca tcacctgttc atgtggatgt cgatgatggc 900 960 agacgcaagg tgacaaatga aggattggag caaggctatt gtgttgttcc gagcaaacaa 1020 agacttatcc ttctaatttc ctttttgaaa aagaacctaa ataaaaagat tatggtattt ttctcgactt gcaagtcggt acaattccat acggaaatca tgaaaataag cgacgtggat 1080 gtctctgata ttcatggagg catggatcag aacagaagaa ctaaaacctt tttcgacttc 1140 1200 atgaaagcaa agaaaggtat cttgttatgt actgatgttg ctgctcgtgg tctcgatatt ccttccgtgg actggattat acagtatgat ccaccagaca agccaacgga atatatccat 1260 agggttggtc gaacagcccg tggagaagga gcaaagggaa aggcattact tgtcttgatt 1320 cctgaagaac ttcagtttat tcgctacctg aaggctgcga aagtacctgt taaagagctt gagttcaatg agaagaggct tagtaatgtt caatctgcgc tggagaaatg tgttgccaag qactacaatc tgaacaagtt agccaaagat gcgtacaggg cttatctctc agcatacaat 1500 teacactett tgaaagacat etttaatgtt cacegacttg accteetgge tgttgetgaa 1560 togttotgot totottogco gootaaagtg aatotgaaca tagaaagtgg agotgggaag 1620 qtgaggaagg cgagaaagca gcaaggtcgc aatggcttca gtccttacag tccctatggc 1680

- (2) INFORMATION FOR SEQ ID NO:1043:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 568 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..568
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596100
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:
- Met Val Glu Ser Asp Lys Ser Ser Val Glu Glu Leu Lys Lys Arg Val 1 5 10 15
- Arg Lys Arg Ser Arg Gly Lys Lys Asn Glu Gln Gln Lys Ala Glu Glu 20 25 30
- Lys Thr His Thr Val Glu Glu Asn Ala Asp Glu Thr Gln Lys Lys Ser 35 40 45
- Glu Lys Lys Val Lys Lys Val Arg Gly Lys Ile Glu Glu Glu Glu Glu 50 55
- Lys Val Glu Ala Met Glu Asp Gly Glu Asp Glu Lys Asn Ile Val Ile 65 70 75 80
- Val Gly Lys Gly Ile Met Thr Asn Val Thr Phe Asp Ser Leu Asp Leu 85 90 95
- Ser Glu Gln Thr Ser Ile Ala Ile Lys Asp Met Gly Phe Gln Tyr Met 100 105 110
- Thr Gln Ile Gln Ala Gly Ser Ile Gln Pro Leu Leu Glu Gly Lys Asp 115 120 125
- Val Leu Gly Ala Ala Arg Thr Gly Ser Gly Lys Thr Leu Ala Phe Leu 130 135 140
- Ile Pro Ala Val Glu Leu Leu Phe Lys Glu Arg Phe Ser Pro Arg Asn 145 150 155 160
- Gly Thr Gly Val Ile Val Ile Cys Pro Thr Arg Glu Leu Ala Ile Gln 165 170 175
- Thr Lys Asn Val Ala Glu Glu Leu Leu Lys His His Ser Gln Thr Val
- Ser Met Val Ile Gly Gly Asn Asn Arg Arg Ser Glu Ala Gln Arg Ile
- Ala Ser Gly Ser Asn Leu Val Ile Ala Thr Pro Gly Arg Leu Leu Asp 210 215 220 His Leu Gln Asn Thr Lys Ala Phe Ile Tyr Lys His Leu Lys Cys Leu
- 225 230 235 240
 Val Ile Asp Glu Ala Asp Arg Ile Leu Glu Glu Asp Phe Glu Glu Asp
- 245 250 255 Met Asn Lys Ile Leu Lys Ile Leu Pro Lys Thr Arg Gln Thr Ala Leu
- 260 265 270

 Phe Ser Ala Thr Gln Thr Ser Lys Val Lys Asp Leu Ala Arg Val Ser
- 275 280 285

 Leu Thr Ser Pro Val His Val Asp Val Asp Asp Gly Arg Arg Lys Val
- 290 295 300
 Thr Asn Glu Gly Leu Glu Gln Gly Tyr Cys Val Val Pro Ser Lys Gln
- Thr Ash Giu Giy Leu Giu Gin Giy Tyr Cys var var Fio Ser Bys Gin 305 310 315 320 Arg Leu Ile Leu Leu Ile Ser Phe Leu Lys Lys Ash Leu Ash Lys Lys
- 325 330 335

 Ile Met Val Phe Phe Ser Thr Cys Lys Ser Val Gln Phe His Thr Glu
- 340 345 350

 Ile Met Lys Ile Ser Asp Val Asp Val Ser Asp Ile His Gly Gly Met 355 360 365
- Asp Gln Asn Arg Arg Thr Lys Thr Phe Phe Asp Phe Met Lys Ala Lys 370 375 380
- Lys Gly Ile Leu Leu Cys Thr Asp Val Ala Ala Arg Gly Leu Asp Ile

 385
 5390
 400

 Pro
 Ser
 Val
 Asp
 Trp
 Ile
 Ile
 Gln
 Tyr
 Asp
 Pro
 Pro
 Asp
 Lys
 Pro
 Thr
 Thr
 Als
 Lys
 Als
 Als

450 455 460 Lys Arg Leu Ser Asn Val Gln Ser Ala Leu Glu Lys Cys Val Ala Lys 465 470 475 480

Asp Tyr Asn Leu Asn Lys Leu Ala Lys Asp Ala Tyr Arg Ala Tyr Leu 485 490 495

Ser Ala Tyr Asn Ser His Ser Leu Lys Asp Ile Phe Asn Val His Arg 500 505 510

Leu Asp Leu Leu Ala Val Ala Glu Ser Phe Cys Phe Ser Ser Pro Pro 515 520 525

Lys Val Asn Leu Asn Ile Glu Ser Gly Ala Gly Lys Val Arg Lys Ala 530 540

Arg Lys Gln Gln Gly Arg Asn Gly Phe Ser Pro Tyr Ser Pro Tyr Gly 545 550 555 560

Lys Ser Thr Pro Thr Lys Glu Ala 565

- (2) INFORMATION FOR SEQ ID NO:1044:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044: Met Glu Asp Glu Asp Glu Lys Asn Ile Val Ile Val Gly Lys Gly

1 5 10 15

Ile Met Thr Asn Val Thr Phe Asp Ser Leu Asp Leu Ser Glu Gln Thr
20 25 30

Ser Ile Ala Ile Lys Asp Met Gly Phe Gln Tyr Met Thr Gln Ile Gln 35 40 45

Ala Gly Ser Ile Gln Pro Leu Leu Glu Gly Lys Asp Val Leu Gly Ala 50 55 60

Ala Arg Thr Gly Ser Gly Lys Thr Leu Ala Phe Leu Ile Pro Ala Val 65 70 75 80

Glu Leu Leu Phe Lys Glu Arg Phe Ser Pro Arg Asn Gly Thr Gly Val 85 90 95

Ile Val Ile Cys Pro Thr Arg Glu Leu Ala Ile Gln Thr Lys Asn Val

Ala Glu Glu Leu Leu Lys His His Ser Gln Thr Val Ser Met Val Ile 115 120 125

Gly Gly Asn Asn Arg Arg Ser Glu Ala Gln Arg Ile Ala Ser Gly Ser 130 135 140

Asn Leu Val Ile Ala Thr Pro Gly Arg Leu Leu Asp His Leu Gln Asn 145 150 150 155 160

Thr Lys Ala Phe Ile Tyr Lys His Leu Lys Cys Leu Val Ile Asp Glu 165 170 175

Ala Asp Arg Ile Leu Glu Glu Asn Phe Glu Glu Asp Met Asn Lys Ile 180 185 190

Leu Lys Ile Leu Pro Lys Thr Arg Gln Thr Ala Leu Phe Ser Ala Thr
195 200 205

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Gln Thr Ser Lys Val Lys Asp Leu Ala Arg Val Ser Leu Thr Ser Pro
                      215
Val His Val Asp Val Asp Asp Gly Arg Arg Lys Val Thr Asn Glu Gly
                 230
                                    235
Leu Glu Gln Gly Tyr Cys Val Val Pro Ser Lys Gln Arg Leu Ile Leu
              245
                                250
Leu Ile Ser Phe Leu Lys Lys Asn Leu Asn Lys Ile Met Val Phe
          260
                             265
                                               270
Phe Ser Thr Cys Lys Ser Val Gln Phe His Thr Glu Ile Met Lys Ile
       275
                        280
                                           285
Ser Asp Val Asp Val Ser Asp Ile His Gly Gly Met Asp Gln Asn Arg
                                       300
                  295
Arg Thr Lys Thr Phe Phe Asp Phe Met Lys Ala Lys Lys Gly Ile Leu
               310
                                   315
Leu Cys Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Ser Val Asp
              325
                                330
Trp Ile Ile Gln Tyr Asp Pro Pro Asp Lys Pro Thr Glu Tyr Ile His
          340
                            345
Arg Val Gly Arg Thr Ala Arg Gly Glu Gly Ala Lys Gly Lys Ala Leu
                         360
Leu Val Leu Ile Pro Glu Glu Leu Gln Phe Ile Arg Tyr Leu Lys Ala
                     375
                                       380
Ala Lys Val Pro Val Lys Glu Leu Glu Phe Asn Glu Lys Arg Leu Ser
                 390
                                   395
Asn Val Gln Ser Ala Leu Glu Lys Cys Val Ala Lys Asp Tyr Asn Leu
                                410
             405
Asn Lys Leu Ala Lys Asp Ala Tyr Arg Ala Tyr Leu Ser Ala Tyr Asn
                            425
          420
Ser His Ser Leu Lys Asp Ile Phe Asn Val His Arg Leu Asp Leu Leu
                        440
Ala Val Ala Glu Ser Phe Cys Phe Ser Ser Pro Pro Lys Val Asn Leu
                     455
Asn Ile Glu Ser Gly Ala Gly Lys Val Arg Lys Ala Arg Lys Gln Gln
                470
                                   475
Gly Arg Asn Gly Phe Ser Pro Tyr Ser Pro Tyr Gly Lys Ser Thr Pro
                                490
Thr Lys Glu Ala
          500
```

- (2) INFORMATION FOR SEQ ID NO:1045:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1173
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596137
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045: 60 atgactgata ttaacaccaa caacgagatc gttggcaaca ccacagttgc tgagaccgcg 120 gatgaggaag ctttgcacct tgcgaaagag cttgaaatga cacagatcac cgattctgat 180 atggataatg tgcgccgaaa tctgttcggt aatggttcaa ccaacactac cataccagcc tctgtttccc aagggatgat gtcacacttg tttgatggca aatccgggtt caaaacgtgg 240 caagaaaaga tgcgctacta tttggtcagc ataaacatgg aaaggtacct cccagaggat 300 ccaccaatag ttccgcaagg tgactattgt tgcaaaggtc taatcctgaa ccgcttggtg 360 aacgatctgt ttgaccttta cagcaaggcc aagtcttcca aaacactgtg gctaacttta 420 gagaacaagt ataagactga tgagtctaga atgcaaagat tctcaactgc gaagtttctg 480 540 aatttcaaga tggtggactc caaaccaatc atggaacagg tggaggctct tcaacgtatc 600 tgtcaagaga tagagttgga agggatgtcg atctgcaacg tcttcaagac gaattgcttg atcaagaagc taccnccggg atggtcagat ttcaagaatt accttaactt caaacgtaag 660

qcaatqactt ttqatqatct catccqaaqq ttaatqattq taqqcaacaa tcqtqqqqct cacgcgggtg ctcagaatca agggcatgat gttaatgtag ctgagcataa ggccaagctg 780 aaaggcaagg gaaaagggtt ctctattcct cagaagaact tgaagattgg acacaaggct 840 gatgtttgca agagcaaagc caaggatgtc aagagccagg caaacctaac tgaagaggat 900 960 atggttgcag tggtcactga atgtaacatg gtggacgaca accaagtgaa gtggtactac gacactggtg caaccacaca catctgcaca gataggacca tgttctccac ctatgtgaat 1020 aacaagtcaa acgaacaact cttcatgggc aacacggcga tgtctaagat tgaaggtaag 1080 ggaaaagtgg ttctgaaggt gacttcggga cgtgagctta ctctgcaaaa cgtgaagcat 1140 gtacctgaca tgcggaagaa tctcatctct tga

- (2) INFORMATION FOR SEQ ID NO:1046:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..390
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

Met Thr Asp Ile Asn Thr Asn Asn Glu Ile Val Gly Asn Thr Thr Val 1 5 10 15

Ala Glu Thr Ala Asp Glu Glu Ala Leu His Leu Ala Lys Glu Leu Glu 20 25 30

Met Thr Gln Ile Thr Asp Ser Asp Met Asp Asn Val Arg Arg Asn Leu 35 40 45

Phe Gly Asn Gly Ser Thr Asn Thr Thr Ile Pro Ala Ser Val Ser Gln 50 60

Gly Met Met Ser His Leu Phe Asp Gly Lys Ser Gly Phe Lys Thr Trp 65 70 75 80

Gln Glu Lys Met Arg Tyr Tyr Leu Val Ser Ile Asn Met Glu Arg Tyr 85 90 95

Leu Pro Glu Asp Pro Pro Ile Val Pro Gln Gly Asp Tyr Cys Cys Lys
100 105 110

Gly Leu Ile Leu Asn Arg Leu Val Asn Asp Leu Phe Asp Leu Tyr Ser 115 120 125

Lys Ala Lys Ser Ser Lys Thr Leu Trp Leu Thr Leu Glu Asn Lys Tyr 130 135 140

Asn Phe Lys Met Val Asp Ser Lys Pro Ile Met Glu Gln Val Glu Ala 165 170 175

Leu Gln Arg Ile Cys Gln Glu Ile Glu Leu Glu Gly Met Ser Ile Cys 180 185 190

Asn Val Phe Lys Thr Asn Cys Leu Ile Lys Lys Leu Xaa Pro Gly Trp 195 200 205

Ser Asp Phe Lys Asn Tyr Leu Asn Phe Lys Arg Lys Ala Met Thr Phe 210 220

Asp Asp Leu Ile Arg Arg Leu Met Ile Val Gly Asn Asn Arg Gly Ala 225 230 235 240

His Ala Gly Ala Gln Asn Gln Gly His Asp Val Asn Val Ala Glu His 245 250 255

Lys Ala Lys Leu Lys Gly Lys Gly Lys Gly Phe Ser Ile Pro Gln Lys 260 265 270

Asn Leu Lys Ile Gly His Lys Ala Asp Val Cys Lys Ser Lys Ala Lys $275 \hspace{1.5cm} 280 \hspace{1.5cm} 285$

Asp Val Lys Ser Gln Ala Asn Leu Thr Glu Glu Asp Met Val Ala Val 290 295 300

Val Thr Glu Cys Asn Met Val Asp Asp Asn Gln Val Lys Trp Tyr Tyr 305 310 315 320

Asp Thr Gly Ala Thr Thr His Ile Cys Thr Asp Arg Thr Met Phe Ser 325 330 335

Thr Tyr Val Asn Asn Lys Ser Asn Glu Gln Leu Phe Met Gly Asn Thr 340 345 350

Ala Met Ser Lys Ile Glu Gly Lys Gly Lys Val Val Leu Lys Val Thr 355 360 365

Ser Gly Arg Glu Leu Thr Leu Gln Asn Val Lys His Val Pro Asp Met 370 375 380

Arg Lys Asn Leu Ile Ser

385 390

- (2) INFORMATION FOR SEQ ID NO:1047:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..358
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596140
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:
- Met Thr Gln Ile Thr Asp Ser Asp Met Asp Asn Val Arg Arg Asn Leu
 1 10 15
- Phe Gly Asn Gly Ser Thr Asn Thr Thr Ile Pro Ala Ser Val Ser Gln 20 25 30
- Gly Met Met Ser His Leu Phe Asp Gly Lys Ser Gly Phe Lys Thr Trp 35 40 45
- Gln Glu Lys Met Arg Tyr Tyr Leu Val Ser Ile Asn Met Glu Arg Tyr 50 55 60
- Leu Pro Glu Asp Pro Pro Ile Val Pro Gln Gly Asp Tyr Cys Cys Lys 65 70 75 80
- Gly Leu Ile Leu Asn Arg Leu Val Asn Asp Leu Phe Asp Leu Tyr Ser
- Lys Ala Lys Ser Ser Lys Thr Leu Trp Leu Thr Leu Glu Asn Lys Tyr
 100 105 110
- Lys Thr Asp Glu Ser Arg Met Gln Arg Phe Ser Thr Ala Lys Phe Leu 115 120 125 Asn Phe Lys Met Val Asp Ser Lys Pro Ile Met Glu Gln Val Glu Ala
- 130 135 140
 Leu Gln Arg Ile Cys Gln Glu Ile Glu Leu Glu Gly Met Ser Ile Cys
- 145 150 155 160
 Asn Val Phe Lys Thr Asn Cys Leu Ile Lys Lys Leu Xaa Pro Gly Trp
- 165 170 175 Ser Asp Phe Lys Asn Tyr Leu Asn Phe Lys Arg Lys Ala Met Thr Phe
- Asp Asp Leu Ile Arg Arg Leu Met Ile Val Gly Asn Asp Arg Gly Ala
 195 200 205
- His Ala Gly Ala Gln Asn Gln Gly His Asp Val Asn Val Ala Glu His
 210 215 220
- Lys Ala Lys Leu Lys Gly Lys Gly Lys Gly Phe Ser Ile Pro Gln Lys 225 230 235 240
- Asn Leu Lys Ile Gly His Lys Ala Asp Val Cys Lys Ser Lys Ala Lys 245 250 255
- Asp Val Lys Ser Gln Ala Asn Leu Thr Glu Glu Asp Met Val Ala Val
 260 265 270
- Val Thr Glu Cys Asn Met Val Asp Asp Asn Gln Val Lys Trp Tyr Tyr
- Asp Thr Gly Ala Thr Thr His Ile Cys Thr Asp Arg Thr Met Phe Ser 290 295 300

 Thr Tyr Val Asn Asn Lys Ser Asn Glu Gln Leu Phe Met Gly Asn Thr

Arg Lys Asn Leu Ile Ser 355

- (2) INFORMATION FOR SEQ ID NO:1048:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1509
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596141
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

atgccgaagt acttagagga ttacgttcta cttgctgaag aagaaagtga atatctcctc 60 tctgtaataa acgaggaacc ttgggattat gctgaagcaa aagaaacaca agagtggaga 120 180 qaaqcqtqtq aqqacqaaat cqcttcaatt qaqaaqaaca aqacatqqqa tttaqtqqaa 240 cttcctcaag gagctaagcc aatcgggctc aaatgggtgt ttaagctaaa gaagaacgca 300 qaaqqqaaca taaacaaqta taaqqcaaqa ctcqtqqcta aaqqttacqt acaacqacat 360 ggcatagatt ttgacgaagt ctttgcccct gtagcacgaa tcgaaacagt ccgcttcatc 420 attgccctag ctgcttcaaa cggatgggaa gtgcatcatc tcgatgtcaa aacagcattc 480 ttacacggtg aattaaaaga gatagtattt gtttcacaac cagaaggatt cacagagaaa gggagttcta gcttaaagct cattaatgac ttcaagaagg gaatggcgtc caagtttgag 540 atgagtgatc tcgggttact cacatactat cttggaatcg aagtaattca gtataatgga 600 ggaattatgt tgaaacaagg gagatatgca gagaagatcc tagacgaaac caagatgagt 660 gattgcaacg cagttcacat tccaatggac tccggtttga agctgtcaaa agcgggaaca 720 780 gagaaaggaa gtcatgactc ggagacagag aagaacattg agccaaaaga gtatagaaga aacattggat gtcttcggta tctacttcac acacgacctg acctctcata ctgtgttggt 840 900 gtgttgagta gatacatgca agaacctaaa gaaggtcatg gagtagctat gaagcagatt atgagatact tgcgtggcac tacttcctat ggactatctt tcaagcgagg agacaaatcg 960 1020 gggctaatag gtttcagtga tagcagtcac aatgtagacg aggatgatgg gaggagcaca accggacata tattctacct tgatggctct ctgataactt ggtgtacaca aaagcaagaa actgtggctt tatcgtcttg tgaggctgag tttatggcag ccactgaagg agctaagcag 1200 qcaatttggt tgcaagaatt acttggagag gtaacaggag aagcatgcaa gaaggtgaga ctactcattg acaacaaatc ggcgatagca cttgccaaga atccagtatt tcacggccgg agcaaacaca ttcataagag gtaccatttc attcgtgagt atgttgagaa tgagcaaata gaagtggaac acgttcccgg ggaagaacag aaggcaaatc ttctaacaaa ggcacttgga aqaatcaaat tcaaaqaqat qaqaqaqcta qttqqaqttc aaqagttqtc gaagtqtqaq ttcaagctta agggagtgaa tgttgataag cttgaagtta gcttaaggaa taagctaacc 1500 aaatcctaa

- (2) INFORMATION FOR SEQ ID NO:1049:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..502
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596142
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

Met Pro Lys Tyr Leu Glu Asp Tyr Val Leu Leu Ala Glu Glu Glu Ser
1 5 10 15
Glu Tyr Leu Leu Ser Val Ile Asn Glu Glu Pro Trp Asp Tyr Ala Glu

Ala Lys Glu Thr Gln Glu Trp Arg Glu Ala Cys Glu Asp Glu Ile Ala Ser Ile Glu Lys Asn Lys Thr Trp Asp Leu Val Glu Leu Pro Gln Gly 55 Ala Lys Pro Ile Gly Leu Lys Trp Val Phe Lys Leu Lys Lys Asn Ala 70 Glu Gly Asn Ile Asn Lys Tyr Lys Ala Arg Leu Val Ala Lys Gly Tyr 90 Val Gln Arg His Gly Ile Asp Phe Asp Glu Val Phe Ala Pro Val Ala 100 105 Arg Ile Glu Thr Val Arg Phe Ile Ile Ala Leu Ala Ala Ser Asn Gly 120 115 125 Trp Glu Val His His Leu Asp Val Lys Thr Ala Phe Leu His Gly Glu 140 135 Leu Lys Glu Ile Val Phe Val Ser Gln Pro Glu Gly Phe Thr Glu Lys 155 150 Gly Ser Ser Ser Leu Lys Leu Ile Asn Asp Phe Lys Lys Gly Met Ala 165 170 175 Ser Lys Phe Glu Met Ser Asp Leu Gly Leu Leu Thr Tyr Tyr Leu Gly 185 190 180 Ile Glu Val Ile Gln Tyr Asn Gly Gly Ile Met Leu Lys Gln Gly Arg 195 200 Tyr Ala Glu Lys Ile Leu Asp Glu Thr Lys Met Ser Asp Cys Asn Ala 215 Val His Ile Pro Met Asp Ser Gly Leu Lys Leu Ser Lys Ala Gly Thr 230 235 Glu Lys Gly Ser His Asp Ser Glu Thr Glu Lys Asn Ile Glu Pro Lys 250 245 Glu Tyr Arg Arg Asn Ile Gly Cys Leu Arg Tyr Leu Leu His Thr Arg 260 265 Pro Asp Leu Ser Tyr Cys Val Gly Val Leu Ser Arg Tyr Met Gln Glu 280 Pro Lys Glu Gly His Gly Val Ala Met Lys Gln Ile Met Arg Tyr Leu 295 300 Arg Gly Thr Thr Ser Tyr Gly Leu Ser Phe Lys Arg Gly Asp Lys Ser 310 315 Gly Leu Ile Gly Phe Ser Asp Ser Ser His Asn Val Asp Glu Asp Asp 325 330 Gly Arg Ser Thr Thr Gly His Ile Phe Tyr Leu Asp Gly Ser Leu Ile 340 345 Thr Trp Cys Thr Gln Lys Gln Glu Thr Val Ala Leu Ser Ser Cys Glu 355 360 Ala Glu Phe Met Ala Ala Thr Glu Gly Ala Lys Gln Ala Ile Trp Leu 370 375 380 Gln Glu Leu Gly Glu Val Thr Gly Glu Ala Cys Lys Val Arg 390 395 400 Leu Leu Ile Asp Asn Lys Ser Ala Ile Ala Leu Ala Lys Asn Pro Val 405 410 Phe His Gly Arg Ser Lys His Ile His Lys Arg Tyr His Phe Ile Arg 420 425 Glu Tyr Val Glu Asn Glu Gln Ile Glu Val Glu His Val Pro Gly Glu 435 440 Glu Gln Lys Ala Asn Leu Leu Thr Lys Ala Leu Gly Arg Ile Lys Phe 455 Lys Glu Met Arg Glu Leu Val Gly Val Gln Glu Leu Ser Lys Cys Glu 470 475 Phe Lys Leu Lys Gly Val Asn Val Asp Lys Leu Glu Val Ser Leu Arg 485 490 Asn Lys Leu Thr Lys Ser

(2) INFORMATION FOR SEQ ID NO:1050:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..328
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596144
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:
- Leu Gly Ile Glu Val Ile Gln Tyr Asn Gly Gly Ile Met Leu Lys Gln 20 25 30
- Gly Arg Tyr Ala Glu Lys Ile Leu Asp Glu Thr Lys Met Ser Asp Cys
- 35 40 45
- Asn Ala Val His Ile Pro Met Asp Ser Gly Leu Lys Leu Ser Lys Ala 50 55 60
- Gly Thr Glu Lys Gly Ser His Asp Ser Glu Thr Glu Lys Asn Ile Glu 65 70 75 80
- Pro Lys Glu Tyr Arg Arg Asn Ile Gly Cys Leu Arg Tyr Leu Leu His 85 90 95
- Thr Arg Pro Asp Leu Ser Tyr Cys Val Gly Val Leu Ser Arg Tyr Met 100 105 110
- Gln Glu Pro Lys Glu Gly His Gly Val Ala Met Lys Gln Ile Met Arg 115 120 125
- Tyr Leu Arg Gly Thr Thr Ser Tyr Gly Leu Ser Phe Lys Arg Gly Asp 130 135 140
- Lys Ser Gly Leu Ile Gly Phe Ser Asp Ser Ser His Asn Val Asp Glu 145 150 150 160
- Asp Asp Gly Arg Ser Thr Thr Gly His Ile Phe Tyr Leu Asp Gly Ser 165 170 175
- Leu Ile Thr Trp Cys Thr Gln Lys Gln Glu Thr Val Ala Leu Ser Ser 180 185 190
- Cys Glu Ala Glu Phe Met Ala Ala Thr Glu Gly Ala Lys Gln Ala Ile
 195 200 205
- Trp Leu Gl
n Glu Leu Leu Gly Glu Val Thr Gly Glu Ala Cys Lys Lys 210 215 220
- Val Arg Leu Leu Ile Asp Asn Lys Ser Ala Ile Ala Leu Ala Lys Asn 225 230 235 240
- Pro Val Phe His Gly Arg Ser Lys His Ile His Lys Arg Tyr His Phe 245 250 255
- Ile Arg Glu Tyr Val Glu As
n Glu Gl
n Ile Glu Val Glu His Val Pro $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$
- Gly Glu Glu Gln Lys Ala Asn Leu Leu Thr Lys Ala Leu Gly Arg Ile 275 280 285
- Lys Phe Lys Glu Met Arg Glu Leu Val Gly Val Gln Glu Leu Ser Lys 290 295 300
- Cys Glu Phe Lys Leu Lys Gly Val As
n Val Asp Lys Leu Glu Val Ser 305 310 315 320
- Leu Arg Asn Lys Leu Thr Lys Ser 325
- (2) INFORMATION FOR SEQ ID NO:1051:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1508

(D) OTHER INFORMATION: / Ceres Seq. ID 1596153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051: taaaaccatt ctcaattctc gtcaacgaca acaacataac tgttcgtcga tcttggtata 60 tctacaggaa actaagaaat tgggtttgga gaaatggctc gaacaaagaa cgcaggtata 120 tctatgtgga gaagttcttc cttagggctg tggctgatct agagttgtgc aaaacatttc 180 cqtqqqqaaq atttqtattt qaaqaaaatq tqaaaqacat tttctatttq attaaaaaqt 240 gcaatgaagt agttggtcca caaaaggtgt ttcctagttt tgttatgcct ttggagtatc 300 360 tagcatttga ggcgatccca gttctcagga aaaatttctg cgaagatatt gaatccgcag atcctcagtg ttcccggatg tgtaaaagga agtttaaatc aagcactatg aaagggtttc 420 480 caatgtcaga tgtgtatgac aaactcggta caactaagga cattcagagt atcttggctc caactcctga tgagaagcta cttttggaaa gaattatgga taaggagttt ggagtgaatg 540 600 atgtcgatga tctaatagct gatggctgga agaaacgtct agttgatgag gagaggacta tatgttttga accgttgctc aatgaagatg tagcacaccg gagctttgtg gctaatatag 660 720 ctttgtctac tgtggtaaaa gctccaagaa aagccgcagt ggaaaagaaa ggcaagggaa 780 aggctgctgc agctctgact agtccaagtg atggaggttt gactgaggtt gtaaacgaaa 840 tgaagaattt gatggagaat ggatttaagt ccatgaacaa gaggatgaaa gatttcaacg 900 cttgtggttc aaaggagatt gatgataaag aaaacgagct ggaggaaggg agtgatgcag 960 agactgagat acacaaagag gtggctcaag gtgataagga gagagaggtt ggagaaacag agactgagat ngacaaagag gtggctcaag gtgacagtga taaggaggtg gctgaaagtg 1020 1080 agaaggacaa agtggtggct gaaagtgaga aggagaaaga ggtggctgaa agtgagattg 1140 gggtggctga aagtgagaag gacaaagagg tgcctcaaga tgatgagatg gatggaggta aggtggctga gagtgatgga gagatggatg gagagaagga caaagaggtg cctcaagatg 1200 atgagatgga tggagagaag gagaaagagg tggctgagcc aagtgagatt ggggtgcctg 1260 aaagtgagaa ggacatagag gtggctgata gtgagaagga gaaagaggtg cctcaagatg 1320 ctaaggtggc tgagccaagt aagaagcgag gaaaggcaca tgaggatgga gatgatccta 1380 1440 gtaaagaagg agttaaaaag ccaaaggtgg tcaagaagct ggcagagtcg aggacggatg ctaagccggt gtatcggagt cctatacaaa cgaggtatag gaggaaaaag acaaagaaga 1500 atgtttaa

- (2) INFORMATION FOR SEQ ID NO:1052:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..501
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596154
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052: Lys Pro Phe Ser Ile Leu Val Asn Asp Asn Asn Ile Thr Val Arg Arg 10 5 Ser Trp Tyr Ile Tyr Arg Lys Leu Arg Asn Trp Val Trp Arg Asn Gly 30 25 20 Ser Asn Lys Glu Arg Arg Tyr Ile Tyr Val Glu Lys Phe Phe Leu Arg 35 Ala Val Ala Asp Leu Glu Leu Cys Lys Thr Phe Pro Trp Gly Arg Phe 55 60 Val Phe Glu Glu Asn Val Lys Asp Ile Phe Tyr Leu Ile Lys Lys Cys 75 70 Asn Glu Val Val Gly Pro Gln Lys Val Phe Pro Ser Phe Val Met Pro 90 85 Leu Glu Tyr Leu Ala Phe Glu Ala Ile Pro Val Leu Arg Lys Asn Phe 110 105 100 Cys Glu Asp Ile Glu Ser Ala Asp Pro Gln Cys Ser Arg Met Cys Lys 125 120 115 Arg Lys Phe Lys Ser Ser Thr Met Lys Gly Phe Pro Met Ser Asp Val 135 140 130 Tyr Asp Lys Leu Gly Thr Thr Lys Asp Ile Gln Ser Ile Leu Ala Pro

155 150 145 Thr Pro Asp Glu Lys Leu Leu Glu Arg Ile Met Asp Lys Glu Phe 165 170 Gly Val Asn Asp Val Asp Asp Leu Ile Ala Asp Gly Trp Lys Lys Arg 180 185 Leu Val Asp Glu Glu Arg Thr Ile Cys Phe Glu Pro Leu Leu Asn Glu 205 195 200 Asp Val Ala His Arg Ser Phe Val Ala Asn Ile Ala Leu Ser Thr Val 215 220 Val Lys Ala Pro Arg Lys Ala Ala Val Glu Lys Lys Gly Lys 230 235 Ala Ala Ala Leu Thr Ser Pro Ser Asp Gly Gly Leu Thr Glu Val 250 245 Val Asn Glu Met Lys Asn Leu Met Glu Asn Gly Phe Lys Ser Met Asn 260 265 Lys Arg Met Lys Asp Phe Asn Ala Cys Gly Ser Lys Glu Ile Asp Asp 280 Lys Glu Asn Glu Leu Glu Glu Gly Ser Asp Ala Glu Thr Glu Ile His 300 295 Lys Glu Val Ala Gln Gly Asp Lys Glu Arg Glu Val Gly Glu Thr Glu 310 315 Thr Glu Xaa Asp Lys Glu Val Ala Gln Gly Asp Ser Asp Lys Glu Val 325 330 Ala Glu Ser Glu Lys Asp Lys Val Val Ala Glu Ser Glu Lys Glu Lys 345 Glu Val Ala Glu Ser Glu Ile Gly Val Ala Glu Ser Glu Lys Asp Lys 365 360 Glu Val Pro Gln Asp Asp Glu Met Asp Gly Gly Lys Val Ala Glu Ser 380 375 Asp Gly Glu Met Asp Gly Glu Lys Asp Lys Glu Val Pro Gln Asp Asp 390 395 Glu Met Asp Gly Glu Lys Glu Lys Glu Val Ala Glu Pro Ser Glu Ile 410 405 Gly Val Pro Glu Ser Glu Lys Asp Ile Glu Val Ala Asp Ser Glu Lys 430 420 425 Glu Lys Glu Val Pro Gln Asp Ala Lys Val Ala Glu Pro Ser Lys Lys 440 445 Arg Gly Lys Ala His Glu Asp Gly Asp Asp Pro Ser Lys Glu Gly Val 455 460 Lys Lys Pro Lys Val Val Lys Lys Leu Ala Glu Ser Arg Thr Asp Ala 475 470 Lys Pro Val Tyr Arg Ser Pro Ile Gln Thr Arg Tyr Arg Arg Lys Lys 490 485 Thr Lys Lys Asn Val 500

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..407
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

Met Pro Leu Glu Tyr Leu Ala Phe Glu Ala Ile Pro Val Leu Arg Lys
1 5 10 15

Asn Phe Cys Glu Asp Ile Glu Ser Ala Asp Pro Gln Cys Ser Arg Met

Cys Lys Arg Lys Phe Lys Ser Ser Thr Met Lys Gly Phe Pro Met Ser 40 Asp Val Tyr Asp Lys Leu Gly Thr Thr Lys Asp Ile Gln Ser Ile Leu 55 Ala Pro Thr Pro Asp Glu Lys Leu Leu Glu Arg Ile Met Asp Lys 70 75 Glu Phe Gly Val Asn Asp Val Asp Asp Leu Ile Ala Asp Gly Trp Lys 90 Lys Arg Leu Val Asp Glu Glu Arg Thr Ile Cys Phe Glu Pro Leu Leu 100 105 110 Asn Glu Asp Val Ala His Arg Ser Phe Val Ala Asn Ile Ala Leu Ser 115 120 125 Thr Val Val Lys Ala Pro Arg Lys Ala Ala Val Glu Lys Lys Gly Lys 130 135 140 Gly Lys Ala Ala Ala Leu Thr Ser Pro Ser Asp Gly Gly Leu Thr 150 155 Glu Val Val Asn Glu Met Lys Asn Leu Met Glu Asn Gly Phe Lys Ser 165 170 175 Met Asn Lys Arg Met Lys Asp Phe Asn Ala Cys Gly Ser Lys Glu Ile 180 185 190 Asp Asp Lys Glu Asn Glu Leu Glu Glu Gly Ser Asp Ala Glu Thr Glu 195 200 205 Ile His Lys Glu Val Ala Gln Gly Asp Lys Glu Arg Glu Val Gly Glu 210 215 220 Thr Glu Thr Glu Xaa Asp Lys Glu Val Ala Gln Gly Asp Ser Asp Lys 225 230 235 Glu Val Ala Glu Ser Glu Lys Asp Lys Val Val Ala Glu Ser Glu Lys 245 250 255 Glu Lys Glu Val Ala Glu Ser Glu Ile Gly Val Ala Glu Ser Glu Lys 260 265 Asp Lys Glu Val Pro Gln Asp Asp Glu Met Asp Gly Gly Lys Val Ala 275 280 Glu Ser Asp Gly Glu Met Asp Gly Glu Lys Asp Lys Glu Val Pro Gln 295 Asp Asp Glu Met Asp Gly Glu Lys Glu Lys Glu Val Ala Glu Pro Ser 315 305 310 Glu Ile Gly Val Pro Glu Ser Glu Lys Asp Ile Glu Val Ala Asp Ser 330 325 Glu Lys Glu Lys Glu Val Pro Gln Asp Ala Lys Val Ala Glu Pro Ser 345 Lys Lys Arg Gly Lys Ala His Glu Asp Gly Asp Pro Ser Lys Glu 360 Gly Val Lys Lys Pro Lys Val Val Lys Lys Leu Ala Glu Ser Arg Thr 370 375 380 Asp Ala Lys Pro Val Tyr Arg Ser Pro Ile Gln Thr Arg Tyr Arg Arg 390 395 Lys Lys Thr Lys Lys Asn Val 405

- (2) INFORMATION FOR SEQ ID NO:1054:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..376
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596156
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

Met Cys Lys Arg Lys Phe Lys Ser Ser Thr Met Lys Gly Phe Pro Met

Ser Asp Val Tyr Asp Lys Leu Gly Thr Thr Lys Asp Ile Gln Ser Ile 25 Leu Ala Pro Thr Pro Asp Glu Lys Leu Leu Leu Glu Arg Ile Met Asp 40 Lys Glu Phe Gly Val Asn Asp Val Asp Asp Leu Ile Ala Asp Gly Trp 55 Lys Lys Arg Leu Val Asp Glu Glu Arg Thr Ile Cys Phe Glu Pro Leu 75 Leu Asn Glu Asp Val Ala His Arg Ser Phe Val Ala Asn Ile Ala Leu 90 Ser Thr Val Val Lys Ala Pro Arg Lys Ala Ala Val Glu Lys Lys Gly 100 105 Lys Gly Lys Ala Ala Ala Ala Leu Thr Ser Pro Ser Asp Gly Gly Leu 120 Thr Glu Val Val Asn Glu Met Lys Asn Leu Met Glu Asn Gly Phe Lys 135 Ser Met Asn Lys Arg Met Lys Asp Phe Asn Ala Cys Gly Ser Lys Glu 150 155 Ile Asp Asp Lys Glu Asn Glu Leu Glu Glu Gly Ser Asp Ala Glu Thr 170 Glu Ile His Lys Glu Val Ala Gln Gly Asp Lys Glu Arg Glu Val Gly 185 Glu Thr Glu Thr Glu Xaa Asp Lys Glu Val Ala Gln Gly Asp Ser Asp 200 205 Lys Glu Val Ala Glu Ser Glu Lys Asp Lys Val Val Ala Glu Ser Glu 215 220 Lys Glu Lys Glu Val Ala Glu Ser Glu Ile Gly Val Ala Glu Ser Glu 225 230 235 240 Lys Asp Lys Glu Val Pro Gln Asp Asp Glu Met Asp Gly Gly Lys Val 250 255 245 Ala Glu Ser Asp Gly Glu Met Asp Gly Glu Lys Asp Lys Glu Val Pro 265 270 Gln Asp Asp Glu Met Asp Gly Glu Lys Glu Lys Glu Val Ala Glu Pro 275 280 285 Ser Glu Ile Gly Val Pro Glu Ser Glu Lys Asp Ile Glu Val Ala Asp 295 300 Ser Glu Lys Glu Lys Glu Val Pro Gln Asp Ala Lys Val Ala Glu Pro 310 315 Ser Lys Lys Arg Gly Lys Ala His Glu Asp Gly Asp Pro Ser Lys 330 335 325 Glu Gly Val Lys Lys Pro Lys Val Val Lys Lys Leu Ala Glu Ser Arg 340 345 350 Thr Asp Ala Lys Pro Val Tyr Arg Ser Pro Ile Gln Thr Arg Tyr Arg 355 360 Arg Lys Lys Thr Lys Lys Asn Val 370 375 (2) INFORMATION FOR SEQ ID NO:1055:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1071 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1071
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

atggetettt etteacette aagaateete tgttttgete ttgeettate egetgettet eteteeete etteegette tteeeacgat tacteeateg ttggataete eecegaggat

ttggaatctc atgacaaact catagaactc ttcgaaaact ggatctcaaa ttttgagaaa qcttatqaaa ccqttqaaqa qaaqtttctt aggttcqaaq ttttcaagga taatctaaaq cacatcqatq aqactaacaa gaaaqggaaa agctactggc tcgggctcaa cgagtttgcg 300 gatttgagcc atgaggagtt caagaaaatg tatttagggc tcaagactga tatagtgaga 360 cgcgatgaaq aaagatctta cgcaqagttc gcttacaggg acgtcgaagc tgttcctaag 420 tctgttgact qgaqaaagaa aggagctgtg gcggaagtta agaaccaggg ctcttgtgga 480 agttgttggg cgttttcgac agtagcagct gtcgaaggta taaacaagat tgtgacagga 540 600 aacttgacaa cattgtcaga acaagaactc atagactgtg acacgaccta caacaatggc tgcaacggtg gtctcatgga ctatgccttt gagtacattg ttaagaacgg aggtctacgc 660 aaqqaaqaaq attatcctta ctctatqqaa qaaqqaactt qcqaqatqca aaaqgatqaa 720 totgaaacag taaccattaa tggacaccaa gacgtaccta ctaatgatga gaagagtoto 780 ttgaaggcat tggctcatca gcctctcagt gtcgccattg atgcatctgg tagagagttc 840 cagttctata gcggcggcgt gtttgatggg cggtgcgggg ttgatcttga ccacggtgtg 900 gctgcggttg ggtatggatc aagcaagggt tcagattaca tcattgtgaa gaattcttgg 960 ggaccaaaat ggggagaaaa aggttacatc aggctgaaga ggaacactgg gaaaccagag 1020 ggtctctgtg gaatcaacaa gatggcttct ttccccacca aaactaagtg a

- (2) INFORMATION FOR SEQ ID NO:1056:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 356 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

230

245

- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056: Met Ala Leu Ser Ser Pro Ser Arg Ile Leu Cys Phe Ala Leu Ala Leu 5 10 Ser Ala Ala Ser Leu Ser Leu Ser Phe Ala Ser Ser His Asp Tyr Ser 20 25 Ile Val Gly Tyr Ser Pro Glu Asp Leu Glu Ser His Asp Lys Leu Ile 4.0 4.5 Glu Leu Phe Glu Asn Trp Ile Ser Asn Phe Glu Lys Ala Tyr Glu Thr 55 Val Glu Glu Lys Phe Leu Arg Phe Glu Val Phe Lys Asp Asn Leu Lys 70 75 His Ile Asp Glu Thr Asn Lys Lys Gly Lys Ser Tyr Trp Leu Gly Leu 8.5 90 Asn Glu Phe Ala Asp Leu Ser His Glu Glu Phe Lys Lys Met Tyr Leu 100 105 110 Gly Leu Lys Thr Asp Ile Val Arg Arg Asp Glu Glu Arg Ser Tyr Ala 120 125 Glu Phe Ala Tyr Arg Asp Val Glu Ala Val Pro Lys Ser Val Asp Trp 135 Arg Lys Lys Gly Ala Val Ala Glu Val Lys Asn Gln Gly Ser Cys Gly 155 150 Ser Cys Trp Ala Phe Ser Thr Val Ala Ala Val Glu Gly Ile Asn Lys 165 170 Ile Val Thr Gly Asn Leu Thr Thr Leu Ser Glu Gln Glu Leu Ile Asp 180 185 Cys Asp Thr Thr Tyr Asn Asn Gly Cys Asn Gly Gly Leu Met Asp Tyr 195 200 Ala Phe Glu Tyr Ile Val Lys Asn Gly Gly Leu Arg Lys Glu Glu Asp 215 Tyr Pro Tyr Ser Met Glu Glu Gly Thr Cys Glu Met Gln Lys Asp Glu

Ser Glu Thr Val Thr Ile Asn Gly His Gln Asp Val Pro Thr Asn Asp

Glu Lys Ser Leu Leu Lys Ala Leu Ala His Gln Pro Leu Ser Val Ala

235

250

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                         265
Ile Asp Ala Ser Gly Arg Glu Phe Gln Phe Tyr Ser Gly Gly Val Phe
 275 280 285
Asp Gly Arg Cys Gly Val Asp Leu Asp His Gly Val Ala Ala Val Gly
                  295 300
Tyr Gly Ser Ser Lys Gly Ser Asp Tyr Ile Ile Val Lys Asn Ser Trp
305 310 315 320
Gly Pro Lys Trp Gly Glu Lys Gly Tyr Ile Arg Leu Lys Arg Asn Thr
           325 330 335
Gly Lys Pro Glu Gly Leu Cys Gly Ile Asn Lys Met Ala Ser Phe Pro
                345
Thr Lys Thr Lys
      355
(2) INFORMATION FOR SEQ ID NO:1057:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 247 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
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- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596161
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:
- Met Tyr Leu Gly Leu Lys Thr Asp Ile Val Arg Arg Asp Glu Glu Arg 1 5 10
- Ser Tyr Ala Glu Phe Ala Tyr Arg Asp Val Glu Ala Val Pro Lys Ser 20 25
- Val Asp Trp Arg Lys Lys Gly Ala Val Ala Glu Val Lys Asn Gln Gly 35 40
- Ser Cys Gly Ser Cys Trp Ala Phe Ser Thr Val Ala Ala Val Glu Gly 50 55 60
- Ile Asn Lys Ile Val Thr Gly Asn Leu Thr Thr Leu Ser Glu Gln Glu 70 75 80
- Leu Ile Asp Cys Asp Thr Thr Tyr Asn Asn Gly Cys Asn Gly Gly Leu 90 85
- Met Asp Tyr Ala Phe Glu Tyr Ile Val Lys Asn Gly Gly Leu Arg Lys 100 105
- Glu Glu Asp Tyr Pro Tyr Ser Met Glu Glu Gly Thr Cys Glu Met Gln 115 120 125
- Lys Asp Glu Ser Glu Thr Val Thr Ile Asn Gly His Gln Asp Val Pro 130 135 140
- Thr Asn Asp Glu Lys Ser Leu Leu Lys Ala Leu Ala His Gln Pro Leu 145 150 155 160
- Ser Val Ala Ile Asp Ala Ser Gly Arg Glu Phe Gln Phe Tyr Ser Gly 165 170
- Gly Val Phe Asp Gly Arg Cys Gly Val Asp Leu Asp His Gly Val Ala 185 190 180
- Ala Val Gly Tyr Gly Ser Ser Lys Gly Ser Asp Tyr Ile Ile Val Lys 200 205
- Asn Ser Trp Gly Pro Lys Trp Gly Glu Lys Gly Tyr Ile Arg Leu Lys 215 220 Arg Asn Thr Gly Lys Pro Glu Gly Leu Cys Gly Ile Asn Lys Met Ala
- 230 235 Ser Phe Pro Thr Lys Thr Lys
- 245 (2) INFORMATION FOR SEQ ID NO:1058:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..441
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058: gatcttttca ttgctggtac tgatacatca tcaaccacta tacaatggat catggcggag 60 120 atcattaacc atcccaagat tcttgagagg ctaagagaag aaatcgattt tgttgtaggg aaaacaaggt tgattcaaga aactgaccta ccgaacctcc tttacttgca agcgataatc 180 aaagaagggc taagattgca tccaccgggg ccactcttac caagaacggt ccaagaaagc 240 ggcagaagag gttgtccagg aacaaatcta gcttatgctt ctgtaggaac cgcggttgga 300 gtaatggtgc agttctttga ttggaaaatt gaaggagaga aagtcaacat gaatgaggct 360 420 gctggaacaa tggtattgac catggctcac cctcttaagt gcactcctgt tcctcgaacc ctaaaccgtt taccttcgta g
- (2) INFORMATION FOR SEQ ID NO:1059:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596205
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Asp Leu Phe Ile Ala Gly Thr Asp Thr Ser Ser Thr Thr Ile Gln Trp $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Ile Met Ala Glu Ile Ile Asn His Pro Lys Ile Leu Glu Arg Leu Arg
20 25 30

Glu Glu Ile Asp Phe Val Val Gly Lys Thr Arg Leu Ile Gln Glu Thr 35 40 45 Asp Leu Pro Asn Leu Leu Tyr Leu Gln Ala Ile Ile Lys Glu Gly Leu

50 55 60
Arg Leu His Pro Pro Gly Pro Leu Leu Pro Arg Thr Val Gln Glu Ser

65 70 75 80
Gly Arg Arg Gly Cys Pro Gly Thr Asn Leu Ala Tyr Ala Ser Val Gly

85 90 95
Thr Ala Val Gly Val Met Val Gln Phe Phe Asp Trp Lys Ile Glu Gly

100 105 110 Glu Lys Val Asn Met Asn Glu Ala Ala Gly Thr Met Val Leu Thr Met 115 120 125

Ala His Pro Leu Lys Cys Thr Pro Val Pro Arg Thr Leu Asn Arg Leu 130 135 140

Pro Ser

145

- (2) INFORMATION FOR SEQ ID NO:1060:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596206
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

Met Ala Glu Ile Ile Asn His Pro Lys Ile Leu Glu Arg Leu Arg Glu

1				5					10					15	
			20					25					Glu 30		
Leu	Pro	Asn 35	Leu	Leu	Tyr	Leu	Gln 40	Ala	Ile	Ile	Lys	Glu 45	Gly	Leu	Arg
Leu	His 50	Pro	Pro	Gly	Pro	Leu 55	Leu	Pro	Arg	Thr	Val 60	Gln	Glu	Ser	Gly
Arg 65		Gly	Суѕ	Pro	Gly 70	Thr	Asn	Leu	Ala	Tyr 75	Ala	Ser	Val	Gly	Thr 80
Ala	Val	Gly	Val	Met 85	Val	Gln	Phe	Phe	Asp 90	Trp	Lys	Ile	Glu	Gly 95	Glu
Lys	Val	Asn	Met 100	Asn	Glu	Ala	Ala	Gly 105	Thr	Met	Val	Leu	Thr 110	Met	Ala
His	Pro	Leu 115	Lys	Cys	Thr	Pro	Val 120	Pro	Arg	Thr	Leu	Asn 125	Arg	Leu	Pro
Ser															

(2) INFORMATION FOR SEQ ID NO:1061:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..442
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061: tnttcgtttc aaacgcatgc tggccgaggc gagggggctc cacgatagcg aagtggctcg 60 ggetteteaa aeggetagge gegagaeate gaaggttttt ategeeaaac teaaageege 120 cgagcagaag gtgtcgctcc ttgccaggat caacgaccag tttatgaact tatcccaggc 180 gcgagctaat gcgcaactga tcaaggcact tgaggaaggt ggggtattgg caactgagaa 240 300 ggaccaggtt gaggaatggc tgaaagactt cgccaatacc gagctgaaag aggaactcaa 360 ggetectact eccgaececa ettetttaag teegggegge cacagategg ttgagaetet 420 tgccgacgag gcgggggtca ctgatcagtc taggtcgctt ctgcctgccg aagatattcg cccgtctgaa gagctcgact aa
- (2) INFORMATION FOR SEQ ID NO:1062:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

Xaa Arg Phe Lys Arg Met Leu Ala Glu Ala Arg Gly Leu His Asp Ser 1 5 5 10 10 15 Glu Val Ala Arg Ala Ser Gln Thr Ala Arg Arg Glu Thr Ser Lys Val 20 25 25 30

Phe Ile Ala Lys Leu Lys Ala Ala Glu Gln Lys Val Ser Leu Leu Ala 35 40 45

Arg Ile Asn Asp Gln Phe Met Asn Leu Ser Gln Ala Arg Ala Asn Ala 50 55 60

Gln Leu Ile Lys Ala Leu Glu Glu Gly Gly Val Leu Ala Thr Glu Lys 65 70 75 80

Asp Gln Val Glu Glu Trp Leu Lys Asp Phe Ala Asn Thr Glu Leu Lys 85 90 95

- (2) INFORMATION FOR SEQ ID NO:1063:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

145

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596254
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Leu Ala Glu Ala Arg Gly Leu His Asp Ser Glu Val Ala Arg Ala 1 5 10 15

Ser Gln Thr Ala Arg Arg Glu Thr Ser Lys Val Phe Ile Ala Lys Leu 20 25 30

Lys Ala Ala Glu Gln Lys Val Ser Leu Leu Ala Arg Ile Asn Asp Gln 35 40 45

Phe Met Asn Leu Ser Gln Ala Arg Ala Asn Ala Gln Leu Ile Lys Ala 50 60

Leu Glu Glu Gly Gly Val Leu Ala Thr Glu Lys Asp Gln Val Glu Glu 65 70 75 80

Trp Leu Lys Asp Phe Ala Asn Thr Glu Leu Lys Glu Glu Leu Lys Ala 85 90 95

Pro Thr Pro Asp Pro Thr Ser Leu Ser Pro Gly Gly His Arg Ser Val 100 105 110 Glu Thr Leu Ala Asp Glu Ala Gly Val Thr Asp Gln Ser Arg Ser Leu

115 120 125

Leu Pro Ala Glu Asp Ile Arg Pro Ser Glu Glu Leu Asp
130 135 140

- (2) INFORMATION FOR SEQ ID NO:1064:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596255
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

Met Asn Leu Ser Gln Ala Arg Ala Asn Ala Gln Leu Ile Lys Ala Leu 1 5 10 15

Glu Glu Gly Gly Val Leu Ala Thr Glu Lys Asp Gln Val Glu Glu Trp 20 25 30

Leu Lys Asp Phe Ala Asn Thr Glu Leu Lys Glu Glu Leu Lys Ala Pro 35 40 45

Thr Pro Asp Pro Thr Ser Leu Ser Pro Gly Gly His Arg Ser Val Glu 50 60

Thr Leu Ala Asp Glu Ala Gly Val Thr Asp Gln Ser Arg Ser Leu Leu 65 70 75 80

Pro Ala Glu Asp Ile Arg Pro Ser Glu Glu Leu Asp

60

120

180

240 300

360

420

480

Client Docket No. 80146.003 90 85 (2) INFORMATION FOR SEQ ID NO:1065: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 507 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..507 (D) OTHER INFORMATION: / Ceres Seq. ID 1596264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065: gacgtggtga tctcccaggc catcgaggga aaattggcga gagaagaggc tgagaaagaa gccttcgtca ataaggagaa tgccatcaag atggtcgagc gcgacctgaa gatggactct gaggttgttc gttgtaggcg acttctcgcc gaggcgagag gacttaggaa catcaaagtg gctcgggcta tgcaaacggc aaggcgagaa cttcggaggc cttcaccgcc aagttcaggg tggccgagga gaagatgtcg ctcttcgagg atgctaacga ccagtttatc gtgggctaat ccacaactga tcaaggcgct tgaagatggc agatctttgg cgaccgagaa aaaacaggtc gaggagtggc tgaaggattt tgccgatgca gaggtgaacc ttgttcgtct cacatctgaa ctgaaggaag agctcaaagc ccctgctcct gaaccagctc ctctaagccc tcgaggtaat agatcggtcg agactcttgc ggattag (2) INFORMATION FOR SEQ ID NO:1066: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..168 (D) OTHER INFORMATION: / Ceres Seq. ID 1596265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066: Asp Val Val Ile Ser Gln Ala Ile Glu Gly Lys Leu Ala Arg Glu Glu 10 Ala Glu Lys Glu Ala Phe Val Asn Lys Glu Asn Ala Ile Lys Met Val 25 Glu Arg Asp Leu Lys Met Asp Ser Glu Val Val Arg Cys Arg Arg Leu 40 Leu Ala Glu Ala Arg Gly Leu Arg Asn Ile Lys Val Ala Arg Ala Met 60 55 Gln Thr Ala Arg Arg Glu Leu Arg Arg Pro Ser Pro Pro Ser Ser Gly 75 70 Trp Pro Arg Arg Arg Cys Arg Ser Ser Arg Met Leu Thr Thr Ser Leu 90 85 Ser Trp Ala Asn Pro Gln Leu Ile Lys Ala Leu Glu Asp Gly Arg Ser 110 105 100 Leu Ala Thr Glu Lys Lys Gln Val Glu Glu Trp Leu Lys Asp Phe Ala 125 120 Asp Ala Glu Val Asn Leu Val Arg Leu Thr Ser Glu Leu Lys Glu Glu 140 135 Leu Lys Ala Pro Ala Pro Glu Pro Ala Pro Leu Ser Pro Arg Gly Asn 155 150 Arg Ser Val Glu Thr Leu Ala Asp

- 165 (2) INFORMATION FOR SEQ ID NO:1067:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..138
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:
- Met Val Glu Arg Asp Leu Lys Met Asp Ser Glu Val Val Arg Cys Arg 1 5 10 15
- Arg Leu Leu Ala Glu Ala Arg Gly Leu Arg Asn Ile Lys Val Ala Arg 20 25 30
- Ala Met Gln Thr Ala Arg Arg Glu Leu Arg Arg Pro Ser Pro Pro Ser 35 40 45
- Ser Gly Trp Pro Arg Arg Cys Arg Ser Ser Arg Met Leu Thr Thr 50 55 60
- Ser Leu Ser Trp Ala Asn Pro Gln Leu Ile Lys Ala Leu Glu Asp Gly 70 75 80
- Arg Ser Leu Ala Thr Glu Lys Lys Gln Val Glu Glu Trp Leu Lys Asp 85 90 95
- Phe Ala Asp Ala Glu Val Asn Leu Val Arg Leu Thr Ser Glu Leu Lys
 100 105 110
- Glu Glu Leu Lys Ala Pro Ala Pro Glu Pro Ala Pro Leu Ser Pro Arg 115 120 125
- Gly Asn Arg Ser Val Glu Thr Leu Ala Asp 130 135
- (2) INFORMATION FOR SEQ ID NO:1068:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:
- Met Asp Ser Glu Val Val Arg Cys Arg Arg Leu Leu Ala Glu Ala Arg

 1 10 15
- Gly Leu Arg Asn Ile Lys Val Ala Arg Ala Met Gln Thr Ala Arg Arg 20 25 30
- Glu Leu Arg Arg Pro Ser Pro Pro Ser Ser Gly Trp Pro Arg Arg Arg 35 40 45
- Cys Arg Ser Ser Arg Met Leu Thr Thr Ser Leu Ser Trp Ala Asn Pro 50 55 60
- Gln Leu Ile Lys Ala Leu Glu Asp Gly Arg Ser Leu Ala Thr Glu Lys 65 70 75 80
- Lys Gln Val Glu Glu Trp Leu Lys Asp Phe Ala Asp Ala Glu Val Asn 85 90 95
- Leu Val Arg Leu Thr Ser Glu Leu Lys Glu Glu Leu Lys Ala Pro Ala 100 105 110
- Pro Glu Pro Ala Pro Leu Ser Pro Arg Gly Asn Arg Ser Val Glu Thr 115 120 125

Leu Ala Asp

130

- (2) INFORMATION FOR SEQ ID NO:1069:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1767 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

1620

1680

1740

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1767
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596280
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069: 60 atggtgaagg tetteatgga egattttteg gtetatggee cetetttete eteatgtttg ttgaatcttg gcagggtact gaccaggtgc gaagagatca atcttgttct caattgggaa 120 aagtgtcatt tcatggtgaa ggaaggcata atgttgggtc acaagatatt agagaagggt atagaggttg acaagggaaa gattgaagtg atgataagat ttattaagaa cttctccaag 240 300 ataqccatqc cqttaaccaq actattqaqc aaggaqaccq agtttqaatt cqatqaqgac 360 tgcctcaaat cctttcacac catcaaggaa gctttggtat ctgctcctgt tgttcgagct cctaattggg actatgcgtt cgagattatg tgtgatgcat cagattacgc cgtaggagct 420 gttatagaca agaagcttca cgtcatatat tacgccaggc ggacgttgga tgaagctcaa 480 540 ggaagatatg caacaactga gaaggagctt ccagctgttg aattcgcatt taagaagttt 600 agaagctatg tggttggatc caaggtcatt gtctatacag accatgcagc tttgaggcat ctattettta gtgggageta caacaggaaa gagttecace aactgaacge tgttgaggga agatetecat ggtatgetaa teaegteaac tatttggcat teaaagtgga geeteecaac 720 ttgaccagtt atgaaaggaa gaagtttttc agagacatac accattacta ttgggatgaa 780 840 ccttatttct acactctttg taaagataag atctacagga gatgcgtcct aaaagatgaa 900 gtagaaggta ttttgctgca ttgccatggc tccgcatatg gtggccactt tgcaacattc aagacaatgt caaagattct gcaagcaggc ttctggtggc caccaatgtt taaggatgtt 960 gaggagtttg tttcaaaatg tgattcatgc cagagaaagg gcaacatcag cagaagaaat 1020 gagatgcctc agaacccaat cttggaagtt gagatctttg atgtatgggg aattgatttt 1080 atgggtccat tcctattttc atacggtaac aaatatatat tggtcgccgt agattatgta 1140 tctaagtggg tcgaagctat tgccagtcct accaacgatg caaaagttat gctaaaactg 1200 ttcaagacca taatcttccc gagatttgga gttcccaggg tagtaataag taatggtgga 1260 gagcatttca tcaacaaggg ttttgaaaac cttctgaaga agcatggagt aaagcacaag 1320 gtcgccactc cttatcatcc acattcaagc gggcaggttg agatttccaa cagggagata 1380 aaaqcaattc tqaaaacact qttqqqatta caaqqaaaga ctggtctgca aagctcggtg 1440 acqcactgtg ggcttatagg acagctttca agacccccat tggagagaac taagcttttc 1500 catgacaaga agatcatcac taaggatttc caggctggtg atcagatgct gctattcaac 1560
- (2) INFORMATION FOR SEQ ID NO:1070:

catctccagg aacttcttga tgattaa

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..588
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596281

tegegettga aactetttee gggaaagett aagteeagat ggtetggtee ettttgtate

actgaagtac qtccttatgq agcagtcact ctagctggta agagtggaga tttcacagta

aatggtcaaa ggctcaagaa atacttagca gatcaaatcc ttccagaggt gacqtcqgtt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

Met Val Lys Val Phe Met Asp Asp Phe Ser Val Tyr Gly Pro Ser Phe 1 5 10 15 Ser Ser Cys Leu Leu Asn Leu Gly Arg Val Leu Thr Arg Cys Glu Glu

20 25 30

Ile Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Lys Glu 35 40 45

Gly Ile Met Leu Gly His Lys Ile Leu Glu Lys Gly Ile Glu Val Asp 50 60

Lys Gly Lys Ile Glu Val Met Ile Arg Phe Ile Lys Asn Phe Ser Lys 65 70 75 80

Ile Ala Met Pro Leu Thr Arg Leu Leu Ser Lys Glu Thr Glu Phe Glu 85 90 95 Phe Asp Glu Asp Cys Leu Lys Ser Phe His Thr Ile Lys Glu Ala Leu

105 100 Val Ser Ala Pro Val Val Arg Ala Pro Asn Trp Asp Tyr Ala Phe Glu 115 120 125 Ile Met Cys Asp Ala Ser Asp Tyr Ala Val Gly Ala Val Ile Asp Lys 130 135 Lys Leu His Val Ile Tyr Tyr Ala Arg Arg Thr Leu Asp Glu Ala Gln 145 150 155 Gly Arg Tyr Ala Thr Thr Glu Lys Glu Leu Pro Ala Val Glu Phe Ala 165 170 Phe Lys Lys Phe Arg Ser Tyr Val Val Gly Ser Lys Val Ile Val Tyr 180 185 Thr Asp His Ala Ala Leu Arg His Leu Phe Phe Ser Gly Ser Tyr Asn 195 200 205 Arg Lys Glu Phe His Gln Leu Asn Ala Val Glu Gly Arg Ser Pro Trp 210 215 220 Tyr Ala Asn His Val Asn Tyr Leu Ala Phe Lys Val Glu Pro Pro Asn 230 235 Leu Thr Ser Tyr Glu Arg Lys Lys Phe Phe Arg Asp Ile His His Tyr 245 250 Tyr Trp Asp Glu Pro Tyr Phe Tyr Thr Leu Cys Lys Asp Lys Ile Tyr 260 265 270 Arg Arg Cys Val Leu Lys Asp Glu Val Glu Gly Ile Leu Leu His Cys 275 280 285 His Gly Ser Ala Tyr Gly Gly His Phe Ala Thr Phe Lys Thr Met Ser 295 300 Lys Ile Leu Gln Ala Gly Phe Trp Trp Pro Pro Met Phe Lys Asp Val 310 315 320 Glu Glu Phe Val Ser Lys Cys Asp Ser Cys Gln Arg Lys Gly Asn Ile 325 330 Ser Arg Arg Asn Glu Met Pro Gln Asn Pro Ile Leu Glu Val Glu Ile 345 350 340 Phe Asp Val Trp Gly Ile Asp Phe Met Gly Pro Phe Leu Phe Ser Tyr 360 365 355 Gly Asn Lys Tyr Ile Leu Val Ala Val Asp Tyr Val Ser Lys Trp Val 375 380 Glu Ala Ile Ala Ser Pro Thr Asn Asp Ala Lys Val Met Leu Lys Leu 390 395 400 Phe Lys Thr Ile Ile Phe Pro Arg Phe Gly Val Pro Arg Val Val Ile 405 410 415 Ser Asn Gly Gly Glu His Phe Ile Asn Lys Gly Phe Glu Asn Leu Leu 420 425 430 Lys Lys His Gly Val Lys His Lys Val Ala Thr Pro Tyr His Pro His 435 440 445 Ser Ser Gly Gln Val Glu Ile Ser Asn Arg Glu Ile Lys Ala Ile Leu 460 455 Lys Thr Leu Leu Gly Leu Gln Gly Lys Thr Gly Leu Gln Ser Ser Val 475 480 470 Thr His Cys Gly Leu Ile Gly Gln Leu Ser Arg Pro Pro Leu Glu Arg 490 495 485 Thr Lys Leu Phe His Asp Lys Lys Ile Ile Thr Lys Asp Phe Gln Ala 500 505 510 Gly Asp Gln Met Leu Leu Phe Asn Ser Arg Leu Lys Leu Phe Pro Gly 515 520 Lys Leu Lys Ser Arg Trp Ser Gly Pro Phe Cys Ile Thr Glu Val Arg 540 535 Pro Tyr Gly Ala Val Thr Leu Ala Gly Lys Ser Gly Asp Phe Thr Val 555 560 550 Asn Gly Gln Arg Leu Lys Lys Tyr Leu Ala Asp Gln Ile Leu Pro Glu 570 565 Val Thr Ser Val His Leu Gln Glu Leu Leu Asp Asp 580 585

- (2) INFORMATION FOR SEQ ID NO:1071:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..583
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596283
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:
- Met Asp Asp Phe Ser Val Tyr Gly Pro Ser Phe Ser Ser Cys Leu Leu 1 5 10 15
- Asn Leu Gly Arg Val Leu Thr Arg Cys Glu Glu Ile Asn Leu Val Leu 20 25 30
- Asn Trp Glu Lys Cys His Phe Met Val Lys Glu Gly Ile Met Leu Gly 35 40 45
- His Lys Ile Leu Glu Lys Gly Ile Glu Val Asp Lys Gly Lys Ile Glu 50 55 60
- Val Met Ile Arg Phe Ile Lys Asn Phe Ser Lys Ile Ala Met Pro Leu 65 70 75 80
- Thr Arg Leu Leu Ser Lys Glu Thr Glu Phe Glu Phe Asp Glu Asp Cys 85 90 95
- Leu Lys Ser Phe His Thr Ile Lys Glu Ala Leu Val Ser Ala Pro Val 100 105 110
- Val Arg Ala Pro Asn Trp Asp Tyr Ala Phe Glu Ile Met Cys Asp Ala 115 120 125
- Ser Asp Tyr Ala Val Gly Ala Val Ile Asp Lys Lys Leu His Val Ile 130 135 140
- Tyr Tyr Ala Arg Arg Thr Leu Asp Glu Ala Gln Gly Arg Tyr Ala Thr 145 150 150 160
- Thr Glu Lys Glu Leu Pro Ala Val Glu Phe Ala Phe Lys Lys Phe Arg 165 170 175
- Ser Tyr Val Val Gly Ser Lys Val Ile Val Tyr Thr Asp His Ala Ala 180 185 190
- Leu Arg His Leu Phe Phe Ser Gly Ser Tyr Asn Arg Lys Glu Phe His 195 200 205 205 Gln Leu Asn Ala Val Glu Gly Arg Ser Pro Trp Tyr Ala Asn His Val
- 210 215 220
 Asn Tyr Leu Ala Phe Lys Val Glu Pro Pro Asn Leu Thr Ser Tyr Glu
- 225 230 235 240
 Arg Lys Lys Phe Phe Arg Asp Ile His His Tyr Tyr Trp Asp Glu Pro
- 245 250 255

 Tyr Phe Tyr Thr Leu Cys Lys Asp Lys Ile Tyr Arg Arg Cys Val Leu
- 260 265 270

 Lys Asp Glu Val Glu Gly Ile Leu Leu His Cys His Gly Ser Ala Tyr
- 275 280 285
 Gly Gly His Phe Ala Thr Phe Lys Thr Met Ser Lys Ile Leu Gln Ala
- 290 295 300

 Gly Phe Trp Trp Pro Pro Met Phe Lys Asp Val Glu Glu Phe Val Ser
 305 310 315 320
- 305 310 315 320 Lys Cys Asp Ser Cys Gln Arg Lys Gly Asn Ile Ser Arg Arg Asn Glu
- 325 330 335

 Met Pro Gln Asn Pro Ile Leu Glu Val Glu Ile Phe Asp Val Trp Gly
 340 345 350
- Ile Asp Phe Met Gly Pro Phe Leu Phe Ser Tyr Gly Asn Lys Tyr Ile
- Leu Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Ser 370 375 380
- Pro Thr Asn Asp Ala Lys Val Met Leu Lys Leu Phe Lys Thr Ile Ile

```
395
                   390
385
Phe Pro Arg Phe Gly Val Pro Arg Val Val Ile Ser Asn Gly Gly Glu
               405 410
His Phe Ile Asn Lys Gly Phe Glu Asn Leu Leu Lys Lys His Gly Val
                              425
           420
Lys His Lys Val Ala Thr Pro Tyr His Pro His Ser Ser Gly Gln Val
                                              445
                           440
       435
Glu Ile Ser Asn Arg Glu Ile Lys Ala Ile Leu Lys Thr Leu Leu Gly
                                          460
                       455
Leu Gln Gly Lys Thr Gly Leu Gln Ser Ser Val Thr His Cys Gly Leu
                                      475
                   470
Ile Gly Gln Leu Ser Arg Pro Pro Leu Glu Arg Thr Lys Leu Phe His
                                                      495
                                   490
               485
Asp Lys Lys Ile Ile Thr Lys Asp Phe Gln Ala Gly Asp Gln Met Leu
                                                  510
                               505
           500
Leu Phe Asn Ser Arg Leu Lys Leu Phe Pro Gly Lys Leu Lys Ser Arg
                                               525
                           520
        515
Trp Ser Gly Pro Phe Cys Ile Thr Glu Val Arg Pro Tyr Gly Ala Val
                       535
Thr Leu Ala Gly Lys Ser Gly Asp Phe Thr Val Asn Gly Gln Arg Leu
                                       555
                   550
Lys Lys Tyr Leu Ala Asp Gln Ile Leu Pro Glu Val Thr Ser Val His
                                   570
               565
Leu Gln Glu Leu Leu Asp Asp
            580
```

- (2) INFORMATION FOR SEQ ID NO:1072:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..490
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596332
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072: atggctgcgg ttgatatacc acttgatcat catgttttca atgtcccaaa aggatataat 60 gcaccacaac aagtacatat aactcaaggt gattatgatg gtaaagctgt tatcatctct 120 tgggttacac ctgatgaacc tggttctagc caagtacatt acggtgcggt tcaggggaaa 180 tatgagtttg ttgctcaagg gacttaccat aactacacgt tttacaagta taagtctggc 240 300 tttattcatc actgccttgt ctctgacctt gagcatgata caaaatacta ttacaagatt gaaagcggtg aatcttctcg agagttttgg tttgttacac caccacatgt acatccagat 360 gettectaca agtttggtat tataggegat atgggteaga catteaacte gttatecaeg 420 ttggaacatt acatggagag tggagctcag gctgttttat ttcttggaga tctttcttat 480 gctgatagat
- (2) INFORMATION FOR SEQ ID NO:1073:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..163
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596333
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:
- Met Ala Ala Val Asp Ile Pro Leu Asp His His Val Phe Asn Val Pro 1 5 10 15 Lys Gly Tyr Asn Ala Pro Gln Gln Val His Ile Thr Gln Gly Asp Tyr

60

120

180

240

25 20 Asp Gly Lys Ala Val Ile Ile Ser Trp Val Thr Pro Asp Glu Pro Gly 40 Ser Ser Gln Val His Tyr Gly Ala Val Gln Gly Lys Tyr Glu Phe Val 55 Ala Gln Gly Thr Tyr His Asn Tyr Thr Phe Tyr Lys Tyr Lys Ser Gly 70 75 Phe Ile His His Cys Leu Val Ser Asp Leu Glu His Asp Thr Lys Tyr 85 90 Tyr Tyr Lys Ile Glu Ser Gly Glu Ser Ser Arg Glu Phe Trp Phe Val 100 105 Thr Pro Pro His Val His Pro Asp Ala Ser Tyr Lys Phe Gly Ile Ile 120 Gly Asp Met Gly Gln Thr Phe Asn Ser Leu Ser Thr Leu Glu His Tyr 135 Met Glu Ser Gly Ala Gln Ala Val Leu Phe Leu Gly Asp Leu Ser Tyr Ala Asp Arg

- (2) INFORMATION FOR SEQ ID NO:1074:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596335
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Met Val Lys Leu Leu Ser Ser Leu Gly Leu His Leu Met Asn Leu 1 5 10 15

Val Leu Ala Lys Tyr Ile Thr Val Arg Phe Arg Gly Asn Met Ser Leu 20 25 30

Leu Leu Lys Gly Leu Thr Ile Thr Thr Arg Phe Thr Ser Ile Ser Leu 35 40 45

Ala Leu Phe Ile Thr Ala Leu Ser Leu Thr Leu Ser Met Ile Gln Asn 50 55 60

Thr Ile Thr Arg Leu Lys Ala Val Asn Leu Leu Glu Ser Phe Gly Leu 65 70 75 80

Leu His His His Met Tyr Ile Gln Met Leu Pro Thr Ser Leu Val Leu 85 90 95

- (2) INFORMATION FOR SEQ ID NO:1075:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..441
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

ccgtggcttt ggtctgcagg aaatcatgaa gtagattaca tgccatacat gggggaggtg acacctttca ggaattacct tcagcgttac actacgcctt acttagcctc aaaaagtagc agtcctcttt ggtacgctgt taggcgtgca tctgctcata tcattgtcct ctccagctat tcgccttttg tgaagtatac cccgcaatgg cactggctta gtgaagagct tacaagagtt

gatagggaga aaacaccttg gctaattgtt ttgatgcacg tcccaatata caacagtaat 300 gaagcacatt tcatggaggg tgaaagcatg cgagcagctt ttgaagagtg gtttgtccaa 360 cacaaagttg atgtaatctt tgctgggcat gttcatgcct acgagagatc ggtactttcg 420 tattaccata antccgcata g

- (2) INFORMATION FOR SEQ ID NO:1076:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596337
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

Pro Trp Leu Trp Ser Ala Gly Asn His Glu Val Asp Tyr Met Pro Tyr

1 10 15

Met Gly Glu Val Thr Pro Phe Arg Asn Tyr Leu Gln Arg Tyr Thr Thr 20 25 30

Pro Tyr Leu Ala Ser Lys Ser Ser Ser Pro Leu Trp Tyr Ala Val Arg 35 40 45

Arg Ala Ser Ala His Ile Ile Val Leu Ser Ser Tyr Ser Pro Phe Val 50 55 60

Lys Tyr Thr Pro Gln Trp His Trp Leu Ser Glu Glu Leu Thr Arg Val 65 70 75 80

Asp Arg Glu Lys Thr Pro Trp Leu Ile Val Leu Met His Val Pro Ile 85 90 95

Tyr Asn Ser Asn Glu Ala His Phe Met Glu Gly Glu Ser Met Arg Ala 100 105 110

Ala Phe Glu Glu Trp Phe Val Gln His Lys Val Asp Val Ile Phe Ala 115 120 125

Gly His Val His Ala Tyr Glu Arg Ser Val Leu Ser Tyr Tyr His Xaa 130 135 140

Ser Ala

145

- (2) INFORMATION FOR SEQ ID NO:1077:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596338
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

Met Pro Tyr Met Gly Glu Val Thr Pro Phe Arg Asn Tyr Leu Gln Arg 1 5 10 15

Tyr Thr Thr Pro Tyr Leu Ala Ser Lys Ser Ser Ser Pro Leu Trp Tyr 20 25 30

Ala Val Arg Arg Ala Ser Ala His Ile Ile Val Leu Ser Ser Tyr Ser 35 40 45

Pro Phe Val Lys Tyr Thr Pro Gln Trp His Trp Leu Ser Glu Glu Leu
50 55 60

Thr Arg Val Asp Arg Glu Lys Thr Pro Trp Leu Ile Val Leu Met His 65 70 75 80

Val Pro Ile Tyr Asn Ser Asn Glu Ala His Phe Met Glu Gly Glu Ser 85 90 95 Met Arg Ala Ala Phe Glu Glu Trp Phe Val Gln His Lys Val Asp Val

100 105 Ile Phe Ala Gly His Val His Ala Tyr Glu Arg Ser Val Leu Ser Tyr 120 125 Tyr His Xaa Ser Ala 130 (2) INFORMATION FOR SEQ ID NO:1078: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..130 (D) OTHER INFORMATION: / Ceres Seq. ID 1596339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078: Met Gly Glu Val Thr Pro Phe Arg Asn Tyr Leu Gln Arg Tyr Thr Thr 10 Pro Tyr Leu Ala Ser Lys Ser Ser Ser Pro Leu Trp Tyr Ala Val Arg 25 Arg Ala Ser Ala His Ile Ile Val Leu Ser Ser Tyr Ser Pro Phe Val 40 Lys Tyr Thr Pro Gln Trp His Trp Leu Ser Glu Glu Leu Thr Arg Val 55 Asp Arg Glu Lys Thr Pro Trp Leu Ile Val Leu Met His Val Pro Ile 70 75 Tyr Asn Ser Asn Glu Ala His Phe Met Glu Gly Glu Ser Met Arg Ala 8.5 90 Ala Phe Glu Glu Trp Phe Val Gln His Lys Val Asp Val Ile Phe Ala 100 105 Gly His Val His Ala Tyr Glu Arg Ser Val Leu Ser Tyr Tyr His Xaa 120 Ser Ala 130 (2) INFORMATION FOR SEQ ID NO:1079: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..306 (D) OTHER INFORMATION: / Ceres Seq. ID 1596343 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079: atggtgatcc catggggtga tctagactca ctcgccatgc ttcagagaca actcgqcgtc 60 gacattotog taacaggoca tacccaccag ttcacagcot acaaacacga gggaggagtg 120 qtqataaacc ctggctcagc aaccggagct tacagcagca taaaccaaga cgttaaccca 180 agetttgtee ttatggaeat egatggttte egagetgtag tetatgteta tgagetaatt 240 gatggagaag ttaaagtcga caagattgag ttcaagaagc cccctactac cagctctggt 300 ccttag (2) INFORMATION FOR SEQ ID NO:1080: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596344
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

Met Val Ile Pro Trp Gly Asp Leu Asp Ser Leu Ala Met Leu Gln Arg 1 5 10 15

Gln Leu Gly Val Asp Ile Leu Val Thr Gly His Thr His Gln Phe Thr $20 \\ 25 \\ 30$

Ala Tyr Lys His Glu Gly Gly Val Val Ile Asn Pro Gly Ser Ala Thr 35 40 45

Gly Ala Tyr Ser Ser Ile Asn Gln Asp Val Asn Pro Ser Phe Val Leu 50 55 60

Met Asp Ile Asp Gly Phe Arg Ala Val Val Tyr Val Tyr Glu Leu Ile 65 70 75 80

Asp Gly Glu Val Lys Val Asp Lys Ile Glu Phe Lys Lys Pro Pro Thr
85 90 95

Thr Ser Ser Gly Pro

- (2) INFORMATION FOR SEQ ID NO:1081:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596346
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

Met Leu Gln Arg Gln Leu Gly Val Asp Ile Leu Val Thr Gly His Thr 1 5 10 15

Gly Ser Ala Thr Gly Ala Tyr Ser Ser Ile Asn Gln Asp Val Asn Pro 35 40 45

Ser Phe Val Leu Met Asp Ile Asp Gly Phe Arg Ala Val Val Tyr Val
50 55 60

Tyr Glu Leu Ile Asp Gly Glu Val Lys Val Asp Lys Ile Glu Phe Lys 65 70 75 80

Lys Pro Pro Thr Thr Ser Ser Gly Pro 85

- (2) INFORMATION FOR SEQ ID NO:1082:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..366
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596350
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

atggccttta cgcacgtttg tctatggacg ctactcgcct tcgtgctgac ctggacggtg 60 ttctgcgtta ccaacaggaa gaagaaggcg ccggaattgg cagatgcggc agcagaggag 120 agaagagaca gtgctgctga tgttatcatc gtcggggctg gtgtgggtgg ctcggctctc 180 gcatattetc ttgctaagga cgggcgccga gtacttgtga tagagaggaga tatgagagaa 240 ccagagagaa tgatgggtga gtttatgcag ccaggaggac gactcatgct ttctaagctt 300 ggccttgaag tgttcaacta tgatttaaat cgcagtaaaa ctctaaccat gattccaact 360 tcttga

(2) INFORMATION FOR SEQ ID NO:1083: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..121 (D) OTHER INFORMATION: / Ceres Seq. ID 1596351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083: Met Ala Phe Thr His Val Cys Leu Trp Thr Leu Leu Ala Phe Val Leu 10 Thr Trp Thr Val Phe Cys Val Thr Asn Arg Lys Lys Ala Pro Glu 30 25 20 Leu Ala Asp Ala Ala Glu Glu Arg Arg Asp Ser Ala Ala Asp Val 45 40 Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ser Leu 60 55 Ala Lys Asp Gly Arg Arg Val Leu Val Ile Glu Arg Asp Met Arg Glu 75 70 Pro Glu Arg Met Met Gly Glu Phe Met Gln Pro Gly Gly Arg Leu Met 90 85 Leu Ser Lys Leu Gly Leu Glu Val Phe Asn Tyr Asp Leu Asn Arg Ser 110 105 100 Lys Thr Leu Thr Met Ile Pro Thr Ser 120 115 (2) INFORMATION FOR SEQ ID NO:1084: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 483 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..483 (D) OTHER INFORMATION: / Ceres Seq. ID 1596368 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084: atggagagag aaggcgcgtc cacaatttgc cctctcgagc tggtcagcca attgttcctg 60 tectgegacg gttttgaatt gteeggtgtt ttgtteceae atgttgeett ceaettteet 120 ccgaaggata agaaagaggc gttatcgata aacaccaccg catgtgcgat gagaggcagc 180 gctcgggtct taagaggcag atgcttgagg cgcgcatcgc ttgtgtggaa aggaatccaa 240 300 gatcccgacc atgcttcgga tgtacctccg cagttgaagt caagttcagg acctgcgtct gegtegggtg aagtgateee tietgaaage gaagatgatg atgaaggaga agacagcaae 360 acctggaaac acgtcaaaac caagcctaag ttggatgata agaacgaaac gtccacttcg 420 aatgctgaac cagcgatgaa ggagtctgtt cctgagcctc ttccaaaaat gtccccgaac 480 (2) INFORMATION FOR SEQ ID NO:1085: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1596369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

Met Glu Arg Glu Gly Ala Ser Thr Ile Cys Pro Leu Glu Leu Val Ser 10 Gln Leu Phe Leu Ser Cys Asp Gly Phe Glu Leu Ser Gly Val Leu Phe 2.0 25 Pro His Val Ala Phe His Phe Pro Pro Lys Asp Lys Lys Glu Ala Leu 40 Ser Ile Asn Thr Thr Ala Cys Ala Met Arg Gly Ser Ala Arg Val Leu 5.5 Arg Gly Arg Cys Leu Arg Arg Ala Ser Leu Val Trp Lys Gly Ile Gln 70 75 Asp Pro Asp His Ala Ser Asp Val Pro Pro Gln Leu Lys Ser Ser Ser 90 85 Gly Pro Ala Ser Ala Ser Gly Glu Val Ile Pro Ser Glu Ser Glu Asp 100 105 Asp Asp Glu Gly Glu Asp Ser Asn Thr Trp Lys His Val Lys Thr Lys 115 120 Pro Lys Leu Asp Asp Lys Asn Glu Thr Ser Thr Ser Asn Ala Glu Pro 135 140 Ala Met Lys Glu Ser Val Pro Glu Pro Leu Pro Lys Met Ser Pro Asn 145 150 155

- (2) INFORMATION FOR SEQ ID NO:1086:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596371
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

Met Arg Gly Ser Ala Arg Val Leu Arg Gly Arg Cys Leu Arg Arg Ala 1 5 10 15

Ser Leu Val Trp Lys Gly Ile Gln Asp Pro Asp His Ala Ser Asp Val 20 25 30

Pro Pro Gln Leu Lys Ser Ser Ser Gly Pro Ala Ser Ala Ser Gly Glu 35 40 45

Val Ile Pro Ser Glu Ser Glu Asp Asp Asp Glu Gly Glu Asp Ser Asn 50 60

Thr Trp Lys His Val Lys Thr Lys Pro Lys Leu Asp Asp Lys Asn Glu 65 70 75 80 Thr Ser Thr Ser Asn Ala Glu Pro Ala Met Lys Glu Ser Val Pro Glu

Pro Leu Pro Lys Met Ser Pro Asn 100

- (2) INFORMATION FOR SEQ ID NO:1087:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 975 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..975
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596407
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

acgtttgtga tagtagatgg atggactgtg accgttgcat gtgttggcga ctcgcgctgc atcttggata ctaagggtgg ttcagtttct aaccttactg ttgatcacag gcttgaagat 180 aatacagaag agagggaacg cgttactgcg agtggtggag aagttggcag gctaagcatt 240 gttggaggcg ttgagaagct cactattgaa attctgcaga ttggtccact acggtgttgg 300 cctggaggtc tctgcctttc aaggtctatt ggggatatgg atgttgggga gttcattgtt 360 ccagttccct ttgtaaagca agtgaagcta tcaaaccttg gaggaaggct tatcattgca 420 tcagatggca tatgggatgc tctctcctca gaagtcgcag ctaaaacttg ccgtgggtta 480 tctgctgaac ttgctgctag acaagtagtt aaggaagcat tgagaagaag gggacttaag 540 gatgacacaa cttgcattgt ggtcgacata atcccacccg aaaacttcca agaaccaccg 600 ccttcacctc ctaaqaaqca caacaacttc tttaaatcat tactcttcag aaagaaatca 660 aactcatcta acaaactctc caagaaactt tccactgttg gtattgttga agagctcttc 720 780 qaaqaaqqtt cqccaatqct cqctqaaaqq ttaqqatcaq gtqactqttc taaqqaatca acaacaggag gagggatatt cacgtgtgcc atatgccaac tagacctagc tccaagcgag 840 ggaatatcag tccacgcagg ttcaatcttc tcgacaagtc taaaaccgtg gcaaggaccg 900 960 ttcttatgca cagattqtcq tgacaaaaaa gacgcgatgg aagggaaacg tccaagtgga gttaaagtca tctag

- (2) INFORMATION FOR SEQ ID NO:1088:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..324
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088: Met Asn Asp Ile Trp Phe Ile Pro Leu Leu Met Pro Gly Glu Thr Ser 5 10 Gly Thr Thr Ala Thr Phe Val Ile Val Asp Gly Trp Thr Val Thr Val 20 25 Ala Cys Val Gly Asp Ser Arg Cys Ile Leu Asp Thr Lys Gly Gly Ser 40 Val Ser Asn Leu Thr Val Asp His Arg Leu Glu Asp Asn Thr Glu Glu 55 60 Arg Glu Arg Val Thr Ala Ser Gly Gly Glu Val Gly Arg Leu Ser Ile 75 70 Val Gly Gly Val Glu Lys Leu Thr Ile Glu Ile Leu Gln Ile Gly Pro 85 90 Leu Arg Cys Trp Pro Gly Gly Leu Cys Leu Ser Arg Ser Ile Gly Asp 100 105 110 Met Asp Val Gly Glu Phe Ile Val Pro Val Pro Phe Val Lys Gln Val 120 125 Lys Leu Ser Asn Leu Gly Gly Arg Leu Ile Ile Ala Ser Asp Gly Ile 135 140 Trp Asp Ala Leu Ser Ser Glu Val Ala Ala Lys Thr Cys Arg Gly Leu 150 155 Ser Ala Glu Leu Ala Ala Arg Gln Val Val Lys Glu Ala Leu Arg Arg 170 175 165 Arg Gly Leu Lys Asp Asp Thr Thr Cys Ile Val Val Asp Ile Ile Pro 1.80 185 190 Pro Glu Asn Phe Gln Glu Pro Pro Pro Ser Pro Pro Lys Lys His Asn 195 200 205 Asn Phe Phe Lys Ser Leu Leu Phe Arg Lys Lys Ser Asn Ser Ser Asn 220 215 Lys Leu Ser Lys Lys Leu Ser Thr Val Gly Ile Val Glu Glu Leu Phe 230 235 Glu Glu Gly Ser Ala Met Leu Ala Glu Arg Leu Gly Ser Gly Asp Cys 250 245 Ser Lys Glu Ser Thr Thr Gly Gly Gly Ile Phe Thr Cys Ala Ile Cys

Gln Leu Asp Leu Ala Pro Ser Glu Gly Ile Ser Val His Ala Gly Ser 285

Ile Phe Ser Thr Ser Leu Lys Pro Trp Gln Gly Pro Phe Leu Cys Thr 290

Asp Cys Arg Asp Lys Lys Asp Ala Met Glu Gly Lys Arg Pro Ser Gly 305

Val Lys Val Ile

- (2) INFORMATION FOR SEQ ID NO:1089:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..314
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596410
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:
- Met Pro Gly Glu Thr Ser Gly Thr Thr Ala Thr Phe Val Ile Val Asp

 1 10 15
- Gly Trp Thr Val Thr Val Ala Cys Val Gly Asp Ser Arg Cys Ile Leu 20 25 30
- Asp Thr Lys Gly Gly Ser Val Ser Asn Leu Thr Val Asp His Arg Leu 35 40 45
- Glu Asp Asn Thr Glu Glu Arg Glu Arg Val Thr Ala Ser Gly Gly Glu
 50 55 60
- Val Gly Arg Leu Ser Ile Val Gly Gly Val Glu Lys Leu Thr Ile Glu
 65 70 75 80
- Ile Leu Gln Ile Gly Pro Leu Arg Cys Trp Pro Gly Gly Leu Cys Leu 85 90 95
- Ser Arg Ser Ile Gly Asp Met Asp Val Gly Glu Phe Ile Val Pro Val 100 105 110
- Pro Phe Val Lys Gln Val Lys Leu Ser Asn Leu Gly Gly Arg Leu Ile 115 120 125
- Ile Ala Ser Asp Gly Ile Trp Asp Ala Leu Ser Ser Glu Val Ala Ala 130 135 140
- Lys Thr Cys Arg Gly Leu Ser Ala Glu Leu Ala Ala Arg Gln Val Val 145 150 150 160
- Lys Glu Ala Leu Arg Arg Gly Leu Lys Asp Asp Thr Thr Cys Ile 165 170 175
- Val Val Asp Ile Ile Pro Pro Glu Asn Phe Gln Glu Pro Pro Pro Ser 180 185 190
- Pro Pro Lys Lys His Asn Asn Phe Phe Lys Ser Leu Leu Phe Arg Lys 195 200 205
- Lys Ser Asn Ser Ser Asn Lys Leu Ser Lys Leu Ser Thr Val Gly 210 215 220
- Ile Val Glu Glu Leu Phe Glu Glu Gly Ser Ala Met Leu Ala Glu Arg 225 230 235 240
- Leu Gly Ser Gly Asp Cys Ser Lys Glu Ser Thr Thr Gly Gly Gly Ile 245 250 255
- Phe Thr Cys Ala Ile Cys Gln Leu Asp Leu Ala Pro Ser Glu Gly Ile 260 265 270
- Ser Val His Ala Gly Ser Ile Phe Ser Thr Ser Leu Lys Pro Trp Gln 275 280 285
- Gly Pro Phe Leu Cys Thr Asp Cys Arg Asp Lys Lys Asp Ala Met Glu 290 295 300
- Gly Lys Arg Pro Ser Gly Val Lys Val Ile

60

1140

1200

- (2) INFORMATION FOR SEQ ID NO:1090:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1218
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596461
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090: tettetagea aateaegtag actegtegtg cactgeaeag ataettttaa tggagagatg

gagataaata attocaaact tagatototo ttgtttatto cagttgacta tagtaggttt 120 tegatgggat caaacttcat ggagttacca ttgttgaggg ttttagatct ctcatttgcg 180 gattttgaag gagggaagat accetetage attggaaage teatecactt gaagtatttg 240 300 agtttatatc aggcatctgt aacttattta ccttcatctt tgcggaacct gaagtcgctg 360 ctgtatctca atctacgtat aaattctggt cagctgatta acgtgcccaa tgtctttaaa gagatgctag aactgagata cctctcgtta ccattgagaa cacctggtag gacaaagttg 420 gaatteggta atetaettaa attggagaeg ttgataaatt teteaacaaa ggtgagtagt 480 540 gtgacggatc ttcacggtat gacaaggcta aggaatctct ctatcttaat cagtggcgag 600 gagttgcgta tggaaactct atctacaacg cctggaaaat ctctaagtaa attgggacac ttggaaaatc ttactataga atattccgtt aactccgttc ttctcaagca cctgaagttg 660 atatttaggc caatgttacc tgatatgcaa cacttttctt ctcagctaac aaccatatct 720 ctacaacatt gtcttttcga ggaggatccg atgccaattc tagagaaact gctacaattg 780 aaactggttt atttaacgtg gaaagcttat gttgggagga gaatggtttg cacaggtggt 840 gggtttcctc aattgcacaa gctttcaatt gagggactat ttgacttgga agagtggata 900 gtagaagaag gctccatgcc acggcttcat actttgacta ttgattactg taagaaatta 960 aaagagattc catatgggct gagatttatc acttcattaa aggaattgac tatcggcaca 1020 acaaatgaaa gagaatttca gaagaaggtt tccaaaggag gagaagatta ctataaaatc 1080

- tggattatat ttgaggag (2) INFORMATION FOR SEQ ID NO:1091:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..406
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596462

caacacattc ctattattcg atataactgg catccagaac cagaagacaa cgaggtcaag

accactgaga tcttgcgtag catgcagtat aaagggtcag agattatgcg ggagggtgcc

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:
- Ser Ser Ser Lys Ser Arg Arg Leu Val Val His Cys Thr Asp Thr Phe 10
- Asn Gly Glu Met Glu Ile Asn Asn Ser Lys Leu Arg Ser Leu Leu Phe 25 20
- Ile Pro Val Asp Tyr Ser Arg Phe Ser Met Gly Ser Asn Phe Met Glu 40
- Leu Pro Leu Leu Arg Val Leu Asp Leu Ser Phe Ala Asp Phe Glu Gly
- Gly Lys Ile Pro Ser Ser Ile Gly Lys Leu Ile His Leu Lys Tyr Leu 75 70
- Ser Leu Tyr Gln Ala Ser Val Thr Tyr Leu Pro Ser Ser Leu Arg Asn 90 85
- Leu Lys Ser Leu Leu Tyr Leu Asn Leu Arg Ile Asn Ser Gly Gln Leu 105 110 100
- Ile Asn Val Pro Asn Val Phe Lys Glu Met Leu Glu Leu Arg Tyr Leu 125 120 115

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Ser Leu Pro Leu Arg Thr Pro Gly Arg Thr Lys Leu Glu Phe Gly Asn
                 135
Leu Leu Lys Leu Glu Thr Leu Ile Asn Phe Ser Thr Lys Val Ser Ser
                     155
      150
Val Thr Asp Leu His Gly Met Thr Arg Leu Arg Asn Leu Ser Ile Leu
           165 170
Ile Ser Gly Glu Glu Leu Arg Met Glu Thr Leu Ser Thr Thr Pro Gly
         180 185 190
Lys Ser Leu Ser Lys Leu Gly His Leu Glu Asn Leu Thr Ile Glu Tyr
                          205
            200
Ser Val Asn Ser Val Leu Leu Lys His Leu Lys Leu Ile Phe Arg Pro
                 215 220
Met Leu Pro Asp Met Gln His Phe Ser Ser Gln Leu Thr Thr Ile Ser
      230 235
Leu Gln His Cys Leu Phe Glu Glu Asp Pro Met Pro Ile Leu Glu Lys
                  250 255
           245
Leu Leu Gln Leu Lys Leu Val Tyr Leu Thr Trp Lys Ala Tyr Val Gly
                               270
                      265
         260
Arg Arg Met Val Cys Thr Gly Gly Gly Phe Pro Gln Leu His Lys Leu
             280
     275
Ser Ile Glu Gly Leu Phe Asp Leu Glu Glu Trp Ile Val Glu Gly
                         300
                 295
Ser Met Pro Arg Leu His Thr Leu Thr Ile Asp Tyr Cys Lys Leu
      310 315
Lys Glu Ile Pro Tyr Gly Leu Arg Phe Ile Thr Ser Leu Lys Glu Leu
                           330
          325
Thr Ile Gly Thr Thr Asn Glu Arg Glu Phe Gln Lys Lys Val Ser Lys
                        345
         340
Gly Gly Glu Asp Tyr Tyr Lys Ile Gln His Ile Pro Ile Ile Arg Tyr
                     360 365
Asn Trp His Pro Glu Pro Glu Asp Asn Glu Val Lys Thr Thr Glu Ile
   370 375 380
Leu Arg Ser Met Gln Tyr Lys Gly Ser Glu Ile Met Arg Glu Gly Ala
                               395
       390
Trp Ile Ile Phe Glu Glu
            405
```

- (2) INFORMATION FOR SEQ ID NO:1092:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..387
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596463
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:
- Met Glu Ile Asn Asn Ser Lys Leu Arg Ser Leu Leu Phe Ile Pro Val
- Asp Tyr Ser Arg Phe Ser Met Gly Ser Asn Phe Met Glu Leu Pro Leu 20 25 30
- Leu Arg Val Leu Asp Leu Ser Phe Ala Asp Phe Glu Gly Gly Lys Ile 35 40 45
- Pro Ser Ser Ile Gly Lys Leu Ile His Leu Lys Tyr Leu Ser Leu Tyr
- 50 55 60

 Gln Ala Ser Val Thr Tyr Leu Pro Ser Ser Leu Arg Asn Leu Lys Ser
 70 75 80
- Leu Leu Tyr Leu Asn Leu Arg Ile Asn Ser Gly Gln Leu Ile Asn Val 85 90 95
- Pro Asn Val Phe Lys Glu Met Leu Glu Leu Arg Tyr Leu Ser Leu Pro

105 100 Leu Arg Thr Pro Gly Arg Thr Lys Leu Glu Phe Gly Asn Leu Leu Lys 115 120 125 Leu Glu Thr Leu Ile Asn Phe Ser Thr Lys Val Ser Ser Val Thr Asp 130 135 140 Leu His Gly Met Thr Arg Leu Arg Asn Leu Ser Ile Leu Ile Ser Gly 145 150 155 Glu Glu Leu Arg Met Glu Thr Leu Ser Thr Thr Pro Gly Lys Ser Leu 165 170 Ser Lys Leu Gly His Leu Glu Asn Leu Thr Ile Glu Tyr Ser Val Asn 180 185 190 Ser Val Leu Leu Lys His Leu Lys Leu Ile Phe Arg Pro Met Leu Pro 195 200 205 Asp Met Gln His Phe Ser Ser Gln Leu Thr Thr Ile Ser Leu Gln His 210 215 220 Cys Leu Phe Glu Glu Asp Pro Met Pro Ile Leu Glu Lys Leu Leu Gln 225 230 235 240 Leu Lys Leu Val Tyr Leu Thr Trp Lys Ala Tyr Val Gly Arg Arg Met 245 250 255 Val Cys Thr Gly Gly Gly Phe Pro Gln Leu His Lys Leu Ser Ile Glu 260 265 270 Gly Leu Phe Asp Leu Glu Glu Trp Ile Val Glu Glu Gly Ser Met Pro 275 280 285 Arg Leu His Thr Leu Thr Ile Asp Tyr Cys Lys Lys Leu Lys Glu Ile 290 295 300 Pro Tyr Gly Leu Arg Phe Ile Thr Ser Leu Lys Glu Leu Thr Ile Gly 315 320 310 Thr Thr Asn Glu Arg Glu Phe Gln Lys Lys Val Ser Lys Gly Glu 325 330 335 Asp Tyr Tyr Lys Ile Gln His Ile Pro Ile Ile Arg Tyr Asn Trp His 340 345 350 Pro Glu Pro Glu Asp Asn Glu Val Lys Thr Thr Glu Ile Leu Arg Ser 355 360 Met Gln Tyr Lys Gly Ser Glu Ile Met Arg Glu Gly Ala Trp Ile Ile 375 370 Phe Glu Glu 385 (2) INFORMATION FOR SEQ ID NO:1093: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..365
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

Met Gly Ser Asn Phe Met Glu Leu Pro Leu Leu Arg Val Leu Asp Leu 1 5 10

Ser Phe Ala Asp Phe Glu Gly Gly Lys Ile Pro Ser Ser Ile Gly Lys 25 20

Leu Ile His Leu Lys Tyr Leu Ser Leu Tyr Gln Ala Ser Val Thr Tyr 45 40

Leu Pro Ser Ser Leu Arg Asn Leu Lys Ser Leu Leu Tyr Leu Asn Leu 60 55

Arg Ile Asn Ser Gly Gln Leu Ile Asn Val Pro Asn Val Phe Lys Glu 75 70

Met Leu Glu Leu Arg Tyr Leu Ser Leu Pro Leu Arg Thr Pro Gly Arg 85 90

```
Thr Lys Leu Glu Phe Gly Asn Leu Leu Lys Leu Glu Thr Leu Ile Asn
                              105
          100
Phe Ser Thr Lys Val Ser Ser Val Thr Asp Leu His Gly Met Thr Arg
                          120
                                             125
Leu Arg Asn Leu Ser Ile Leu Ile Ser Gly Glu Glu Leu Arg Met Glu
                     135
Thr Leu Ser Thr Thr Pro Gly Lys Ser Leu Ser Lys Leu Gly His Leu
                                     155
                  150
Glu Asn Leu Thr Ile Glu Tyr Ser Val Asn Ser Val Leu Leu Lys His
                                                    175
                                 170
              165
Leu Lys Leu Ile Phe Arg Pro Met Leu Pro Asp Met Gln His Phe Ser
                              185
Ser Gln Leu Thr Thr Ile Ser Leu Gln His Cys Leu Phe Glu Glu Asp
                         200
Pro Met Pro Ile Leu Glu Lys Leu Leu Gln Leu Lys Leu Val Tyr Leu
                                         220
                      215
Thr Trp Lys Ala Tyr Val Gly Arg Arg Met Val Cys Thr Gly Gly Gly
                                     235
                  230
Phe Pro Gln Leu His Lys Leu Ser Ile Glu Gly Leu Phe Asp Leu Glu
                                  250
               245
Glu Trp Ile Val Glu Glu Gly Ser Met Pro Arg Leu His Thr Leu Thr
                                                 270
                              265
           2.60
Ile Asp Tyr Cys Lys Lys Leu Lys Glu Ile Pro Tyr Gly Leu Arg Phe
                                             285
                         280
Ile Thr Ser Leu Lys Glu Leu Thr Ile Gly Thr Thr Asn Glu Arg Glu
                                         300
                      295
Phe Gln Lys Lys Val Ser Lys Gly Glu Asp Tyr Tyr Lys Ile Gln
                                      315
                   310
His Ile Pro Ile Ile Arg Tyr Asn Trp His Pro Glu Pro Glu Asp Asn
               325
                                  330
Glu Val Lys Thr Thr Glu Ile Leu Arg Ser Met Gln Tyr Lys Gly Ser
                             345
           340
Glu Ile Met Arg Glu Gly Ala Trp Ile Ile Phe Glu Glu
                          360
        355
```

- (2) INFORMATION FOR SEQ ID NO:1094:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 919 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..919
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094: atgcctctag ctaagcgagg aaggaagaga aaagccgatc caaatgtttc acagagaccc 60 ggagcctcta aacccactac tgcgaaaaga aaccctttac ctagtcaata caacttcaca 120 cccgcggccg agattcctcc tgctaagtct tcccaagggc gagtccgagt tcaaccccaa 180 caagcaaggt cagcagctcc acgagtctcc gactatccac ctcctcaagt tcttttccag 240 aactccgtga atcatgatct ccctgcacct ctttcgtcac aagaagtcca gaatgatgca 300 actaatcgat cgactccaca acatgaccct ccaagttctc cgattcagaa ctctcatgcc 360 agtcaaccat cttcccaagg taacaacttc caagaacgtg ttagttccgt gttaccggaa 420 ctccaagccg ataacataaa ggctctaaac gacattcttc aagtgcctgg tcgtgaggcg 480 540 tggacaactg ttctttctcc catactgatg gaaaaaacaa cttggtttac tcgtgacaca tcttcgaggt tggttcgaaa gattactaga gtatggacaa acaaatttga tggtgtcttc 600 tatagctggt catgtgttcc acaggatcga cgagaaagat acttcctcca gtttgcgaaa 660 atacaccatt gggattcttt gattacagga acaattcagt actattttga agatatatgt 720 caaagacgga tgaaagatat gattagcact gtgaggacta gtcaagagtg tcctaaatgg 780 atcatcgatt cccatatctt ggaaacgatg tgtgcatatt gggataatga agaagcaatt 840 gcaaagagtc tgacatattc caagactcgc atgtttgacc ataatgggct cggtcctcac 900

(ix) FEATURE:

```
atccatttat tagggactc
(2) INFORMATION FOR SEQ ID NO:1095:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 306 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..306
        (D) OTHER INFORMATION: / Ceres Seq. ID 1596523
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:
Met Pro Leu Ala Lys Arg Gly Arg Lys Arg Lys Ala Asp Pro Asn Val
       5 10
Ser Gln Arg Pro Gly Ala Ser Lys Pro Thr Thr Ala Lys Arg Asn Pro
             25
Leu Pro Ser Gln Tyr Asn Phe Thr Pro Ala Ala Glu Ile Pro Pro Ala
                       40
Lys Ser Ser Gln Gly Arg Val Arg Val Gln Pro Gln Gln Ala Arg Ser
                    55
Ala Ala Pro Arg Val Ser Asp Tyr Pro Pro Pro Gln Val Leu Phe Gln
                                75
                70
Asn Ser Val Asn His Asp Leu Pro Ala Pro Leu Ser Ser Gln Glu Val
                             90 95
            85
Gln Asn Asp Ala Thr Asn Arg Ser Thr Pro Gln His Asp Pro Pro Ser
         100 105 110
Ser Pro Ile Gln Asn Ser His Ala Ser Gln Pro Ser Ser Gln Gly Asn
                    120 125
   115
Asn Phe Gln Glu Arg Val Ser Ser Val Leu Pro Glu Leu Gln Ala Asp
                 135 140
Asn Ile Lys Ala Leu Asn Asp Ile Leu Gln Val Pro Gly Arg Glu Ala
     150 155
Trp Thr Thr Val Leu Ser Pro Ile Leu Met Glu Lys Thr Thr Trp Phe
                             170 175
           165
Thr Arg Asp Thr Ser Ser Arg Leu Val Arg Lys Ile Thr Arg Val Trp
                                          190
                        185
         180
Thr Asn Lys Phe Asp Gly Val Phe Tyr Ser Trp Ser Cys Val Pro Gln
                    200 205
      195
Asp Arg Arg Glu Arg Tyr Phe Leu Gln Phe Ala Lys Ile His His Trp
                                    220
                   215
Asp Ser Leu Ile Thr Gly Thr Ile Gln Tyr Tyr Phe Glu Asp Ile Cys
                              235
              230
Gln Arg Arg Met Lys Asp Met Ile Ser Thr Val Arg Thr Ser Gln Glu
                             250 255
              245
Cys Pro Lys Trp Ile Ile Asp Ser His Ile Leu Glu Thr Met Cys Ala
              265 270
 Tyr Trp Asp Asn Glu Glu Ala Ile Ala Lys Ser Leu Thr Tyr Ser Lys
    275 280
 Thr Arg Met Phe Asp His Asn Gly Leu Gly Pro His Ile His Leu Leu
                 295
    290
 Gly Thr
 305
 (2) INFORMATION FOR SEQ ID NO:1096:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 435 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
```

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096: 60 aggaatttca tcgaacatgt tataggcaat gatgagtttg tggtgaataa tgtgtatacg ctaaatatat gggatgttgg tgggcaaaag actataagat cgtattggag gaattacttt 120 gagcagactg atggtttggt ttgggtggtt gatagttctg atcttaggag gttagatgat 180 tgcaagatgg aacttgacaa tctcttgaaa gaagagaggc tagctggttc atctttgctg 240 atactagcaa ataagcagga tattcaaggt gcactaacac ctgatgaaat tggcaaggtg 300 ctaaacttag agtccatgga taaaagccgg cactggaaga tagtgggttg cagcgcatac 360 acgggtgaag gtttgttgga aggattcgat tggttggttc aagacattgc ctccaggatt 420 tacatgcttg actaa

- (2) INFORMATION FOR SEQ ID NO:1097:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097: Arg Asn Phe Ile Glu His Val Ile Gly Asn Asp Glu Phe Val Val Asn
- 1 5 10 15
 Asn Val Tyr Thr Leu Asn Ile Trp Asp Val Gly Gly Gln Lys Thr Ile
- 20 25 30

 Arg Ser Tyr Trp Arg Asn Tyr Phe Glu Gln Thr Asp Gly Leu Val Trp
- 35 40 45
 Val Val Asp Ser Ser Asp Leu Arg Arg Leu Asp Asp Cys Lys Met Glu
- 50 55 60
 Leu Asp Asn Leu Leu Lys Glu Glu Arg Leu Ala Gly Ser Ser Leu Leu
- 65 70 75 80

 Ile Leu Ala Asn Lys Gln Asp Ile Gln Gly Ala Leu Thr Pro Asp Glu
 85 90 95
- Ile Gly Lys Val Leu Asn Leu Glu Ser Met Asp Lys Ser Arg His Trp
- Lys Ile Val Gly Cys Ser Ala Tyr Thr Gly Glu Gly Leu Leu Glu Gly 115 120 125
- Phe Asp Trp Leu Val Gln Asp Ile Ala Ser Arg Ile Tyr Met Leu Asp 130 135 140
- (2) INFORMATION FOR SEQ ID NO:1098:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596534
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:
- Met Glu Leu Asp Asn Leu Leu Lys Glu Glu Arg Leu Ala Gly Ser Ser 1 10 15
- Leu Leu Ile Leu Ala Asn Lys Gln Asp Ile Gln Gly Ala Leu Thr Pro 20 25 30
- Asp Glu Ile Gly Lys Val Leu Asn Leu Glu Ser Met Asp Lys Ser Arg

His Trp Lys Ile Val Gly Cys Ser Ala Tyr Thr Gly Glu Gly Leu Leu 50 60 Glu Gly Phe Asp Trp Leu Val Gln Asp Ile Ala Ser Arg Ile Tyr Met 65 70 70 75 80 80

- (2) INFORMATION FOR SEQ ID NO:1099:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1248
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596611
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099: atggcaaccg tggaatccaa gaaacaagag aagaagtcga gaacgagcaa accaaagaag 60 gataacatga ggatgaggat gttaatgaaa ttggtaatga ctttgagact agtaatagct 120 180 tggagaacac taacacatgt acgggaactc aagaagcggg aacagaaagc tcaagtgctc acggccaagt acaattcaat ggactcgagg gattggatgt tagcatgtga agacgaaatc 240 tattcgataa agaagaacga gactcggagt cttgtagatc ttccatttgg aataaagccg 300 attggtttaa aatgggtatt caaactcaaa cgaaattctg atgtaagtat caataaatac 360 aaagctcgac ttgttgctaa gggttacgtg caacgttatg ggactgattt ctatgaagtc 420 tttgttccag tagcttgtat tgagaaaata attcttgtcg accttgaggc ttcaaatgat 480 tgggagatac aacttgatgt taaaacagct ttcttacatg gagagttaaa ggaaactgtt 540 tatgtcacgc gaccagaaga ttttgtagaa aagggagaag aaggaaaaga accgtcggtt 600 660 tatcggaaaa ctataagtgg tgagtttctt cttgtagcag tttacgtgga tgacttattt gttacaggaa caaatacaac cattattgat gagttcaaag gagagatgac ttcaaatttc 720 aacatgagca accttgggaa attaacttat tatctcggaa ttgaagtgtt tcaacgaaaa 780 840 gaagaaataa ggttgaatca aactcgttat gagatgaaga tattagaaga gactgcaatg 900 gccggaccta tcttactctg tgggagtaat gagtcgttat atgcaaagtc caagagaatc 960 acatggagcg gctatgaggc actgcttaag gcattgaaac ggcaagataa gcaatttggc tccaagattt gctcagtgaa gtcaccgggt taccaagcaa aagagttgtt atacggattg 1020 acaataaatc agcgatatct ctcacgaaga accctgtatt tcatggcgag ggcaaacaca 1080 tccataggcg aagtcgaaca tgttctggga attgagcaaa gggcagacat cttaacaaag 1140 gcccttgtaa gaatgaagtt taaagagatg agagatctca ttggtgttca agatgtgtgt 1200 gaagggatag agcttaggat ctttaggagt tatctaagat gtgtttag
- (2) INFORMATION FOR SEQ ID NO:1100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..415
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596612
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

Met Ala Thr Val Glu Ser Lys Lys Gln Glu Lys Lys Ser Arg Thr Ser 1 5 10 15 15 Lys Pro Lys Lys Asp Asn Met Arg Met Arg Met Leu Met Lys Leu Val

20 25 30

Met Thr Leu Arg Leu Val Ile Ala Trp Arg Thr Leu Thr His Val Arg

35 40 45
Glu Leu Lys Lys Arg Glu Gln Lys Ala Gln Val Leu Thr Ala Lys Tyr
50 55 60

Asn Ser Met Asp Ser Arg Asp Trp Met Leu Ala Cys Glu Asp Glu Ile

70 65 Tyr Ser Ile Lys Lys Asn Glu Thr Arg Ser Leu Val Asp Leu Pro Phe 85 90 Gly Ile Lys Pro Ile Gly Leu Lys Trp Val Phe Lys Leu Lys Arg Asn 100 105 Ser Asp Val Ser Ile Asn Lys Tyr Lys Ala Arg Leu Val Ala Lys Gly 115 120 125 Tyr Val Gln Arg Tyr Gly Thr Asp Phe Tyr Glu Val Phe Val Pro Val 130 135 140 Ala Cys Ile Glu Lys Ile Ile Leu Val Asp Leu Glu Ala Ser Asn Asp 150 155 Trp Glu Ile Gln Leu Asp Val Lys Thr Ala Phe Leu His Gly Glu Leu 165 170 Lys Glu Thr Val Tyr Val Thr Arg Pro Glu Asp Phe Val Glu Lys Gly 180 185 190 Glu Glu Gly Lys Glu Pro Ser Val Tyr Arg Lys Thr Ile Ser Gly Glu 195 200 205 Phe Leu Leu Val Ala Val Tyr Val Asp Asp Leu Phe Val Thr Gly Thr 210 215 220 Asn Thr Thr Ile Ile Asp Glu Phe Lys Gly Glu Met Thr Ser Asn Phe 225 230 235 240 Asn Met Ser Asn Leu Gly Lys Leu Thr Tyr Tyr Leu Gly Ile Glu Val 245 250 255 Phe Gln Arg Lys Glu Glu Ile Arg Leu Asn Gln Thr Arg Tyr Glu Met 260 265 270 Lys Ile Leu Glu Glu Thr Ala Met Ala Gly Pro Ile Leu Leu Cys Gly 280 285 Ser Asn Glu Ser Leu Tyr Ala Lys Ser Lys Arg Ile Thr Trp Ser Gly 290 295 300 Tyr Glu Ala Leu Leu Lys Ala Leu Lys Arg Gln Asp Lys Gln Phe Gly 315 320 305 310 Ser Lys Ile Cys Ser Val Lys Ser Pro Gly Tyr Gln Ala Lys Glu Leu 325 330 335 Leu Tyr Gly Leu Thr Ile Asn Gln Arg Tyr Leu Ser Arg Arg Thr Leu 340 345 Tyr Phe Met Ala Arg Ala Asn Thr Ser Ile Gly Glu Val Glu His Val 355 360 Leu Gly Ile Glu Gln Arg Ala Asp Ile Leu Thr Lys Ala Leu Val Arg 370 375 380 Met Lys Phe Lys Glu Met Arg Asp Leu Ile Gly Val Gln Asp Val Cys 390 395 400 Glu Gly Ile Glu Leu Arg Ile Phe Arg Ser Tyr Leu Arg Cys Val 405 410 (2) INFORMATION FOR SEQ ID NO:1101: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 393 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..393
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596614
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

Met Arg Met Arg Met Leu Met Lys Leu Val Met Thr Leu Arg Leu Val 10 5

Ile Ala Trp Arg Thr Leu Thr His Val Arg Glu Leu Lys Lys Arg Glu 20 25

Gln Lys Ala Gln Val Leu Thr Ala Lys Tyr Asn Ser Met Asp Ser Arg 40

```
Asp Trp Met Leu Ala Cys Glu Asp Glu Ile Tyr Ser Ile Lys Lys Asn
                      55
Glu Thr Arg Ser Leu Val Asp Leu Pro Phe Gly Ile Lys Pro Ile Gly
                                     75
                  70
Leu Lys Trp Val Phe Lys Leu Lys Arg Asn Ser Asp Val Ser Ile Asn
                                 90
              85
Lys Tyr Lys Ala Arg Leu Val Ala Lys Gly Tyr Val Gln Arg Tyr Gly
                             105
          100
Thr Asp Phe Tyr Glu Val Phe Val Pro Val Ala Cys Ile Glu Lys Ile
                                             125
                         120
Ile Leu Val Asp Leu Glu Ala Ser Asn Asp Trp Glu Ile Gln Leu Asp
                                        140
                      135
Val Lys Thr Ala Phe Leu His Gly Glu Leu Lys Glu Thr Val Tyr Val
                                    155
                  150
Thr Arg Pro Glu Asp Phe Val Glu Lys Gly Glu Gly Lys Glu Pro
                                170
                                                     175
Ser Val Tyr Arg Lys Thr Ile Ser Gly Glu Phe Leu Leu Val Ala Val
                             185 190
Tyr Val Asp Asp Leu Phe Val Thr Gly Thr Asn Thr Thr Ile Ile Asp
                                  205
                          200
Glu Phe Lys Gly Glu Met Thr Ser Asn Phe Asn Met Ser Asn Leu Gly
                               220
                      215
Lys Leu Thr Tyr Tyr Leu Gly Ile Glu Val Phe Gln Arg Lys Glu Glu
                                     235
                  230
Ile Arg Leu Asn Gln Thr Arg Tyr Glu Met Lys Ile Leu Glu Glu Thr
                                 250
               245
Ala Met Ala Gly Pro Ile Leu Leu Cys Gly Ser Asn Glu Ser Leu Tyr
                              265
           260
Ala Lys Ser Lys Arg Ile Thr Trp Ser Gly Tyr Glu Ala Leu Leu Lys
                          280
Ala Leu Lys Arg Gln Asp Lys Gln Phe Gly Ser Lys Ile Cys Ser Val
                      295
Lys Ser Pro Gly Tyr Gln Ala Lys Glu Leu Leu Tyr Gly Leu Thr Ile
                                     315
                   310
Asn Gln Arg Tyr Leu Ser Arg Arg Thr Leu Tyr Phe Met Ala Arg Ala
               325
                                  330
Asn Thr Ser Ile Gly Glu Val Glu His Val Leu Gly Ile Glu Gln Arg
                              345
          340
Ala Asp Ile Leu Thr Lys Ala Leu Val Arg Met Lys Phe Lys Glu Met
                                             365
                          360
Arg Asp Leu Ile Gly Val Gln Asp Val Cys Glu Gly Ile Glu Leu Arg
                                          380
                      375
Ile Phe Arg Ser Tyr Leu Arg Cys Val
                  390
(2) INFORMATION FOR SEQ ID NO:1102:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1500 base pairs
          (B) TYPE: nucleic acid
```

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596776
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

atggagetea atgtetaegg attgtggget tatgatgeaa teaeegeget ggeaatgget attgaagaag ctggaataga taacatgact ttcagtaatg cagatcctgg gaaaaatgta totgaacttg aagotottgg tttatotoag tttggtocaa agottotoca gaogototoa 240 acaattcagt tcaqaqqact tqcaqqaqat ttctgttttg tcaatgggca actgcaacca 300 toggtgtttg agattgttaa tgtgatoggt acoggagtaa ggtcagtagg attotggacg

gaggaaaatg gtcttgtgaa gaaactagag cagcaaccga gttgcatgag taatttatct acttggaatg atcatcttaa atacattata tggcctggag aggctggttc tattccaact 420 480 ggatcgaaga ttcctacaaa tgacaagagg ttgcgcattg gagttcctaa gagaattggt 540 ttcactgatc tcgtgaaggt cacaagggat cctatcacca attcaactat agtcacaggt ttttgcatag attattttga ggctgtggtt caagcaatgc cttatgacgt ctcctatgag 600 660 ttcattcctt tcgagaaacc caatggtgaa ccagccggta gttacaacga cttggtccac 720 caaqtqtacc taqqqaqata tqacqccqtt qtqqqaqata cqaccatact ttcqaaaaqq 780 tecetitatg ttgagtteae attaceattt attaaateag gegtaggatt agtegtetee attgaagacc aagtgaaaag agatagtgtc cctttcctga aacccttgtc atgggaactg 840 900 tggttgactt cetttgttet tttetteett attggattta etgtttggge tettgaacat 960 agggataacc cagacttcca tggacctcct aattaccaag ctagtaccat tttatggttt gccttctcta ccatggtttt tgctccaagt acattgaatc ttccttcccc ctctacatct 1020 ctgcatatat tgaagtttct atacatcagt acatcacaaa tattgatgct tacacttaag 1080 ttgctgtccg caggagaga agtatatagc ttcgaggcga gggtcctagt tatcacatgg 1140 tacttcattg tcctcgtgtt aactctgagt tacacagcca gtttggcgtc gcttttgaca 1200 tcacaacaac taaatccaac cataaccagc atgagtagct tgcttcaaag aggagaacga 1260 gtgggttatc agagaacatc attcattctt gggaaactta aagatacagg nttcccgcaa 1320 tctagccttg tgccttttga tactgcagaa gaatgcgacg agcttctgag caaaggatca 1380 aaaaaaggcg gtgtctctgc agctttctta gaaatccctt acttgagaat ctttcttagt 1440 aattattgca acacttataa gattgttgaa gtacccttca aggttgatgg attcggcttt 1500

- (2) INFORMATION FOR SEQ ID NO:1103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596777
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

Met Glu Leu Asn Val Tyr Gly Leu Trp Ala Tyr Asp Ala Ile Thr Ala 1 $$ 5 $$ 10 $$ 15 Leu Ala Met Ala Ile Glu Glu Ala Gly Ile Asp Asn Met Thr Phe Ser

20 25 30

Asn Ala Asp Pro Gly Lys Asn Val Ser Glu Leu Glu Ala Leu Gly Leu
35 40 45

Ser Gln Phe Gly Pro Lys Leu Leu Gln Thr Leu Ser Thr Ile Gln Phe 50 55 60

Arg Gly Leu Ala Gly Asp Phe Cys Phe Val Asn Gly Gln Leu Gln Pro

70

75

80

Ser Val Phe Glu Ile Val Asn Val Ile Gly Thr Gly Val Arg Ser Val 85 90 95

Gly Phe Trp Thr Glu Glu Asn Gly Leu Val Lys Lys Leu Glu Gln Gln 100 105 110

Pro Ser Cys Met Ser Asn Leu Ser Thr Trp Asn Asp His Leu Lys Tyr
115 120 125

Ile Ile Trp Pro Gly Glu Ala Gly Ser Ile Pro Thr Gly Ser Lys Ile 130 135 140

Pro Thr Asn Asp Lys Arg Leu Arg Ile Gly Val Pro Lys Arg Ile Gly
145 150 155 160

Phe Thr Asp Leu Val Lys Val Thr Arg Asp Pro Ile Thr Asn Ser Thr 165 170 175

Ile Val Thr Gly Phe Cys Ile Asp Tyr Phe Glu Ala Val Val Gln Ala 180 185 190

Met Pro Tyr Asp Val Ser Tyr Glu Phe Ile Pro Phe Glu Lys Pro Asn 195 200 205

Gly Glu Pro Ala Gly Ser Tyr Asn Asp Leu Val His Gln Val Tyr Leu 210 220

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Gly Arg Tyr Asp Ala Val Val Gly Asp Thr Thr Ile Leu Ser Lys Arg
                                    235
                 230
Ser Leu Tyr Val Glu Phe Thr Leu Pro Phe Ile Lys Ser Gly Val Gly
                      250
           245
Leu Val Val Ser Ile Glu Asp Gln Val Lys Arg Asp Ser Val Pro Phe
                            265 270
Leu Lys Pro Leu Ser Trp Glu Leu Trp Leu Thr Ser Phe Val Leu Phe
                         280
Phe Leu Ile Gly Phe Thr Val Trp Ala Leu Glu His Arg Asp Asn Pro
                                       300
                     295
Asp Phe His Gly Pro Pro Asn Tyr Gln Ala Ser Thr Ile Leu Trp Phe
                                    315
                  310
Ala Phe Ser Thr Met Val Phe Ala Pro Ser Thr Leu Asn Leu Pro Ser
                                330
Pro Ser Thr Ser Leu His Ile Leu Lys Phe Leu Tyr Ile Ser Thr Ser
                             345
Gln Ile Leu Met Leu Thr Leu Lys Leu Leu Ser Ala Gly Glu Arg Val
                         360
Tyr Ser Phe Glu Ala Arg Val Leu Val Ile Thr Trp Tyr Phe Ile Val
                     375
Leu Val Leu Thr Leu Ser Tyr Thr Ala Ser Leu Ala Ser Leu Leu Thr
                                    395
                  390
Ser Gln Gln Leu Asn Pro Thr Ile Thr Ser Met Ser Ser Leu Leu Gln
                                410
              405
Arg Gly Glu Arg Val Gly Tyr Gln Arg Thr Ser Phe Ile Leu Gly Lys
                             425
          420
Leu Lys Asp Thr Xaa Phe Pro Gln Ser Ser Leu Val Pro Phe Asp Thr
                         440
Ala Glu Glu Cys Asp Glu Leu Leu Ser Lys Gly Ser Lys Lys Gly Gly
                                        460
                     455
Val Ser Ala Ala Phe Leu Glu Ile Pro Tyr Leu Arg Ile Phe Leu Ser
        470
                                  475
Asn Tyr Cys Asn Thr Tyr Lys Ile Val Glu Val Pro Phe Lys Val Asp
                                 490
           485
Gly Phe Gly Phe
           500
```

- (2) INFORMATION FOR SEQ ID NO:1104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..482
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

Met Ala Ile Glu Glu Ala Gly Ile Asp Asn Met Thr Phe Ser Asn Ala 1 5 10 15 Asp Pro Gly Lys Asn Val Ser Glu Leu Glu Ala Leu Gly Leu Ser Gln

sp Pro Gly Lys Asn Val Ser Glu Leu Glu Ala Leu Gly Leu Ser Glu
20 25 30

Phe Gly Pro Lys Leu Leu Gln Thr Leu Ser Thr Ile Gln Phe Arg Gly
35
40
45
Lou Ala Gly Asp Phe Cys Phe Val Asp Gly Gln Leu Gln Pro Ser Val

Leu Ala Gly Asp Phe Cys Phe Val Asn Gly Gln Leu Gln Pro Ser Val 50 55 60

Phe Glu Ile Val Asn Val Ile Gly Thr Gly Val Arg Ser Val Gly Phe 65 70 75 80

Trp Thr Glu Glu Asn Gly Leu Val Lys Lys Leu Glu Gln Gln Pro Ser

85 90 95

Cys Met Ser Asn Leu Ser Thr Trp Asn Asp His Leu Lys Tyr Ile Ile

105 100 Trp Pro Gly Glu Ala Gly Ser Ile Pro Thr Gly Ser Lys Ile Pro Thr 115 120 125 Asn Asp Lys Arg Leu Arg Ile Gly Val Pro Lys Arg Ile Gly Phe Thr 130 135 140 Asp Leu Val Lys Val Thr Arg Asp Pro Ile Thr Asn Ser Thr Ile Val 145 150 155 160 Thr Gly Phe Cys Ile Asp Tyr Phe Glu Ala Val Val Gln Ala Met Pro 165 170 175 Tyr Asp Val Ser Tyr Glu Phe Ile Pro Phe Glu Lys Pro Asn Gly Glu 180 185 190 Pro Ala Gly Ser Tyr Asn Asp Leu Val His Gln Val Tyr Leu Gly Arg 195 200 205 Tyr Asp Ala Val Val Gly Asp Thr Thr Ile Leu Ser Lys Arg Ser Leu 210 215 220 Tyr Val Glu Phe Thr Leu Pro Phe Ile Lys Ser Gly Val Gly Leu Val 225 230 235 240 Val Ser Ile Glu Asp Gln Val Lys Arg Asp Ser Val Pro Phe Leu Lys 245 250 255 Pro Leu Ser Trp Glu Leu Trp Leu Thr Ser Phe Val Leu Phe Phe Leu 260 265 270 Ile Gly Phe Thr Val Trp Ala Leu Glu His Arg Asp Asn Pro Asp Phe 275 280 285 His Gly Pro Pro Asn Tyr Gln Ala Ser Thr Ile Leu Trp Phe Ala Phe 290 295 300 Ser Thr Met Val Phe Ala Pro Ser Thr Leu Asn Leu Pro Ser Pro Ser 305 310 315 320 Thr Ser Leu His Ile Leu Lys Phe Leu Tyr Ile Ser Thr Ser Gln Ile 325 330 335 Leu Met Leu Thr Leu Lys Leu Leu Ser Ala Gly Glu Arg Val Tyr Ser 340 345 Phe Glu Ala Arg Val Leu Val Ile Thr Trp Tyr Phe Ile Val Leu Val 355 360 365 Leu Thr Leu Ser Tyr Thr Ala Ser Leu Ala Ser Leu Leu Thr Ser Gln 375 380 Gln Leu Asn Pro Thr Ile Thr Ser Met Ser Ser Leu Leu Gln Arg Gly 390 395 Glu Arg Val Gly Tyr Gln Arg Thr Ser Phe Ile Leu Gly Lys Leu Lys 405 410 415 Asp Thr Xaa Phe Pro Gln Ser Ser Leu Val Pro Phe Asp Thr Ala Glu 420 425 430 Glu Cys Asp Glu Leu Leu Ser Lys Gly Ser Lys Lys Gly Gly Val Ser 435 440 445 Ala Ala Phe Leu Glu Ile Pro Tyr Leu Arg Ile Phe Leu Ser Asn Tyr 450 455 460 Cys Asn Thr Tyr Lys Ile Val Glu Val Pro Phe Lys Val Asp Gly Phe 470 475

- (2) INFORMATION FOR SEQ ID NO:1105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

Gly Phe

- (A) NAME/KEY: -
- (B) LOCATION: 1..705
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

cgcactttct caccccaaac gattctcgcc cggaaaatga ggtgggaaag ggtccgacaa 60 ctacagcaac aagtgggtct cggtgagtct tnttccgggc ccggtaagag gtggggtcac 120 acttgtaacg ccattaaagg aggtagcttt ctctatgttt tcggtggcta tggcagagat 180 aattgccaaa ccaatcaagt ccatgttttc gacgctgcaa agcagatatg gactcagcca 240 atgatcaatg gcacacetee teeteecagg gacagteaca getgtacaac agteggegae 300 aatctttttg tgtttggtgg tactgatgga gttaaccctc ttaaggattt gtatattcta 360 gatacttctt cacatacttg gaaatgtccg agtgttaggg gagagggacc tgaggcaaga 420 480 gaaggtcata gcgccacact ggttggtaaa aggctgtttg tctttggtgg ctgtgggaaa 540 tcttctggta ttaatgaaga aatctattac aatgacgttt acatatttaa tacagaaact 600 tttgtgtgga aacgggctgt tacaattggg aatcctccat ctgcgcggga tagccattct 660 tgctcatcgt ggaagaacaa acttgttgtt ataggtggcg aagatggaca tgactactat ctgtccgatg ttcatatcct tgatacaggt gaaaaagcat cttga

- (2) INFORMATION FOR SEQ ID NO:1106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..234
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596785
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106: Arg Thr Phe Ser Pro Gln Thr Ile Leu Ala Arg Lys Met Arg Trp Glu 10 Arg Val Arg Gln Leu Gln Gln Gln Val Gly Leu Gly Glu Ser Xaa Ser 25 20 Gly Pro Gly Lys Arg Trp Gly His Thr Cys Asn Ala Ile Lys Gly Gly 40 35 Ser Phe Leu Tyr Val Phe Gly Gly Tyr Gly Arg Asp Asn Cys Gln Thr 55 Asn Gln Val His Val Phe Asp Ala Ala Lys Gln Ile Trp Thr Gln Pro 75 70 Met Ile Asn Gly Thr Pro Pro Pro Pro Arg Asp Ser His Ser Cys Thr 90 85 Thr Val Gly Asp Asn Leu Phe Val Phe Gly Gly Thr Asp Gly Val Asn 100 105 Pro Leu Lys Asp Leu Tyr Ile Leu Asp Thr Ser Ser His Thr Trp Lys 125 120 Cys Pro Ser Val Arg Gly Glu Gly Pro Glu Ala Arg Glu Gly His Ser 135 140 Ala Thr Leu Val Gly Lys Arg Leu Phe Val Phe Gly Gly Cys Gly Lys 150 155 Ser Ser Gly Ile Asn Glu Glu Ile Tyr Tyr Asn Asp Val Tyr Ile Phe 170 165 Asn Thr Glu Thr Phe Val Trp Lys Arg Ala Val Thr Ile Gly Asn Pro 190 180 185 Pro Ser Ala Arg Asp Ser His Ser Cys Ser Ser Trp Lys Asn Lys Leu 205 195 200 Val Val Ile Gly Gly Glu Asp Gly His Asp Tyr Tyr Leu Ser Asp Val 220 215 His Ile Leu Asp Thr Gly Glu Lys Ala Ser 230
- (2) INFORMATION FOR SEQ ID NO:1107:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..222
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596786
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:
- Met Arg Trp Glu Arg Val Arg Gln Leu Gln Gln Gln Val Gly Leu Gly 10
- Glu Ser Xaa Ser Gly Pro Gly Lys Arg Trp Gly His Thr Cys Asn Ala
- Ile Lys Gly Gly Ser Phe Leu Tyr Val Phe Gly Gly Tyr Gly Arg Asp 40
- Asn Cys Gln Thr Asn Gln Val His Val Phe Asp Ala Ala Lys Gln Ile 55
- Trp Thr Gln Pro Met Ile Asn Gly Thr Pro Pro Pro Pro Arg Asp Ser 75
- His Ser Cys Thr Thr Val Gly Asp Asn Leu Phe Val Phe Gly Gly Thr 85 90
- Asp Gly Val Asn Pro Leu Lys Asp Leu Tyr Ile Leu Asp Thr Ser Ser 105
- His Thr Trp Lys Cys Pro Ser Val Arg Gly Glu Gly Pro Glu Ala Arg 120 115
- Glu Gly His Ser Ala Thr Leu Val Gly Lys Arg Leu Phe Val Phe Gly 135
- Gly Cys Gly Lys Ser Ser Gly Ile Asn Glu Glu Ile Tyr Tyr Asn Asp 150 155
- Val Tyr Ile Phe Asn Thr Glu Thr Phe Val Trp Lys Arg Ala Val Thr 170 165
- Ile Gly Asn Pro Pro Ser Ala Arg Asp Ser His Ser Cys Ser Ser Trp 185 180
- Lys Asn Lys Leu Val Val Ile Gly Gly Glu Asp Gly His Asp Tyr Tyr 195 200
- Leu Ser Asp Val His Ile Leu Asp Thr Gly Glu Lys Ala Ser 215 210
- (2) INFORMATION FOR SEQ ID NO:1108:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596787

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:
- Met Ile Asn Gly Thr Pro Pro Pro Pro Arg Asp Ser His Ser Cys Thr
- Thr Val Gly Asp Asn Leu Phe Val Phe Gly Gly Thr Asp Gly Val Asn 25
- Pro Leu Lys Asp Leu Tyr Ile Leu Asp Thr Ser Ser His Thr Trp Lys 40
- Cys Pro Ser Val Arg Gly Glu Gly Pro Glu Ala Arg Glu Gly His Ser 55
- Ala Thr Leu Val Gly Lys Arg Leu Phe Val Phe Gly Gly Cys Gly Lys 75
- Ser Ser Gly Ile Asn Glu Glu Ile Tyr Tyr Asn Asp Val Tyr Ile Phe 90 85
- Asn Thr Glu Thr Phe Val Trp Lys Arg Ala Val Thr Ile Gly Asn Pro 100 105
- Pro Ser Ala Arg Asp Ser His Ser Cys Ser Ser Trp Lys Asn Lys Leu 115 120 125

Val Val Ile Gly Gly Glu Asp Gly His Asp Tyr Tyr Leu Ser Asp Val 130 135 140

His Ile Leu Asp Thr Gly Glu Lys Ala Ser 145

- (2) INFORMATION FOR SEQ ID NO:1109:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1003 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1003
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596800
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109: gaagttttta tctttgagga aaggtacaaa aantgacgtt gctgctgctt tagaacagga 60 120 acttcacact tcgaggtcta tgtttgagca agctcggttc aaccttgtga ctgctctatc 180 aaatgttgaa gctaagaaaa ggtttgaatt tttggaagca gtcagtggaa caatggatgc 240 acatcttcgg tacttcaaac aggtcttgac atatgcgcaa caatccagag aaagatcaaa 300 ttatgaacaa gcagcactta atgaaaagat gcaggagtac aaaagacagg ttgatcgaga 360 gagcaggtgg ggttcaaatg gttctaatgg atcaccaaat ggagatggca tacaagcaat 420 cggtagaagc tctcacaaaa tgatagacgc cgtaatgcaa tctgctgcaa gaggaaaggt 480 gcaaacaata aggcaaggtt atctctctaa acgatcttca aacctgagag gagactggaa 540 aagaaggttt tttgttcttg acagccgggg aatgctctat tattaccgaa aacagtgtag 600 caaaccatct gggtctggaa gccagctttc tggacagaga aatagctccg agcttgggtc tggactgctt agtaggtggc tttcttcgaa taatcatgga catggtggtg tccatgatga 660 720 gaagtotgta gotogtoata cagtgaactt actoacotca acaattaaag togacgotga 780 tcaatcagat ctgaggtttt gctttaggat catatcacct acaaaaaact acacgttgca 840 ggctgagagt gcactcgatc aaatggattg gatagaaaag atcactgggg ttattgcatc 900 actacttagt tctcaggtcc ctgaacaggc tcatattaaa taccaatgca actttggtga ttgtccatcg gctacatttc agcgtcttcc tggtagtccc atgggaagtg gccaccatcg 960
- (2) INFORMATION FOR SEQ ID NO:1110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 amino acids

atctgctagt gaaagtagct catatgaaag ttctgaatat gat

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..334
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

Lys Phe Leu Ser Leu Arg Lys Gly Thr Lys Xaa Asp Val Ala Ala 1 5 10 15
Leu Glu Gln Glu Leu His Thr Ser Arg Ser Met Phe Glu Gln Ala Arg

20 25 30

Phe Asn Leu Val Thr Ala Leu Ser Asn Val Glu Ala Lys Lys Arg Phe
35 40 45

Glu Phe Leu Glu Ala Val Ser Gly Thr Met Asp Ala His Leu Arg Tyr
50 55 60

Phe Lys Gln Val Leu Thr Tyr Ala Gln Gln Ser Arg Glu Arg Ser Asn 65 70 75 80

Tyr Glu Gln Ala Ala Leu Asn Glu Lys Met Gln Glu Tyr Lys Arg Gln
85 90 95

Val Asp Arg Glu Ser Arg Trp Gly Ser Asn Gly Ser Asn Gly Ser Pro 100 105 110

Asn Gly Asp Gly Ile Gln Ala Ile Gly Arg Ser Ser His Lys Met Ile 115 120 125

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Asp Ala Val Met Gln Ser Ala Ala Arg Gly Lys Val Gln Thr Ile Arg
                   135
Gln Gly Tyr Leu Ser Lys Arg Ser Ser Asn Leu Arg Gly Asp Trp Lys
       150
                               155
Arg Arg Phe Phe Val Leu Asp Ser Arg Gly Met Leu Tyr Tyr Arg
      165
                            170
                                            175
Lys Gln Cys Ser Lys Pro Ser Gly Ser Gly Ser Gln Leu Ser Gly Gln
       180
                         185
Arg Asn Ser Ser Glu Leu Gly Ser Gly Leu Leu Ser Arg Trp Leu Ser
                      200
Ser Asn Asn His Gly His Gly Gly Val His Asp Glu Lys Ser Val Ala
 210 215
Arg His Thr Val Asn Leu Leu Thr Ser Thr Ile Lys Val Asp Ala Asp
      230
                                235
Gln Ser Asp Leu Arg Phe Cys Phe Arg Ile Ile Ser Pro Thr Lys Asn
                            250
      245
Tyr Thr Leu Gln Ala Glu Ser Ala Leu Asp Gln Met Asp Trp Ile Glu
                        265
Lys Ile Thr Gly Val Ile Ala Ser Leu Leu Ser Ser Gln Val Pro Glu
            280 285
Gln Ala His Ile Lys Tyr Gln Cys Asn Phe Gly Asp Cys Pro Ser Ala
  290 295
                                   300
Thr Phe Gln Arg Leu Pro Gly Ser Pro Met Gly Ser Gly His His Arg
305 310 315
Ser Ala Ser Glu Ser Ser Ser Tyr Glu Ser Ser Glu Tyr Asp
                   330
         325
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- (2) INFORMATION FOR SEQ ID NO:1111:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..308
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596802
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111: Met Phe Glu Gln Ala Arg Phe Asn Leu Val Thr Ala Leu Ser Asn Val 10 Glu Ala Lys Lys Arg Phe Glu Phe Leu Glu Ala Val Ser Gly Thr Met 20 25 Asp Ala His Leu Arg Tyr Phe Lys Gln Val Leu Thr Tyr Ala Gln Gln 40 Ser Arg Glu Arg Ser Asn Tyr Glu Gln Ala Ala Leu Asn Glu Lys Met 55 Gln Glu Tyr Lys Arg Gln Val Asp Arg Glu Ser Arg Trp Gly Ser Asn 75 70 Gly Ser Asn Gly Ser Pro Asn Gly Asp Gly Ile Gln Ala Ile Gly Arg 90 8.5 Ser Ser His Lys Met Ile Asp Ala Val Met Gln Ser Ala Ala Arg Gly 100 105 Lys Val Gln Thr Ile Arg Gln Gly Tyr Leu Ser Lys Arg Ser Ser Asn 120 125 115 Leu Arg Gly Asp Trp Lys Arg Arg Phe Phe Val Leu Asp Ser Arg Gly 135 140 Met Leu Tyr Tyr Tyr Arg Lys Gln Cys Ser Lys Pro Ser Gly Ser Gly 150 155 Ser Gln Leu Ser Gly Gln Arg Asn Ser Ser Glu Leu Gly Ser Gly Leu 165 170 Leu Ser Arg Trp Leu Ser Ser Asn Asn His Gly His Gly Gly Val His

185 180 Asp Glu Lys Ser Val Ala Arg His Thr Val Asn Leu Leu Thr Ser Thr 205 195 200 Ile Lys Val Asp Ala Asp Gln Ser Asp Leu Arg Phe Cys Phe Arg Ile 220 215 Ile Ser Pro Thr Lys Asn Tyr Thr Leu Gln Ala Glu Ser Ala Leu Asp 235 240 225 230 Gln Met Asp Trp Ile Glu Lys Ile Thr Gly Val Ile Ala Ser Leu Leu 245 250 Ser Ser Gln Val Pro Glu Gln Ala His Ile Lys Tyr Gln Cys Asn Phe 270 265 Gly Asp Cys Pro Ser Ala Thr Phe Gln Arg Leu Pro Gly Ser Pro Met 285 275 280 Gly Ser Gly His His Arg Ser Ala Ser Glu Ser Ser Ser Tyr Glu Ser 290 295 Ser Glu Tyr Asp (2) INFORMATION FOR SEQ ID NO:1112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..277
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596803
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:
- Met Asp Ala His Leu Arg Tyr Phe Lys Gln Val Leu Thr Tyr Ala Gln 1 5 10
- Gln Ser Arg Glu Arg Ser Asn Tyr Glu Gln Ala Ala Leu Asn Glu Lys 20 25 30
- Met Gln Glu Tyr Lys Arg Gln Val Asp Arg Glu Ser Arg Trp Gly Ser 35 40 45
- Asn Gly Ser Asn Gly Ser Pro Asn Gly Asp Gly Ile Gln Ala Ile Gly 50 55 60
- Arg Ser Ser His Lys Met Ile Asp Ala Val Met Gln Ser Ala Ala Arg
 65 70 75 80
- Gly Lys Val Gln Thr Ile Arg Gln Gly Tyr Leu Ser Lys Arg Ser Ser 85 90 95
- Asn Leu Arg Gly Asp Trp Lys Arg Arg Phe Phe Val Leu Asp Ser Arg
- Gly Met Leu Tyr Tyr Tyr Arg Lys Gln Cys Ser Lys Pro Ser Gly Ser 115 120 125
- Gly Ser Gln Leu Ser Gly Gln Arg Asn Ser Ser Glu Leu Gly Ser Gly 130 135 140
- Leu Leu Ser Arg Trp Leu Ser Ser Asn Asn His Gly His Gly Val 145 150 155 160
- His Asp Glu Lys Ser Val Ala Arg His Thr Val Asn Leu Leu Thr Ser 165 170 175
- Thr Ile Lys Val Asp Ala Asp Gln Ser Asp Leu Arg Phe Cys Phe Arg 180 185 190
- Ile Ile Ser Pro Thr Lys Asn Tyr Thr Leu Gln Ala Glu Ser Ala Leu 195 200 205
- Asp Gln Met Asp Trp Ile Glu Lys Ile Thr Gly Val Ile Ala Ser Leu 210 215 220
- Leu Ser Ser Gln Val Pro Glu Gln Ala His Ile Lys Tyr Gln Cys Asn 225 230 235 240
- Phe Gly Asp Cys Pro Ser Ala Thr Phe Gln Arg Leu Pro Gly Ser Pro 245 250 255

Met Gly Ser Gly His His Arg Ser Ala Ser Glu Ser Ser Ser Tyr Glu 260 265 270

Ser Ser Glu Tyr Asp 275

- (2) INFORMATION FOR SEQ ID NO:1113:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1044 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1044
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113: 60 aagtttttat ctttgaggaa aggtacaaaa antgacgttg ctgctgcttt agaacaggaa 120 cttcacactt cgaggtctat gtttgagcaa gctcggttca accttgtgac tgctctatca aatgttgaag ctaagaaaag gtttgaattt ttggaagcag tcagtggaac aatggatgca 180 catcttcggt acttcaaaca gggttacgaa ttactgcatc agatggaacc atatatcaat 240 300 caggictiga catatgogca acaatocaga gaaagatcaa attatgaaca agcagcactt 360 aatgaaaaga tgcaggagta caaaagacag gttgatcgag agagcaggtg gggttcaaat ggttctaatg gatcaccaaa tggagatggc atacaagcaa tcggtagaag ctctcacaaa 420 atgatagacg ccgtaatgca atctgctgca agaggaaagg tgcaaacaat aaggcaaggt 480 tatctctcta aacgatcttc aaacctgaga ggagactgga aaagaaggtt ttttgttctt 540 gacagccggg gaatgctcta ttattaccga aaacagtgta gcaaaccatc tgggtctgga 600 660 agccagcttt ctggacagag aaatagctcc gagcttgggt ctggactgct tagtaggtgg 720 ctttcttcga ataatcatgg acatggtggt gtccatgatg agaagtctgt agctcgtcat 780 acagtgaact tactcacctc aacaattaaa gtcgacgctg atcaatcaga tctgaggttt 840 tgctttagga tcatatcacc tacaaaaaac tacacgttgc aggctgagag tgcactcgat 900 caaatggatt ggatagaaaa gatcactggg gttattgcat cactacttag ttctcaggtc cctgaacagg ctcatattaa ataccaatgc aactttggtg attgtccatc ggctacattt 960 1020 cagcgtcttc ctggtagtcc catgggaagt ggccaccatc gatctgctag tgaaagtagc
- tcatatgaaa gttctgaata tgat (2) INFORMATION FOR SEQ ID NO:1114:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..348
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596805
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Lys Phe Leu Ser Leu Arg Lys Gly Thr Lys Xaa Asp Val Ala Ala Ala 1 5 10 15

Leu Glu Glu Leu His Thr Ser Arg Ser Met Phe Glu Gln Ala Arg 20 25 30

Phe Asn Leu Val Thr Ala Leu Ser Asn Val Glu Ala Lys Lys Arg Phe 35 40 45

Glu Phe Leu Glu Ala Val Ser Gly Thr Met Asp Ala His Leu Arg Tyr
50 60

Phe Lys Gln Gly Tyr Glu Leu Leu His Gln Met Glu Pro Tyr Ile Asn 65 70 75 80

Gln Val Leu Thr Tyr Ala Gln Gln Ser Arg Glu Arg Ser Asn Tyr Glu 85 90 95 Gln Ala Ala Leu Asn Glu Lys Met Gln Glu Tyr Lys Arg Gln Val Asp

100 105 110
Arg Glu Ser Arg Trp Gly Ser Asn Gly Ser Asn Gly Ser Pro Asn Gly

120 115 Asp Gly Ile Gln Ala Ile Gly Arg Ser Ser His Lys Met Ile Asp Ala 130 135 140 Val Met Gln Ser Ala Ala Arg Gly Lys Val Gln Thr Ile Arg Gln Gly 145 150 155 Tyr Leu Ser Lys Arg Ser Ser Asn Leu Arg Gly Asp Trp Lys Arg Arg 165 170 175 Phe Phe Val Leu Asp Ser Arg Gly Met Leu Tyr Tyr Tyr Arg Lys Gln 185 Cys Ser Lys Pro Ser Gly Ser Gly Ser Gln Leu Ser Gly Gln Arg Asn 195 200 Ser Ser Glu Leu Gly Ser Gly Leu Leu Ser Arg Trp Leu Ser Ser Asn 210 215 220 Asn His Gly His Gly Gly Val His Asp Glu Lys Ser Val Ala Arg His 225 230 235 Thr Val Asn Leu Leu Thr Ser Thr Ile Lys Val Asp Ala Asp Gln Ser 250 245 Asp Leu Arg Phe Cys Phe Arg Ile Ile Ser Pro Thr Lys Asn Tyr Thr 260 265 270 Leu Gln Ala Glu Ser Ala Leu Asp Gln Met Asp Trp Ile Glu Lys Ile 275 280 285 Thr Gly Val Ile Ala Ser Leu Leu Ser Ser Gln Val Pro Glu Gln Ala 290 295 300 His Ile Lys Tyr Gln Cys Asn Phe Gly Asp Cys Pro Ser Ala Thr Phe 305 310 315 Gln Arg Leu Pro Gly Ser Pro Met Gly Ser Gly His His Arg Ser Ala 325 330 Ser Glu Ser Ser Ser Tyr Glu Ser Ser Glu Tyr Asp 340 345

- (2) INFORMATION FOR SEQ ID NO:1115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..322
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:
- Met Phe Glu Gln Ala Arg Phe Asn Leu Val Thr Ala Leu Ser Asn Val

 1 10 15 15
- Glu Ala Lys Lys Arg Phe Glu Phe Leu Glu Ala Val Ser Gly Thr Met 20 25 30
- Asp Ala His Leu Arg Tyr Phe Lys Gln Gly Tyr Glu Leu Leu His Gln 35 40 45
- Met Glu Pro Tyr Ile Asn Gln Val Leu Thr Tyr Ala Gln Gln Ser Arg
 50 55 60
- Glu Arg Ser Asn Tyr Glu Gln Ala Ala Leu Asn Glu Lys Met Gln Glu 65 70 75 80
- Tyr Lys Arg Gln Val Asp Arg Glu Ser Arg Trp Gly Ser Asn Gly Ser 85 90 95
- Asn Gly Ser Pro Asn Gly Asp Gly Ile Gln Ala Ile Gly Arg Ser Ser 100 105 110
- His Lys Met Ile Asp Ala Val Met Gln Ser Ala Ala Arg Gly Lys Val
- Gln Thr Ile Arg Gln Gly Tyr Leu Ser Lys Arg Ser Ser Asn Leu Arg 130 135 140
- Gly Asp Trp Lys Arg Arg Phe Phe Val Leu Asp Ser Arg Gly Met Leu 145 150 150

Tyr Tyr Tyr Arg Lys Gln Cys Ser Lys Pro Ser Gly Ser Gly Ser Gln 170 165 Leu Ser Gly Gln Arg Asn Ser Ser Glu Leu Gly Ser Gly Leu Leu Ser 185 180 Arg Trp Leu Ser Ser Asn Asn His Gly His Gly Gly Val His Asp Glu 200 195 Lys Ser Val Ala Arg His Thr Val Asn Leu Leu Thr Ser Thr Ile Lys 215 Val Asp Ala Asp Gln Ser Asp Leu Arg Phe Cys Phe Arg Ile Ile Ser 230 235 Pro Thr Lys Asn Tyr Thr Leu Gln Ala Glu Ser Ala Leu Asp Gln Met 250 245 Asp Trp Ile Glu Lys Ile Thr Gly Val Ile Ala Ser Leu Leu Ser Ser 265 Gln Val Pro Glu Gln Ala His Ile Lys Tyr Gln Cys Asn Phe Gly Asp 280 Cys Pro Ser Ala Thr Phe Gln Arg Leu Pro Gly Ser Pro Met Gly Ser 300 290 295 Gly His His Arg Ser Ala Ser Glu Ser Ser Ser Tyr Glu Ser Ser Glu 315 310 Tyr Asp

- (2) INFORMATION FOR SEQ ID NO:1116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..291
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116: Met Asp Ala His Leu Arg Tyr Phe Lys Gln Gly Tyr Glu Leu Leu His 5 Gln Met Glu Pro Tyr Ile Asn Gln Val Leu Thr Tyr Ala Gln Gln Ser 25 2.0 Arg Glu Arg Ser Asn Tyr Glu Gln Ala Ala Leu Asn Glu Lys Met Gln 40 Glu Tyr Lys Arg Gln Val Asp Arg Glu Ser Arg Trp Gly Ser Asn Gly 60 55 Ser Asn Gly Ser Pro Asn Gly Asp Gly Ile Gln Ala Ile Gly Arg Ser 75 70 Ser His Lys Met Ile Asp Ala Val Met Gln Ser Ala Ala Arg Gly Lys 90 8.5 Val Gln Thr Ile Arg Gln Gly Tyr Leu Ser Lys Arg Ser Ser Asn Leu 110 105 100 Arg Gly Asp Trp Lys Arg Arg Phe Phe Val Leu Asp Ser Arg Gly Met 125 120 Leu Tyr Tyr Tyr Arg Lys Gln Cys Ser Lys Pro Ser Gly Ser Gly Ser 140 135 Gln Leu Ser Gly Gln Arg Asn Ser Ser Glu Leu Gly Ser Gly Leu Leu 150 155 Ser Arg Trp Leu Ser Ser Asn Asn His Gly His Gly Gly Val His Asp 175 170 165 Glu Lys Ser Val Ala Arg His Thr Val Asn Leu Leu Thr Ser Thr Ile 185 180 Lys Val Asp Ala Asp Gln Ser Asp Leu Arg Phe Cys Phe Arg Ile Ile 195 200 205 Ser Pro Thr Lys Asn Tyr Thr Leu Gln Ala Glu Ser Ala Leu Asp Gln

60

₁₂₀

180

240

300

360

Phe Gly Val Val Leu Gly Gly Val Val

(2) INFORMATION FOR SEQ ID NO:1119:

130

135

220 215 210 Met Asp Trp Ile Glu Lys Ile Thr Gly Val Ile Ala Ser Leu Leu Ser 235 230 Ser Gln Val Pro Glu Gln Ala His Ile Lys Tyr Gln Cys Asn Phe Gly 250 245 Asp Cys Pro Ser Ala Thr Phe Gln Arg Leu Pro Gly Ser Pro Met Gly 270 265 260 Ser Gly His His Arg Ser Ala Ser Glu Ser Ser Ser Tyr Glu Ser Ser 285 280 275 Glu Tyr Asp 290 (2) INFORMATION FOR SEQ ID NO:1117: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..412 (D) OTHER INFORMATION: / Ceres Seq. ID 1596885 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117: tttggctatg cgttatccta ggagacttgt gttggctggt tgtttatcgg ctctgattgt tatgactate etetegeta etettggatg ggetgeteet aatetgatet etegeaaatg gactcatcac ataacaacat tgttgttctt tggttttggg ctatggtctt tgtgggacgg tttcaaagaa ggaggaggg gttcggaaga attggctgaa gtcgaagcag aactgagaga agatgaaaac aaaaagcaga atagggcgtt cctcacgcaa tttttctctc caatttttct caaggetttt tegattaatt tetttggaga atggggtgae aagagteage ttgetacaat tggtttagct gcagatgaaa atccatttgg ggtggtcctt ggtggagttg tg (2) INFORMATION FOR SEQ ID NO:1118: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..137 (D) OTHER INFORMATION: / Ceres Seq. ID 1596886 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118: Leu Ala Met Arg Tyr Pro Arg Arg Leu Val Leu Ala Gly Cys Leu Ser 10 Ala Leu Ile Val Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala Ala 30 25 2.0 Pro Asn Leu Ile Ser Arg Lys Trp Thr His His Ile Thr Thr Leu Leu 45 40 Phe Phe Gly Phe Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu Gly 55 60 Gly Gly Gly Ser Glu Glu Leu Ala Glu Val Glu Ala Glu Leu Arg Glu 75 70 Asp Glu Asn Lys Lys Gln Asn Arg Ala Phe Leu Thr Gln Phe Phe Ser 90 Pro Ile Phe Leu Lys Ala Phe Ser Ile Asn Phe Phe Gly Glu Trp Gly 110 105 100 Asp Lys Ser Gln Leu Ala Thr Ile Gly Leu Ala Ala Asp Glu Asn Pro 125 120 115

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596887
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:
- Met Arg Tyr Pro Arg Arg Leu Val Leu Ala Gly Cys Leu Ser Ala Leu 1 5 10 15
- Ile Val Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala Ala Pro Asn 20 25 30
- Leu Ile Ser Arg Lys Trp Thr His His Ile Thr Thr Leu Leu Phe Phe 35 40 45
- Gly Phe Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu Gly Gly 50 55 60
- Gly Ser Glu Glu Leu Ala Glu Val Glu Ala Glu Leu Arg Glu Asp Glu 65 70 75 80
- Asn Lys Lys Gln Asn Arg Ala Phe Leu Thr Gln Phe Phe Ser Pro Ile 85 90 95
- Phe Leu Lys Ala Phe Ser Ile Asn Phe Phe Gly Glu Trp Gly Asp Lys
 100 105 110
- Ser Gln Leu Ala Thr Ile Gly Leu Ala Ala Asp Glu Asn Pro Phe Gly 115 120 125
- Val Val Leu Gly Gly Val Val 130 135
- (2) INFORMATION FOR SEQ ID NO:1120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..117
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:
- Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala Ala Pro Asn Leu Ile 1 5 10
- Ser Arg Lys Trp Thr His His Ile Thr Thr Leu Leu Phe Phe Gly Phe 20 25 30
- Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu Gly Gly Gly Ser 35 40 45
- Glu Glu Leu Ala Glu Val Glu Ala Glu Leu Arg Glu Asp Glu Asn Lys 50 55 60
- Lys Gln Asn Arg Ala Phe Leu Thr Gln Phe Phe Ser Pro Ile Phe Leu 65 70 75 80
- Lys Ala Phe Ser Ile Asn Phe Phe Gly Glu Trp Gly Asp Lys Ser Gln 85 90 95
- Leu Ala Thr Ile Gly Leu Ala Ala Asp Glu Asn Pro Phe Gly Val Val 100 105 110
- Leu Gly Gly Val Val
 - 115
- (2) INFORMATION FOR SEQ ID NO:1121:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2361 base pairs
 - (B) TYPE: nucleic acid

2340

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2361
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596933
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121: atgagctaca aaaatacaaa taactctcac ttgattctct tcaagctgtt acttcttctg 60 atcctttatt ctgcagatct cacagcttca agctcatgtc gaagtgaatg tggaggatgc 120 180 aaatgtggag gaattgcgat cccataccct tttggaatcg gtaagggctg ctatctcgag 240 aagtcatacg aaatcgaatg tottaatact tcaggaaagc ttgtcccctt tctttctgta attagcaaag aagttgttag tatccatctt cctggtaggc aatcctttgg gtcagttcgt 300 360 gtcagaagtc cgataacatc cgcaggatgt tctagtgatg gaaaagactc cgcaccagta atgaacttga cggatagtcc ttttttcgtt agtgacataa acaaccttgt gggagttggt 420 480 tgcagcagca aggtgtcgtt ggagcatata aagcaaaaca tggtgggatg tgagttgaac 540 tgcagtacga ctaacgcgtc ggatagcaac agcatccctt tcttcgacaa aacggggtgc 600 tettttett ataetttege eeaggtttgt acaggaaaca aaceggaaga tatgggatge gatggtaggg gatgttgtca agcgagtcta cctagagagc ctcaacaagt tattggtatc 660 720 agaatagaga gcaatgatgg aaagtcaaca acaagtggag actgtagagt cgccttctta 780 actgatgaat tottcagttt gtcgaagctg accaaaccag aacagttaca tgctaagaga tatgctacat taagtctagg atggataatg cagacgagga atacttcctt cgtcaactcc 840 900 ttggcctgca aaatcagaaa agacacggac actgcttact ctaatgacca gagtataaag tgtatatgcg actacaccat gagcatcatt tctgatatta ggtatgccaa ttgtgaatgc 960 aacctaggtt acaaaggtaa cccatatgat tcggacggat gtagagatat tgatgaatgt 1020 aaagagaatc ccaaatattg taaagaaaca gacacttgtg tgaatttcga gggaggctat 1080 cgctgtgtgg gcgataagac taaagcaata atgatagggg cgggtactgg ttttggggtc 1140 1200 ttagtcctag ttggtggagt atggtggttg agaaagtttc tagtgaagag aaggatggca aagaggaaga agaagttett caaacgtaat ggaggactae tgttgcaaca agaattgaat 1260 1320 acaagacaag gcgttgtcga aaaagcaaga atcttcacct cgaaagagct agagaaagcc actgaaaact tcagcgaaaa cagagttctt ggacatggtg gtcaaggtac tgtgtacaaa 1380 ggtatgcttg tagatggtag aaccgttgca gtcaagaaat caaaagttat agatgaagac 1440 1500 aaacttcaag agttcatcaa tgaggtcgtg attctctccc agataaacca tagacatgta 1560 gtcaaactct tgggatgttg tcttgagaca gaagttccta ttctggttta cgagtttatc 1620 atcaacggaa acctctttaa gcatatccac gaagaagaag ctgatgatta cactatgata tggggaatgc gtctacgcat tgctgtggat attgcaggag ctctttctta tcttcattct 1680 gctgcatctt ctccaattta tcatagagac atcaagtcaa caaatatatt actagacgaa 1740 aagtaccgag ccaaggtggc tgattttgga acatcaaggt cagtaaccat agatcaaact 1800 cattggacaa cggttatttc aggtacggtt gggtatgtgg atccagagta ttaccggtcc 1860 agccaatata ctgaaaagag tgatgtttat agctttggag tcattctagc ggaacttatc 1920 actggagata agcctgtcat aatggtacaa aacactcaag agataatagc cttggcagag 1980 catttcagag ttgccatgaa agagagaaga ctttctgaca tcatggatgc tagaataaga 2040 gatgatagca aaccggaaca agtgatggca gtagcaaatc tggcaatgaa gtgtttgagt 2100 tctagaggaa ggaatcgtcc gaatatgaga gaagttttta cagagttgga aaggatttgt 2160 acgtctccgg aagattcaca ggtgcagaac cggattgacg aagaagaaga agaagatgga 2220 gtagaagaag aagaagaagt tgtgacaata gtacacagag gagattcttg gagcattggt 2280
- aatcctcttc tcacatggtg a (2) INFORMATION FOR SEQ ID NO:1122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 786 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..786
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596934

gttactgctc cagcctcaag tattgtcgct tcacctccat cttcagatgt tgaaccattg

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

Met Ser Tyr Lys Asn Thr Asn Asn Ser His Leu Ile Leu Phe Lys Leu

1.0 1 Leu Leu Leu Ile Leu Tyr Ser Ala Asp Leu Thr Ala Ser Ser Ser Cys Arg Ser Glu Cys Gly Gly Cys Lys Cys Gly Gly Ile Ala Ile Pro Tyr Pro Phe Gly Ile Gly Lys Gly Cys Tyr Leu Glu Lys Ser Tyr Glu 50 55 Ile Glu Cys Leu Asn Thr Ser Gly Lys Leu Val Pro Phe Leu Ser Val 75 70 Ile Ser Lys Glu Val Val Ser Ile His Leu Pro Gly Arg Gln Ser Phe 85 Gly Ser Val Arg Val Arg Ser Pro Ile Thr Ser Ala Gly Cys Ser Ser 100 105 110 Asp Gly Lys Asp Ser Ala Pro Val Met Asn Leu Thr Asp Ser Pro Phe 115 120 Phe Val Ser Asp Ile Asn Asn Leu Val Gly Val Gly Cys Ser Ser Lys 130 135 140 Val Ser Leu Glu His Ile Lys Gln Asn Met Val Gly Cys Glu Leu Asn 150 155 Cys Ser Thr Thr Asn Ala Ser Asp Ser Asn Ser Ile Pro Phe Phe Asp 165 170 Lys Thr Gly Cys Ser Phe Ser Tyr Thr Phe Ala Gln Val Cys Thr Gly 180 185 190 Asn Lys Pro Glu Asp Met Gly Cys Asp Gly Arg Gly Cys Cys Gln Ala 195 200 Ser Leu Pro Arg Glu Pro Gln Gln Val Ile Gly Ile Arg Ile Glu Ser 210 215 220 Asn Asp Gly Lys Ser Thr Thr Ser Gly Asp Cys Arg Val Ala Phe Leu 225 230 235 Thr Asp Glu Phe Phe Ser Leu Ser Lys Leu Thr Lys Pro Glu Gln Leu 245 250 His Ala Lys Arg Tyr Ala Thr Leu Ser Leu Gly Trp Ile Met Gln Thr 260 265 Arg Asn Thr Ser Phe Val Asn Ser Leu Ala Cys Lys Ile Arg Lys Asp 275 280 285 Thr Asp Thr Ala Tyr Ser Asn Asp Gln Ser Ile Lys Cys Ile Cys Asp 290 295 300 Tyr Thr Met Ser Ile Ile Ser Asp Ile Arg Tyr Ala Asn Cys Glu Cys 310 315 320 Asn Leu Gly Tyr Lys Gly Asn Pro Tyr Asp Ser Asp Gly Cys Arg Asp 330 335 325 Ile Asp Glu Cys Lys Glu Asn Pro Lys Tyr Cys Lys Glu Thr Asp Thr 345 350 340 Cys Val Asn Phe Glu Gly Gly Tyr Arg Cys Val Gly Asp Lys Thr Lys 360 355 Ala Ile Met Ile Gly Ala Gly Thr Gly Phe Gly Val Leu Val Leu Val 375 Gly Gly Val Trp Trp Leu Arg Lys Phe Leu Val Lys Arg Arg Met Ala 385 390 395 400 Lys Arg Lys Lys Phe Phe Lys Arg Asn Gly Gly Leu Leu Gln 410 415 405 Gln Glu Leu Asn Thr Arg Gln Gly Val Val Glu Lys Ala Arg Ile Phe 425 430 420 Thr Ser Lys Glu Leu Glu Lys Ala Thr Glu Asn Phe Ser Glu Asn Arg 435 440 Val Leu Gly His Gly Gly Gln Gly Thr Val Tyr Lys Gly Met Leu Val 460 455 Asp Gly Arg Thr Val Ala Val Lys Lys Ser Lys Val Ile Asp Glu Asp 470 475 480 Lys Leu Gln Glu Phe Ile Asn Glu Val Val Ile Leu Ser Gln Ile Asn 490 485

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His Arg His Val Val Lys Leu Leu Gly Cys Cys Leu Glu Thr Glu Val
                          505
         500
Pro Ile Leu Val Tyr Glu Phe Ile Ile Asn Gly Asn Leu Phe Lys His
              520
     515
Ile His Glu Glu Glu Ala Asp Asp Tyr Thr Met Ile Trp Gly Met Arg
                  535
Leu Arg Ile Ala Val Asp Ile Ala Gly Ala Leu Ser Tyr Leu His Ser
                                555
               550
Ala Ala Ser Ser Pro Ile Tyr His Arg Asp Ile Lys Ser Thr Asn Ile
                             570
            565
Leu Leu Asp Glu Lys Tyr Arg Ala Lys Val Ala Asp Phe Gly Thr Ser
                585
                                          590
Arg Ser Val Thr Ile Asp Gln Thr His Trp Thr Thr Val Ile Ser Gly
               600
                                      605
Thr Val Gly Tyr Val Asp Pro Glu Tyr Tyr Arg Ser Ser Gln Tyr Thr
                                   620
                  615
Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Ile Leu Ala Glu Leu Ile
                              635
               630
Thr Gly Asp Lys Pro Val Ile Met Val Gln Asn Thr Gln Glu Ile Ile
                             650
Ala Leu Ala Glu His Phe Arg Val Ala Met Lys Glu Arg Arg Leu Ser
                665
                                          670
Asp Ile Met Asp Ala Arg Ile Arg Asp Asp Ser Lys Pro Glu Gln Val
                      680 685
Met Ala Val Ala Asn Leu Ala Met Lys Cys Leu Ser Ser Arg Gly Arg
                           700
                 695
Asn Arg Pro Asn Met Arg Glu Val Phe Thr Glu Leu Glu Arg Ile Cys
705 710 715
Thr Ser Pro Glu Asp Ser Gln Val Gln Asn Arg Ile Asp Glu Glu
                             730
            725
Glu Glu Asp Gly Val Glu Glu Glu Glu Val Val Thr Ile Val His
                         745
         740
Arg Gly Asp Ser Trp Ser Ile Gly Val Thr Ala Pro Ala Ser Ser Ile
             760 765
Val Ala Ser Pro Pro Ser Ser Asp Val Glu Pro Leu Asn Pro Leu Leu
 770
Thr Trp
785
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- (2) INFORMATION FOR SEQ ID NO:1123:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..666
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596936
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

Met Asn Leu Thr Asp Ser Pro Phe Phe Val Ser Asp Ile Asn Asn Leu 1 5 10 15 Val Gly Val Gly Cys Ser Ser Lys Val Ser Leu Glu His Ile Lys Gln

20 25 30
Asn Met Val Gly Cys Glu Leu Asn Cys Ser Thr Thr Asn Ala Ser Asp

35 40 45
Ser Asn Ser Ile Pro Phe Phe Asp Lys Thr Gly Cys Ser Phe Ser Tyr

50 55 60 Thr Phe Ala Gln Val Cys Thr Gly Asn Lys Pro Glu Asp Met Gly Cys

65 70 75 80
Asp Gly Arg Gly Cys Cys Gln Ala Ser Leu Pro Arg Glu Pro Gln Gln

				85					90					95	
Val	Ile	Gly			Ile	Glu	Ser	Asn 105		Gly	Lys	Ser	Thr 1		Ser
Gly	Asp	Cys 115	Arg	Val	Ala	Phe	Leu 120		Asp	Glu	Phe	Phe 125	Ser	Leu	Ser
_	130	Thr				135					140		Ala		
145					150					155			Val .		160
				165					170					175	
			180					185					Ile 190		
		195					200					205	Gly		
	210					215					220		Glu		
225					230					235			Gly		240
				245					250				Ala	255	
_			260					265					270 Phe		
		275					280					285	Arg		
	290					295					300		Glu		
305					310					315			Gly		320
				325					330				Ala	335	
			340					345					350 Ile		
_		355					360				Val	365	Lys		
	370					375				Leu	380 Val		Glu		Ile
385					390				His	395 Glu			Ala	Asp	400
Tyr	Thr	Met			Gly	Met	: Arg	Leu	410 Arg	, Ile	Ala	Val	Asp	415 Ile	Ala
Gly	Ala			Tyr	Leu	His	s Ser 440			ser	Ser	Pro	Ile		His
Arg			Lys	Ser	Thr	Asr 455	ıle		ı Lev	ı Asp	Glu 460	Lys		Arg	Ala
_		. Ala	a Asp	Phe	Gl _y	Thr	Ser	Arg	g Ser	val 475	. Thr		: Asp	Gln	Thr 480
465 His	Trr	Thr	Thr	Val	. Ile	Sei	Gly	7 Thi	val 490	L Gly		. Val	Asp	Pro 495	Glu
			500	Ser	Glr			505	5				510	ı	Phe
		51.5	5				520)				525)		Met
	530	1				53	5				54()			Val
54	5				550	0				55!	5				Arg 560
Ası	o Ası	o Se	r Ly:	s Pro 565	o Gli õ	u Gl:	n Val	l Me	t Al. 57	a Val	⊥ Alá	a Ası	n Leu	575	Met

```
        Lys
        Cys
        Leu
        Ser
        Ser
        Arg
        Gly
        Arg
        Ash
        Arg
        Pro
        Ash
        Met
        Arg
        Glu
        Val

        Phe
        Thr
        Glu
        Leu
        Glu
        Arg
        Ile
        Cys
        Thr
        Ser
        Pro
        Glu
        Asp
        Ser
        Gln
        Val

        Glu
        Asn
        Arg
        Ile
        Arg
        Glu
        Glu
        Asp
        Gly
        Val
        Glu
        Glu
        Glu
        Arg
        Gly
        Asp
        Ser
        Irp
        Ser
        Ile
        Gly
        Arg
        Gly
        Arg
        Irp
        Ser
        Ile
        Gly
        Arg
        Arg
        Irp
        Ser
        Irp
        Gly
        Arg
        Arg
        Irp
        Irp
```

- Val Glu Pro Leu Asn Pro Leu Leu Thr Trp 660 665
- (2) INFORMATION FOR SEQ ID NO:1124:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596960
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124: 60 atggaggaag aaagagaaaa cactaactct atctacatag tttccgagct acttgaagaa attttccttg gattgccttt gaaatcaatc ctcaaattca aaaccgtctc aaaacaatgg 120 agatcaatcc tggaatcgaa cttgttcgtg gagaggcgta gaactcttca aaagaaccac 240 ccgaaaatcc tggctgctta taactgcgac tactgcacgc ggccgggtat cctccctaag totcagttcg aaggggacga agagatcgtt tatcttcata ccgacgccac gcaaccctcg 300 atgacttgcg acggtttagt ctgcatcacc gaacctagtt ggttcaacgt tttgaacgtc 360 tocaccqqac aactocqaaq atttotaccc qgtocagato caqqaccqca agcaaattgg 420 ctcttgggat tcggtagaga caaagttacg ggcaagtata aaatagtgag gatgtgtttt 480 catgattgtt atgaatttgg gattcttgat attgaatctg gcgaatggag caaactgatg 540 tcacctcctc atataatqcq aqtqqqaaqt aaatcqqtqt qtqtqaatqq atcaatctac 600 tggttacaaa ttagtgtgag ttacataata ctggccttgg atcttcacca agaaacgttc 660 720 aatggtgtct accacctccc ggctacgtgg gtcacgcaag atacccaatt agtgaacctt gaggaccgtc tagccatggc catgacgacc aaagttggqc ctqaatggat actaqaqatc 780 840 tggagcatgg atatagaaga aaaaggatgg agcaagcgtt acacatggag caaggcttac tocataagtt tagcccatag agttgttgta toctggccat ggcaaaaaag gtggttcacg 900 960 ccggtatcgg tttctaagca agggaatctt gtcttctatg ataatcacaa gaggctgttc aaatattatt caggtacaga tgagattcgt tgtctctcct ctaacattaa tgttatatct 1020 1080 tottacqttq aaaatttqqc cccacttccq ttaaaaccaa gccatacqca tcacqatctt 1140 qqqaattcqa attccaaqtt cagcacatcc agatgccact tgtttccgac gcgagctaac ttttaa
- (2) INFORMATION FOR SEQ ID NO:1125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..381
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596961
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

Met Glu Glu Glu Arg Glu Asn Thr Asn Ser Ile Tyr Ile Val Ser Glu

5 10 15

Leu Leu Glu Glu Ile Phe Leu Gly Leu Pro Leu Lys Ser Ile Leu Lys 20 25 30

Phe Lys Thr Val Ser Lys Gln Trp Arg Ser Ile Leu Glu Ser Asn Leu

40 35 Phe Val Glu Arg Arg Arg Thr Leu Gln Lys Asn His Pro Lys Ile Leu 55 60 Ala Ala Tyr Asn Cys Asp Tyr Cys Thr Arg Pro Gly Ile Leu Pro Lys 70 Ser Gln Phe Glu Gly Asp Glu Glu Ile Val Tyr Leu His Thr Asp Ala 90 Thr Gln Pro Ser Met Thr Cys Asp Gly Leu Val Cys Ile Thr Glu Pro 100 105 Ser Trp Phe Asn Val Leu Asn Val Ser Thr Gly Gln Leu Arg Arg Phe 115 120 Leu Pro Gly Pro Asp Pro Gly Pro Gln Ala Asn Trp Leu Leu Gly Phe 135 140 Gly Arg Asp Lys Val Thr Gly Lys Tyr Lys Ile Val Arg Met Cys Phe 155 150 His Asp Cys Tyr Glu Phe Gly Ile Leu Asp Ile Glu Ser Gly Glu Trp 165 170 Ser Lys Leu Met Ser Pro Pro His Ile Met Arg Val Gly Ser Lys Ser 180 185 Val Cys Val Asn Gly Ser Ile Tyr Trp Leu Gln Ile Ser Val Ser Tyr 200 Ile Ile Leu Ala Leu Asp Leu His Gln Glu Thr Phe Asn Gly Val Tyr 215 220 His Leu Pro Ala Thr Trp Val Thr Gln Asp Thr Gln Leu Val Asn Leu 225 230 235 240 Glu Asp Arg Leu Ala Met Ala Met Thr Thr Lys Val Gly Pro Glu Trp 245 250 Ile Leu Glu Ile Trp Ser Met Asp Ile Glu Glu Lys Gly Trp Ser Lys 260 265 270 Arg Tyr Thr Trp Ser Lys Ala Tyr Ser Ile Ser Leu Ala His Arg Val 280 285 Val Val Ser Trp Pro Trp Gln Lys Arg Trp Phe Thr Pro Val Ser Val 295 300 Ser Lys Gln Gly Asn Leu Val Phe Tyr Asp Asn His Lys Arg Leu Phe 315 320 310 Lys Tyr Tyr Ser Gly Thr Asp Glu Ile Arg Cys Leu Ser Ser Asn Ile 330 335 Asn Val Ile Ser Ser Tyr Val Glu Asn Leu Ala Pro Leu Pro Leu Lys 345 Pro Ser His Thr His His Asp Leu Gly Asn Ser Asn Ser Lys Phe Ser 355 360 Thr Ser Arg Cys His Leu Phe Pro Thr Arg Ala Asn Phe 370 375 (2) INFORMATION FOR SEQ ID NO:1126: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..281
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596963
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:
- Met Thr Cys Asp Gly Leu Val Cys Ile Thr Glu Pro Ser Trp Phe Asn 5 10
- Val Leu Asn Val Ser Thr Gly Gln Leu Arg Arg Phe Leu Pro Gly Pro 25
- Asp Pro Gly Pro Gln Ala Asn Trp Leu Leu Gly Phe Gly Arg Asp Lys 40

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Val Thr Gly Lys Tyr Lys Ile Val Arg Met Cys Phe His Asp Cys Tyr
                        55
Glu Phe Gly Ile Leu Asp Ile Glu Ser Gly Glu Trp Ser Lys Leu Met
                                        75
                    70
Ser Pro Pro His Ile Met Arg Val Gly Ser Lys Ser Val Cys Val Asn
                                    90
                85
Gly Ser Ile Tyr Trp Leu Gln Ile Ser Val Ser Tyr Ile Ile Leu Ala
                                                    110
                               105
           100
Leu Asp Leu His Gln Glu Thr Phe Asn Gly Val Tyr His Leu Pro Ala
                                                125
                           120
        115
Thr Trp Val Thr Gln Asp Thr Gln Leu Val Asn Leu Glu Asp Arg Leu
                                            140
                       135
Ala Met Ala Met Thr Thr Lys Val Gly Pro Glu Trp Ile Leu Glu Ile
                                       155
                    150
Trp Ser Met Asp Ile Glu Glu Lys Gly Trp Ser Lys Arg Tyr Thr Trp
                                                        175
                                    170
                165
Ser Lys Ala Tyr Ser Ile Ser Leu Ala His Arg Val Val Ser Trp
                                                    190
                                185
            180
Pro Trp Gln Lys Arg Trp Phe Thr Pro Val Ser Val Ser Lys Gln Gly
                                                205
                            200
Asn Leu Val Phe Tyr Asp Asn His Lys Arg Leu Phe Lys Tyr Tyr Ser
                        215
    210
Gly Thr Asp Glu Ile Arg Cys Leu Ser Ser Asn Ile Asn Val Ile Ser
                                        235
                    230
Ser Tyr Val Glu Asn Leu Ala Pro Leu Pro Leu Lys Pro Ser His Thr
                                   250
                245
His His Asp Leu Gly Asn Ser Asn Ser Lys Phe Ser Thr Ser Arg Cys
                                265
            260
His Leu Phe Pro Thr Arg Ala Asn Phe
                            280
        275
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- (2) INFORMATION FOR SEQ ID NO:1127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596968
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127: atgtttaaga atgctcaaga atttatctcg aaatgtgact catgtcagag aagagggaac 60 120 atcagcagaa ggaatgagat gcctaagaat ctgatcttag aagttgagat ctttgacgtt tggggaatcg attttatggg tccgtttcct ttttcttacg ggaacgatta catactggtc 180 gcagtagact atgtatcaaa atgggtggaa gccatagcca gccccaccaa tgatgttaga 240 300 gttgtgctaa agctgttcaa gacaattatt ttccctagat ttggagtctc gagagttaag 360 catggagtaa agcacaaggt agccactcct tatcatccac agacgagcgg gcaggtggaa 420 atctccaaca gggagataaa agtaattcta gagaaaacag tggggattac gaggaaagat 480 tggtctgcga agctctatga cgcactatgg gcttacagaa caactttcaa gactcctatt ggcacgactc ctttcaacct tctctatgga aagtcctgtc acttacctgt ggaactcaag 540 600 tataaagcca tgtgggcagt taaactcctg aacttcgaca ttaaaaccgc cgaagagaag 660 cggttgatcc aactgaacga tctcaacgag attcgcttag aagcttatga gagttccaaa 720 atctacaagg agcgaaccaa gtctttccat gacaagaaga tagtctcaag agattttaag tatgaagagc tgagggaaat agattctggt tttgagggaa caacaataca ctcgaccaca 780 840 gagcaatcaa actcaacatt gttctggctt cttcacccca ggaaatcact cgaccacacc ctacagggac cgaatgacga tgtggtcgag tatagcgaac gatgcagtca taacttctcc 900 960 atgtcagtaa ttcactcgac cgcggtgctg gtcgcagcag aagaagagag gtcgagtatc atcagagogg tgctggccgc gacgaaggag cagaggtcga gtacccccag ggggaagctg 1020 agacacaaca gggagattot togatggoot gggagcaato acaggoggot attgacgaco 1080 aaatccgctg cttcttccac tgagtggact gtgtga

- (2) INFORMATION FOR SEQ ID NO:1128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..371
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:
- Met Phe Lys Asn Ala Gln Glu Phe Ile Ser Lys Cys Asp Ser Cys Gln 1 10 15
- Arg Arg Gly Asn Ile Ser Arg Arg Asn Glu Met Pro Lys Asn Leu Ile 20 25 30
- Leu Glu Val Glu Ile Phe Asp Val Trp Gly Ile Asp Phe Met Gly Pro
- Phe Pro Phe Ser Tyr Gly Asn Asp Tyr Ile Leu Val Ala Val Asp Tyr
- Val Ser Lys Trp Val Glu Ala Ile Ala Ser Pro Thr Asn Asp Val Arg
- 65 70 75 80
 Val Val Leu Lys Leu Phe Lys Thr Ile Ile Phe Pro Arg Phe Gly Val
- 85 90 95 Ser Arg Val Lys His Gly Val Lys His Lys Val Ala Thr Pro Tyr His
- 100 105 110 Pro Gln Thr Ser Gly Gln Val Glu Ile Ser Asn Arg Glu Ile Lys Val
- 115 120 125 Ile Leu Glu Lys Thr Val Gly Ile Thr Arg Lys Asp Trp Ser Ala Lys
- 130 135 140 Leu Tyr Asp Ala Leu Trp Ala Tyr Arg Thr Thr Phe Lys Thr Pro Ile
- 145 150 155 160 Gly Thr Thr Pro Phe Asn Leu Leu Tyr Gly Lys Ser Cys His Leu Pro
- 165 170 175
 Val Glu Leu Lys Tyr Lys Ala Met Trp Ala Val Lys Leu Leu Asn Phe
- 180 185 190
 Asp Ile Lys Thr Ala Glu Glu Lys Arg Leu Ile Gln Leu Asn Asp Leu
- 195 200 205
 Asn Glu Ile Arg Leu Glu Ala Tyr Glu Ser Ser Lys Ile Tyr Lys Glu
- 210 215 220
 Arg Thr Lys Ser Phe His Asp Lys Lys Ile Val Ser Arg Asp Phe Lys
- 225 230 235 240

 Tyr Glu Glu Leu Arg Glu Ile Asp Ser Gly Phe Glu Gly Thr Thr Ile
 245 250 255
- His Ser Thr Thr Glu Gln Ser Asn Ser Thr Leu Phe Trp Leu Leu His 260 265 270
- Pro Arg Lys Ser Leu Asp His Thr Leu Gln Gly Pro Asn Asp Asp Val 275 280 285
- Val Glu Tyr Ser Glu Arg Cys Ser His Asn Phe Ser Met Ser Val Ile 290 295 300
- His Ser Thr Ala Val Leu Val Ala Ala Glu Glu Glu Arg Ser Ser Ile 305 310 315 320
- Ile Arg Ala Val Leu Ala Ala Thr Lys Glu Gln Arg Ser Ser Thr Pro 325 330 335
- Arg Gly Lys Leu Arg His Asn Arg Glu Ile Leu Arg Trp Pro Gly Ser 340 345 350
- Asn His Arg Arg Leu Leu Thr Thr Lys Ser Ala Ala Ser Ser Thr Glu 355 360 365
- Trp Thr Val
 - 370
- (2) INFORMATION FOR SEQ ID NO:1129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..345
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596971
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:
- Met Pro Lys Asn Leu Ile Leu Glu Val Glu Ile Phe Asp Val Trp Gly
 1 5 10 15
- Ile Asp Phe Met Gly Pro Phe Pro Phe Ser Tyr Gly Asn Asp Tyr Ile 20 25 30
- Leu Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Ser 35 40 45
- Pro Thr Asn Asp Val Arg Val Val Leu Lys Leu Phe Lys Thr Ile Ile 50 55 60
- Phe Pro Arg Phe Gly Val Ser Arg Val Lys His Gly Val Lys His Lys 65 70 75 80
- Val Ala Thr Pro Tyr His Pro Gln Thr Ser Gly Gln Val Glu Ile Ser 85 90 95
- Asn Arg Glu Ile Lys Val Ile Leu Glu Lys Thr Val Gly Ile Thr Arg 100 105 110
- Lys Asp Trp Ser Ala Lys Leu Tyr Asp Ala Leu Trp Ala Tyr Arg Thr
 115 120 125
- Thr Phe Lys Thr Pro Ile Gly Thr Thr Pro Phe Asn Leu Leu Tyr Gly
 130 135 140
- Lys Ser Cys His Leu Pro Val Glu Leu Lys Tyr Lys Ala Met Trp Ala 145 150 155 160
- Val Lys Leu Leu Asn Phe Asp Ile Lys Thr Ala Glu Glu Lys Arg Leu 165 170 175
- Ile Gln Leu Asn Asp Leu Asn Glu Ile Arg Leu Glu Ala Tyr Glu Ser 180 185 190
- Ser Lys Ile Tyr Lys Glu Arg Thr Lys Ser Phe His Asp Lys Lys Ile
 195 200 205
- Val Ser Arg Asp Phe Lys Tyr Glu Glu Leu Arg Glu Ile Asp Ser Gly 210 215 220
 Phe Glu Gly Thr Thr Ile His Ser Thr Thr Glu Gln Ser Asn Ser Thr
- 225 230 235 240
- Leu Phe Trp Leu Leu His Pro Arg Lys Ser Leu Asp His Thr Leu Gln 245 250 255
- Gly Pro Asn Asp Asp Val Val Glu Tyr Ser Glu Arg Cys Ser His Asn 260 265 270
- Phe Ser Met Ser Val Ile His Ser Thr Ala Val Leu Val Ala Ala Glu 275 280 285
- Glu Glu Arg Ser Ser Ile Ile Arg Ala Val Leu Ala Ala Thr Lys Glu 290 295 300 Gln Arg Ser Ser Thr Pro Arg Gly Lys Leu Arg His Asn Arg Glu Ile
- 305 310 315 320 Leu Arg Trp Pro Gly Ser Asn His Arg Arg Leu Leu Thr Thr Lys Ser
- 325 330

 Ala Ala Ser Ser Thr Glu Trp Thr Val
 340 345
- (2) INFORMATION FOR SEQ ID NO:1130:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2554
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596976
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

```
atggagacat cttggagatt tctcagaagt gtttgcttac tttcatttgt ccttgggtcg
                                                                       60
ttttctgttt accaaaccct ttgtcttgtt gacgctcaag aagacgccat tgtaacactg
                                                                      120
caagtagatg cttctaacgt gacacggcga ccgattcccg aaactctatt tgggatcttc
                                                                      180
tttgaggaaa taaatcatgc tggagcaggt ggactatggg ctgaacttgt tagcaataga
                                                                      240
ggatttgaag ctggtggaca aatcattcct tccaatatct ggccttggtc cattattgga
                                                                      300
gatgaatcat ccatttatgt tgttacagac cgttcttcgt gttttgagcg taacaagatt
                                                                      360
getettagaa tggaagteet ttgtgacage aattettgte caacaggagg egteggggtt
                                                                      420
tataacccgg gttactgggg catgaacatt gaaaaaggga agaaatacaa agtggtgttc
                                                                      480
tatgtgcgtt cgactggcga catcgatgtt tctgtgtcgt ttacaagttc gaatggatca
                                                                      540
                                                                      600
tcgactcttg cgtcagaaaa tactatagct ttggcttctg atgtttccag ttggacaaaa
                                                                       660
atggaaatgc ttttagaagc aaatggaaca gataatggtg caagacttca atttacaact
                                                                       720
acaaaaaaag gttcaatttg gtttgaccaa gtctcagcca tacctatgga tacttacaag
                                                                       780
ggacatggtt tcagaaatga ccttttccaa atgatggtcg atctaaaacc gcggtttatc
                                                                       840
cgattcccgg gcaatgcatt ccgctggaaa gaaaccgtgg gagcttggga agagagacct
                                                                       900
ggccattatg gtgatgtttg gaagtactgg actgatgatg cccttggcca ctttgaattc
                                                                       960
tttcaacttg cagaagacct tggtgcatcc ccaatatggg tgtttaacaa tgggataagt
cacaatgatc aagttgaaac aaaaaatgtc atgccttttg ttcaagaagc gattgacggt
                                                                      1020
                                                                      1080
atagagtttg ctcgtggaga ttctaattct acatggggat cggttcgagc tgcaatggga
catccagage cttttgaact aaaatatgtt geggttggga atgaagattg ttttaaaagt
                                                                      1140
ttctacagag gaaactatct tgaattctac gatgctatca aaaaagctta tccagacatt
                                                                      1200
aaaatcatct ccaactgcga tgcatcgtct aaaccgctcg atcaccctgc tgattacttt
                                                                      1260
gattaccaca tttacactct tgcaagagac ttgttttcca agtcccatga ttttgacaat
                                                                      1320
acaccgcgca acggaccaaa ggcttttgtt agcgaatacg ctgtaagcaa aacggatgct
                                                                      1380
aaaaatggaa accttttggc cgctctcggg gaagcagctt tcctccttgg tttggaaaag
                                                                      1440
aacagtggca ttgtaggaat ggttagctat gcacctctct ttgtcaacac aaacgataga
                                                                      1500
aggtggatcc cggatgcaat agtttttaac tcgtctcatc tatatggaac tcctagctat
                                                                      1560
tgggtccaac agttcttcac cgagtcaagc ggagcaactc ttctcaattc tacacttaat
                                                                      1620
ggagacactt cttctgttga agcatctgcc atctctttcc aaaccaatgg caaagattac
                                                                      1680
atacagatca aggctgtaaa ctttggagaa caatcagtaa atctaaaggt agcagtgaca
                                                                      1740
ggactgatcg caaaatttta tggatcgaag aagaaaatac ttacatctgc caatgtgatg
                                                                      1800
                                                                      1860
gatgagaact ctttttcaaa cccaaagatg attgtgccac aagaaagttt gctggagatg
actgaggagg aggaacttat gtttgttctc ccgccgcact cgttctcttc ctttgatttg
                                                                      1920
ttgaaagaat ctgaaaatgt cctcaagatg ccaaaatctg attcatacaa gaaaacttca
                                                                      1980
acaatgagca agatggctcc cttgatcgcc ttattcactg gcctttgcgg cttcaagaaa
                                                                      2040
aacgctcggc cattgggaac gatcgagaca atgaatcagt catctccacg ggagaccaaa
                                                                      2100
gaaagagaac aaacaaggaa tgacttccag aacaaggaaa ctgatgactt gtggaacaag
                                                                      2160
gaaagcgatg atcgagatac taatgcattt aatgacgata gtagtgaagc ggactctgag
                                                                      2220
cttccgttgc ctccaggaag aaaaggaaca atacgtggaa catattcgtg taacaacatg
                                                                      2280
gtgttaagaa gatccttgtc tactaagaag aaactgagtg cgagcctaac gatccaaata
                                                                      2340
ccgagatcat tgtccatggt cctcaaacgt gacaaggagg aggataaatc tgtgaggaag
                                                                      2400
                                                                      2460
 aagaaactga acgcaaataa ttcgattctg gtacgtccaa ttatacttgg agagagatgt
                                                                      2520
 agggttettg atgeggaace aggagatgaa gateanagee aaagaatgge agagaacaga
 atatatcgtc ctagatccat gagttcgatc tcga
```

- (2) INFORMATION FOR SEQ ID NO:1131:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 851 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..851
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596977
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

Met Glu Thr Ser Trp Arg Phe Leu Arg Ser Val Cys Leu Leu Ser Phe 10 Val Leu Gly Ser Phe Ser Val Tyr Gln Thr Leu Cys Leu Val Asp Ala 25 Gln Glu Asp Ala Ile Val Thr Leu Gln Val Asp Ala Ser Asn Val Thr 40 Arg Arg Pro Ile Pro Glu Thr Leu Phe Gly Ile Phe Phe Glu Glu Ile 55 60 Asn His Ala Gly Ala Gly Gly Leu Trp Ala Glu Leu Val Ser Asn Arg 70 75 Gly Phe Glu Ala Gly Gly Gln Ile Ile Pro Ser Asn Ile Trp Pro Trp 85 90 Ser Ile Ile Gly Asp Glu Ser Ser Ile Tyr Val Val Thr Asp Arg Ser 105 Ser Cys Phe Glu Arg Asn Lys Ile Ala Leu Arg Met Glu Val Leu Cys 120 Asp Ser Asn Ser Cys Pro Thr Gly Gly Val Gly Val Tyr Asn Pro Gly 135 Tyr Trp Gly Met Asn Ile Glu Lys Gly Lys Lys Tyr Lys Val Val Phe 150 155 Tyr Val Arg Ser Thr Gly Asp Ile Asp Val Ser Val Ser Phe Thr Ser 170 165 Ser Asn Gly Ser Ser Thr Leu Ala Ser Glu Asn Thr Ile Ala Leu Ala 180 185 Ser Asp Val Ser Ser Trp Thr Lys Met Glu Met Leu Leu Glu Ala Asn 200 Gly Thr Asp Asn Gly Ala Arg Leu Gln Phe Thr Thr Lys Lys Gly 215 220 Ser Ile Trp Phe Asp Gln Val Ser Ala Ile Pro Met Asp Thr Tyr Lys 230 235 Gly His Gly Phe Arg Asn Asp Leu Phe Gln Met Met Val Asp Leu Lys 250 245 Pro Arg Phe Ile Arg Phe Pro Gly Asn Ala Phe Arg Trp Lys Glu Thr 265 260 Val Gly Ala Trp Glu Glu Arg Pro Gly His Tyr Gly Asp Val Trp Lys 280 285 Tyr Trp Thr Asp Asp Ala Leu Gly His Phe Glu Phe Phe Gln Leu Ala 295 300 Glu Asp Leu Gly Ala Ser Pro Ile Trp Val Phe Asn Asn Gly Ile Ser 310 315 His Asn Asp Gln Val Glu Thr Lys Asn Val Met Pro Phe Val Gln Glu 325 330 Ala Ile Asp Gly Ile Glu Phe Ala Arg Gly Asp Ser Asn Ser Thr Trp 345 340 Gly Ser Val Arg Ala Ala Met Gly His Pro Glu Pro Phe Glu Leu Lys 360 365 Tyr Val Ala Val Gly Asn Glu Asp Cys Phe Lys Ser Phe Tyr Arg Gly 380 375 Asn Tyr Leu Glu Phe Tyr Asp Ala Ile Lys Lys Ala Tyr Pro Asp Ile 390 395 Lys Ile Ile Ser Asn Cys Asp Ala Ser Ser Lys Pro Leu Asp His Pro 405 410Ala Asp Tyr Phe Asp Tyr His Ile Tyr Thr Leu Ala Arg Asp Leu Phe 420 425 Ser Lys Ser His Asp Phe Asp Asn Thr Pro Arg Asn Gly Pro Lys Ala 440 Phe Val Ser Glu Tyr Ala Val Ser Lys Thr Asp Ala Lys Asn Gly Asn 455 460 Leu Leu Ala Ala Leu Gly Glu Ala Ala Phe Leu Leu Gly Leu Glu Lys 470 475 480 Asn Ser Gly Ile Val Gly Met Val Ser Tyr Ala Pro Leu Phe Val Asn

490 485 Thr Asn Asp Arg Arg Trp Ile Pro Asp Ala Ile Val Phe Asn Ser Ser 505 510 His Leu Tyr Gly Thr Pro Ser Tyr Trp Val Gln Gln Phe Phe Thr Glu 520 525 515 Ser Ser Gly Ala Thr Leu Leu Asn Ser Thr Leu Asn Gly Asp Thr Ser 535 Ser Val Glu Ala Ser Ala Ile Ser Phe Gln Thr Asn Gly Lys Asp Tyr 550 555 Ile Gln Ile Lys Ala Val Asn Phe Gly Glu Gln Ser Val Asn Leu Lys 565 570 Val Ala Val Thr Gly Leu Ile Ala Lys Phe Tyr Gly Ser Lys Lys 585 Ile Leu Thr Ser Ala Asn Val Met Asp Glu Asn Ser Phe Ser Asn Pro 595 600 605 Lys Met Ile Val Pro Gln Glu Ser Leu Leu Glu Met Thr Glu Glu 610 615 Glu Leu Met Phe Val Leu Pro Pro His Ser Phe Ser Ser Phe Asp Leu 625 630 635 Leu Lys Glu Ser Glu Asn Val Leu Lys Met Pro Lys Ser Asp Ser Tyr 645 650 655 Lys Lys Thr Ser Thr Met Ser Lys Met Ala Pro Leu Ile Ala Leu Phe 660 665 670 Thr Gly Leu Cys Gly Phe Lys Lys Asn Ala Arg Pro Leu Gly Thr Ile 675 680 685 Glu Thr Met Asn Gln Ser Ser Pro Arg Glu Thr Lys Glu Arg Glu Gln 690 695 700 Thr Arg Asn Asp Phe Gln Asn Lys Glu Thr Asp Asp Leu Trp Asn Lys 705 710 715 720 Glu Ser Asp Asp Arg Asp Thr Asn Ala Phe Asn Asp Asp Ser Ser Glu 725 730 735 Ala Asp Ser Glu Leu Pro Leu Pro Pro Gly Arg Lys Gly Thr Ile Arg 740 745 750 Gly Thr Tyr Ser Cys Asn Asn Met Val Leu Arg Arg Ser Leu Ser Thr 755 760 765 Lys Lys Lys Leu Ser Ala Ser Leu Thr Ile Gln Ile Pro Arg Ser Leu 775 780 Ser Met Val Leu Lys Arg Asp Lys Glu Glu Asp Lys Ser Val Arg Lys 785 790 795 800 Lys Lys Leu Asn Ala Asn Asn Ser Ile Leu Val Arg Pro Ile Ile Leu 810 815 805 Gly Glu Arg Cys Arg Val Leu Asp Ala Glu Pro Gly Asp Glu Asp Xaa 820 825 Ser Gln Arg Met Ala Glu Asn Arg Ile Tyr Arg Pro Arg Ser Met Ser 835 Ser Ile Ser 850

(2) INFORMATION FOR SEQ ID NO:1132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 728 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..728
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

Met Glu Val Leu Cys Asp Ser Asn Ser Cys Pro Thr Gly Gly Val Gly
1 5 10 15

Val Tyr Asn Pro Gly Tyr Trp Gly Met Asn Ile Glu Lys Gly Lys 25 Tyr Lys Val Val Phe Tyr Val Arg Ser Thr Gly Asp Ile Asp Val Ser 40 Val Ser Phe Thr Ser Ser Asn Gly Ser Ser Thr Leu Ala Ser Glu Asn Thr Ile Ala Leu Ala Ser Asp Val Ser Ser Trp Thr Lys Met Glu Met 70 75 Leu Leu Glu Ala Asn Gly Thr Asp Asn Gly Ala Arg Leu Gln Phe Thr 90 8.5 Thr Thr Lys Lys Gly Ser Ile Trp Phe Asp Gln Val Ser Ala Ile Pro 105 100 Met Asp Thr Tyr Lys Gly His Gly Phe Arg Asn Asp Leu Phe Gln Met 125 120 115 Met Val Asp Leu Lys Pro Arg Phe Ile Arg Phe Pro Gly Asn Ala Phe 140 135 Arg Trp Lys Glu Thr Val Gly Ala Trp Glu Glu Arg Pro Gly His Tyr 150 155 Gly Asp Val Trp Lys Tyr Trp Thr Asp Asp Ala Leu Gly His Phe Glu 165 170 Phe Phe Gln Leu Ala Glu Asp Leu Gly Ala Ser Pro Ile Trp Val Phe 185 180 Asn Asn Gly Ile Ser His Asn Asp Gln Val Glu Thr Lys Asn Val Met 200 Pro Phe Val Gln Glu Ala Ile Asp Gly Ile Glu Phe Ala Arg Gly Asp 220 215 Ser Asn Ser Thr Trp Gly Ser Val Arg Ala Ala Met Gly His Pro Glu 235 230 Pro Phe Glu Leu Lys Tyr Val Ala Val Gly Asn Glu Asp Cys Phe Lys 250 245 Ser Phe Tyr Arg Gly Asn Tyr Leu Glu Phe Tyr Asp Ala Ile Lys Lys 265 Ala Tyr Pro Asp Ile Lys Ile Ile Ser Asn Cys Asp Ala Ser Ser Lys 280 Pro Leu Asp His Pro Ala Asp Tyr Phe Asp Tyr His Ile Tyr Thr Leu 300 295 Ala Arg Asp Leu Phe Ser Lys Ser His Asp Phe Asp Asn Thr Pro Arg 315 310 Asn Gly Pro Lys Ala Phe Val Ser Glu Tyr Ala Val Ser Lys Thr Asp 330 Ala Lys Asn Gly Asn Leu Leu Ala Ala Leu Gly Glu Ala Ala Phe Leu 345 340 Leu Gly Leu Glu Lys Asn Ser Gly Ile Val Gly Met Val Ser Tyr Ala 365 360 Pro Leu Phe Val Asn Thr Asn Asp Arg Arg Trp Ile Pro Asp Ala Ile 380 375 Val Phe Asn Ser Ser His Leu Tyr Gly Thr Pro Ser Tyr Trp Val Gln 390 395 Gln Phe Phe Thr Glu Ser Ser Gly Ala Thr Leu Leu Asn Ser Thr Leu 405 410 Asn Gly Asp Thr Ser Ser Val Glu Ala Ser Ala Ile Ser Phe Gln Thr 425 420 Asn Gly Lys Asp Tyr Ile Gln Ile Lys Ala Val Asn Phe Gly Glu Gln 440 Ser Val Asn Leu Lys Val Ala Val Thr Gly Leu Ile Ala Lys Phe Tyr 460 455 Gly Ser Lys Lys Ile Leu Thr Ser Ala Asn Val Met Asp Glu Asn 475 470 Ser Phe Ser Asn Pro Lys Met Ile Val Pro Gln Glu Ser Leu Leu Glu 490 485 Met Thr Glu Glu Glu Leu Met Phe Val Leu Pro Pro His Ser Phe

			500					505					510		
		515					520			Asn		525			
	530					535				Met	540				
545					550					Phe 555					560
				565					570	Ser				575	
Lys	Glu	Arg	Glu 580	Gln	Thr	Arg	Asn	Asp 585	Phe	Gln	Asn	Lys	Glu 590	Thr	Asp
Asp	Leu	Trp 595	Asn	Lys	Glu	Ser	Asp 600	Asp	Arg	Asp	Thr	Asn 605	Ala	Phe	Asn
Asp	Asp 610	Ser	Ser	Glu	Ala	Asp 615	Ser	Glu	Leu	Pro	Leu 620	Pro	Pro	Gly	Arg
Lys 625	Gly	Thr	Ile	Arg	Gly 630	Thr	Tyr	Ser	Cys	Asn 635	Asn	Met	Val	Leu	Arg 640
Arg	Ser	Leu	Ser	Thr 645	Lys	Lys	Lys	Leu	Ser 650	Ala	Ser	Leu	Thr	Ile 655	Gln
Ile	Pro	Arg	Ser 660	Leu	Ser	Met	Val	Leu 665	Lys	Arg	Asp	Lys	Glu 670	Glu	Asp
Lys	Ser	Val 675	Arg	Lys	Lys	Lys	Leu 680	Asn	Ala	Asn	Asn	Ser 685	Ile	Leu	Val
Arg	Pro 690	Ile	Ile	Leu	Gly	Glu 695	Arg	Cys	Arg	Val	Leu 700	Asp	Ala	Glu	Pro
Gly 705		Glu	Asp	Xaa	Ser 710	Gln	Arg	Met	Ala	Glu 715	Asn	Arg	Ile	Tyr	Arg 720
	Arg	Ser	Met	Ser 725	Ser	Ile	Ser								

- (2) INFORMATION FOR SEQ ID NO:1133:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..729
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596980
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133: atgtccggtg cacaatctag tgattcgttg ccagagattt cacggccgac tgcaacagaa 60 120 tgtcaagagg tgaaatccga tgaagcactc actgaaccca accctgattg ggctctagtt 180 ctcgtcaaag acccatcgcc tccactcatc atcgaggttg aggatgagac tctgccttca atcgacagtg ttcagaaccc taaaccgaag gatcatgagg ctgccccctc gcaaccctct 240 300 gttgcatctc gattgcgcaa gaggaagtca tctgctgctg atccacgcat caaaaggatg 360 aagcagggaa agggagttac cggactgatt cgaacggtta ttaagttcaa cccgttcact gagaatctag tgtttgagtt ctgggctaat ctgcccacta tgaaggtaga cacgtataag 420 480 gtcagagtct tggtgcgcaa tcgggagtat gagctctcac ctgggaagat caacgagatg 540 tatggtctcc cttttgttga tgctagacag cagcgaatgg atatcgctgg tctggttgat gaacaagtgg ctgaatttct cactggtggg aaagtcagtg ttctgagcaa gcttcagaca 600 660 tggatgcgag agcaaacgtg gcaagctaag gcggatgatg tggagagcca aggatggaag 720 ctgacttggc gtggtgtcaa agacaagaat taccaagaag atatggaaga tatcatctcg aagatttag
- (2) INFORMATION FOR SEQ ID NO:1134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met Ser Gly Ala Gln Ser Ser Asp Ser Leu Pro Glu Ile Ser Arg Pro

1 10 15

Thr Ala Thr Glu Cys Gln Glu Val Lys Ser Asp Glu Ala Leu Thr Glu

Thr Ala Thr Glu Cys Gln Glu Val Lys Ser Asp Glu Ala Leu Thr Glu
20 25 30

Pro Asn Pro Asp Trp Ala Leu Val Leu Val Lys Asp Pro Ser Pro Pro 35 40 45

Leu Ile Ile Glu Val Glu Asp Glu Thr Leu Pro Ser Ile Asp Ser Val 50 55 60

Gln Asn Pro Lys Pro Lys Asp His Glu Ala Ala Pro Ser Gln Pro Ser 65 70 75 80

Val Ala Ser Arg Leu Arg Lys Arg Lys Ser Ser Ala Ala Asp Pro Arg 85 90 95

Ile Lys Arg Met Lys Gln Gly Lys Gly Val Thr Gly Leu Ile Arg Thr 100 105 110

Val Ile Lys Phe Asn Pro Phe Thr Glu Asn Leu Val Phe Glu Phe Trp
115 120 125

Ala Asn Leu Pro Thr Met Lys Val Asp Thr Tyr Lys Val Arg Val Leu 130 135 140

Val Arg Asn Arg Glu Tyr Glu Leu Ser Pro Gly Lys Ile Asn Glu Met 145 150 155 160

Tyr Gly Leu Pro Phe Val Asp Ala Arg Gln Gln Arg Met Asp Ile Ala 165 170 175

Gly Leu Val Asp Glu Gln Val Ala Glu Phe Leu Thr Gly Gly Lys Val 180 185 190

Ser Val Leu Ser Lys Leu Gln Thr Trp Met Arg Glu Gln Thr Trp Gln 195 200 205

Ala Lys Ala Asp Asp Val Glu Ser Gln Gly Trp Lys Leu Thr Trp Arg 210 215 220

Gly Val Lys Asp Lys Asn Tyr Gln Glu Asp Met Glu Asp Ile Ile Ser 225 230 235 240

Lys Ile

(2) INFORMATION FOR SEQ ID NO:1135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

Met Lys Gln Gly Lys Gly Val Thr Gly Leu Ile Arg Thr Val Ile Lys 1 5 10 15

Phe Asn Pro Phe Thr Glu Asn Leu Val Phe Glu Phe Trp Ala Asn Leu 20 25 30

Pro Thr Met Lys Val Asp Thr Tyr Lys Val Arg Val Leu Val Arg Asn 35 40 45

Arg Glu Tyr Glu Leu Ser Pro Gly Lys Ile Asn Glu Met Tyr Gly Leu
50 55 60

Pro Phe Val Asp Ala Arg Gln Gln Arg Met Asp Ile Ala Gly Leu Val 65 70 75 80

Asp Glu Gln Val Ala Glu Phe Leu Thr Gly Gly Lys Val Ser Val Leu
85 90 95

```
Ser Lys Leu Gln Thr Trp Met Arg Glu Gln Thr Trp Gln Ala Lys Ala
100 105 110
```

Asp Asp Val Glu Ser Gln Gly Trp Lys Leu Thr Trp Arg Gly Val Lys 115 120 125

Asp Lys Asn Tyr Gln Glu Asp Met Glu Asp Ile Ile Ser Lys Ile 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596991
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136: ccgacgaggg agaaacactt ggtccttaat ggcggcaaca gaaaccctac tggagaagtg 60 gtcgctagaa gtgcagccag agattatcaa aacagtacga agaaacgatc atccaagaac 120 ctcatcaaag ggcaatggac ggcggaagaa gacaggaagt tgataaggtt ggtgaggcaa 180 catggggaga ggaaatgggc aatgatatcg gagaaacttg agggaagagc aggcaaacaa 240 300 tgtcgtgaga gatggcataa tcatctccgt cctgatatta agaaagatgg atggagtgaa 360 gaagaagaga gggttcttgt ggaatcacac atgagaatcg ggaacaaatg ggcagagatc gctaaactca taccaggacg gactgagaat tctatcaaga accattggaa tgcgaccaag 420 agacgtcaaa attcaaaacg caaacacaaa cgcgaatcaa acgctgataa caatgataga 480 gatgcctctc catcagctaa aagaccatgc attctccaag actacatcaa aagtatcgag 540 agaaataaca ttaacaagga caatgacgag aagaagaatg agaacaccat cagtgttatt 600 tctacaccta atcttgatca gatctattct gatggtgatt ccgcgtcgtc catccttggc 660 720 ggtccatatg acgaagagct agattacttt caaaatatct ttgcaaacca tccgatttct cttgagaatt taggtttgag ccaaacttcg gatgaggtaa ctcagtcttc atcatctggg 780 ttcatgatca agaaccctaa ccctaacttg cacgacagtg ttggaattca tcatcaagag 840 gcaacgatca cageteegge gaatacaeee caeettgegt etgatateta ettatettat 900 960 ttattgaacg gtacgacgtc ttcatactcc gacactcatt ttccgtcttc ctcatcttcc acgtcatcca ccaccgtaga gcatggaggc cacaacgagt ttcttgagcc tcaagctaac 1020 tctacaagtg aaagaagaga aatggatctg atagagatgc tctctggttc tattcaaggt 1080
- (2) INFORMATION FOR SEQ ID NO:1137:

agcaacatct gcttcccgtt ggtctag

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..368
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

Thr Gly Glu Val Val Ala Arg Ser Ala Ala Arg Asp Tyr Gln Asn Ser 20 25 30

Thr Lys Lys Arg Ser Ser Lys Asn Leu Ile Lys Gly Gln Trp Thr Ala 35 40 45

Glu Glu Asp Arg Lys Leu Ile Arg Leu Val Arg Gln His Gly Glu Arg
50 55 60

Lys Trp Ala Met Ile Ser Glu Lys Leu Glu Gly Arg Ala Gly Lys Gln 65 70 75 80

Cys Arg Glu Arg Trp His Asn His Leu Arg Pro Asp Ile Lys Lys Asp

Gly Trp Ser Glu Glu Glu Glu Arg Val Leu Val Glu Ser His Met Arg 105 Ile Gly Asn Lys Trp Ala Glu Ile Ala Lys Leu Ile Pro Gly Arg Thr 115 120 Glu Asn Ser Ile Lys Asn His Trp Asn Ala Thr Lys Arg Arg Gln Asn 135 140 Ser Lys Arg Lys His Lys Arg Glu Ser Asn Ala Asp Asn Asn Asp Arg 150 155 Asp Ala Ser Pro Ser Ala Lys Arg Pro Cys Ile Leu Gln Asp Tyr Ile 165 170 175 Lys Ser Ile Glu Arg Asn Asn Ile Asn Lys Asp Asn Asp Glu Lys Lys 185 Asn Glu Asn Thr Ile Ser Val Ile Ser Thr Pro Asn Leu Asp Gln Ile 205 200 Tyr Ser Asp Gly Asp Ser Ala Ser Ser Ile Leu Gly Gly Pro Tyr Asp 220 215 Glu Glu Leu Asp Tyr Phe Gln Asn Ile Phe Ala Asn His Pro Ile Ser 230 235 Leu Glu Asn Leu Gly Leu Ser Gln Thr Ser Asp Glu Val Thr Gln Ser 245 250 Ser Ser Ser Gly Phe Met Ile Lys Asn Pro Asn Pro Asn Leu His Asp 265 270 260 Ser Val Gly Ile His His Gln Glu Ala Thr Ile Thr Ala Pro Ala Asn 280 285 Thr Pro His Leu Ala Ser Asp Ile Tyr Leu Ser Tyr Leu Leu Asn Gly 300 295 Thr Thr Ser Ser Tyr Ser Asp Thr His Phe Pro Ser Ser Ser Ser 310 315 320 Thr Ser Ser Thr Thr Val Glu His Gly Gly His Asn Glu Phe Leu Glu 325 330 335 Pro Gln Ala Asn Ser Thr Ser Glu Arg Arg Glu Met Asp Leu Ile Glu 340 345 350 Met Leu Ser Gly Ser Ile Gln Gly Ser Asn Ile Cys Phe Pro Leu Val 355

- (2) INFORMATION FOR SEQ ID NO:1138:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..301
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596993
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

Met Ile Ser Glu Lys Leu Glu Gly Arg Ala Gly Lys Gln Cys Arg Glu
1 5 10 15

Arg Trp His Asn His Leu Arg Pro Asp Ile Lys Lys Asp Gly Trp Ser 20 25 30

Glu Glu Glu Glu Arg Val Leu Val Glu Ser His Met Arg Ile Gly Asn 35 40 45

Lys Trp Ala Glu Ile Ala Lys Leu Ile Pro Gly Arg Thr Glu Asn Ser 50 55 60

Ile Lys Asn His Trp Asn Ala Thr Lys Arg Arg Gln Asn Ser Lys Arg 65 70 75 80

Lys His Lys Arg Glu Ser Asn Ala Asp Asn Asn Asp Arg Asp Ala Ser 85 90 95
Pro Ser Ala Lys Arg Pro Cys Ile Leu Gln Asp Tyr Ile Lys Ser Ile

105 110 100 Glu Arg Asn Asn Ile Asn Lys Asp Asn Asp Glu Lys Lys Asn Glu Asn 115 120 125 Thr Ile Ser Val Ile Ser Thr Pro Asn Leu Asp Gln Ile Tyr Ser Asp 130 135 140 Gly Asp Ser Ala Ser Ser Ile Leu Gly Gly Pro Tyr Asp Glu Glu Leu 145 150 155 160 Asp Tyr Phe Gln Asn Ile Phe Ala Asn His Pro Ile Ser Leu Glu Asn 165 170 175 Leu Gly Leu Ser Gln Thr Ser Asp Glu Val Thr Gln Ser Ser Ser 180 185 190 Gly Phe Met Ile Lys Asn Pro Asn Pro Asn Leu His Asp Ser Val Gly 200 205 195 Ile His His Gln Glu Ala Thr Ile Thr Ala Pro Ala Asn Thr Pro His 210 215 Leu Ala Ser Asp Ile Tyr Leu Ser Tyr Leu Leu Asn Gly Thr Thr Ser 230 235 240 Ser Tyr Ser Asp Thr His Phe Pro Ser Ser Ser Ser Thr Ser Ser 245 250 255 Thr Thr Val Glu His Gly Gly His Asn Glu Phe Leu Glu Pro Gln Ala 260 265 270 Asn Ser Thr Ser Glu Arg Arg Glu Met Asp Leu Ile Glu Met Leu Ser 275 280 285 Gly Ser Ile Gln Gly Ser Asn Ile Cys Phe Pro Leu Val 295 (2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..258
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1596994
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

Met Arg Ile Gly Asn Lys Trp Ala Glu Ile Ala Lys Leu Ile Pro Gly
1 5 10 15

Arg Thr Glu Asn Ser Ile Lys Asn His Trp Asn Ala Thr Lys Arg Arg 20 25 30

Gln Asn Ser Lys Arg Lys His Lys Arg Glu Ser Asn Ala Asp Asn Asn 35 40 45

Asp Arg Asp Ala Ser Pro Ser Ala Lys Arg Pro Cys Ile Leu Gln Asp 50 55 60

Tyr Ile Lys Ser Ile Glu Arg Asn Asn Ile Asn Lys Asp Asn Asp Glu 65 70 75 80

Lys Lys Asn Glu Asn Thr Ile Ser Val Ile Ser Thr Pro Asn Leu Asp 85 90 95

Gln Ile Tyr Ser Asp Gly Asp Ser Ala Ser Ser Ile Leu Gly Gly Pro 100 105 110

Tyr Asp Glu Glu Leu Asp Tyr Phe Gln Asn Ile Phe Ala Asn His Pro

Ile Ser Leu Glu Asn Leu Gly Leu Ser Gln Thr Ser Asp Glu Val Thr
130 135 140

Gln Ser Ser Ser Gly Phe Met Ile Lys Asn Pro Asn Pro Asn Leu 145 150 155 160

His Asp Ser Val Gly Ile His His Gln Glu Ala Thr Ile Thr Ala Pro 165 170 175

Ala Asn Thr Pro His Leu Ala Ser Asp Ile Tyr Leu Ser Tyr Leu Leu
180 185 190

(A) THEODMANION FOR CEO ID 1

- (2) INFORMATION FOR SEQ ID NO:1140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1075 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

Leu Val

- (A) NAME/KEY: -
- (B) LOCATION: 1..1075
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140: 60 ctcaagctca aactctaaag gtgtaggtga agtcatcatt ataagaccag agtgaactga 120 taatgctgtg aagaacaggt ttacaacact ttgtaagaag agagccaagc atgaagctat 180 gactaaagac agcaactcaa acaccaaaag aatgttgttc ttagacggta tcagtacacc gcgaaaatcc gagaatgaaa ctcctattgc taagaaattg aagagaagtc acattctaga 240 300 tctcacagag atcagtaact atggaagggc cgaggcatgt gtgaatcagc agataaggtc 360 tccattttcg gttttagctc gaaatgccac tggtattgat agcttggaag aacagaatca aacaagcaat gtgaatgaga gtgatggtga agggatgttt cttaagaagg atgatccaaa 420 agttacaget ttgatgeaac aagetgaact tttaagetee ttggegeaga aagttaatge 480 agacaacaca gaacagagta tggagaatgc ttggaaggtt cttcaggact tcttgaataa 540 aggcaaggag aatgatttat tcagatatgg aatacctgat atagatttta agatcgagga 600 660 atttaaggac cttatagagg atttgaggag tggttatgaa gacaatcaat tatcttggag 720 gcaacctgat cttcatgact caccagctag ctctgagtat agttccggat caaccatcat 780 ggtggatcag tctggtgata aaacacaacc attctcagca gatactcaga cagaacataa gcaagttgga gaggagttgc tcgtcccgaa aaatcctgat gagaatatgc ccatctcggg 840 cgaagaaaag ttcagctcgc ctattcaggt cacgccattg ttcagatctt tggcagacgg 900 tataccaagt ccacagttct ccgaaagtgt aagcttcgca ccttctttgt tcatcataca 960 atacttaggc tttgaaaaat caatgagtct taaaagactg attgcttttg taggagagga 1020 gcttcctgct aaaaacacta gggatcgagt cctcatctcc atgtccaagt gctaa
- (2) INFORMATION FOR SEQ ID NO:1141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597000
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:
- Met Thr Lys Asp Ser Asn Ser Asn Thr Lys Arg Met Leu Phe Leu Asp 1 5 10
- Gly Ile Ser Thr Pro Arg Lys Ser Glu Asn Glu Thr Pro Ile Ala Lys
 20 25 30
- Lys Leu Lys Arg Ser His Ile Leu Asp Leu Thr Glu Ile Ser Asn Tyr 35 40 45
- Gly Arg Ala Glu Ala Cys Val Asn Gln Gln Ile Arg Ser Pro Phe Ser 50 55 60
- Val Leu Ala Arg Asn Ala Thr Gly Ile Asp Ser Leu Glu Glu Gln Asn

70 75 Gln Thr Ser Asn Val Asn Glu Ser Asp Gly Glu Gly Met Phe Leu Lys 85 90 95 Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln Gln Ala Glu Leu Leu 100 105 110 Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn Thr Glu Gln Ser Met 115 120 125 Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu Asn Lys Gly Lys Glu 130 135 140 Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile Asp Phe Lys Ile Glu 145 150 155 160 Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser Gly Tyr Glu Asp Asn 165 170 175 Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp Ser Pro Ala Ser Ser 180 185 190 Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp Gln Ser Gly Asp Lys 195 200 205 Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu His Lys Gln Val Gly 210 215 220 Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu Asn Met Pro Ile Ser 225 230 235 240 Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val Thr Pro Leu Phe Arg 245 250 255 Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe Ser Glu Ser Val Ser 260 265 270 Phe Ala Pro Ser Leu Phe Ile Ile Gln Tyr Leu Gly Phe Glu Lys Ser 275 280 Met Ser Leu Lys Arg Leu Ile Ala Phe Val Gly Glu Glu Leu Pro Ala 290 295 300 Lys Asn Thr Arg Asp Arg Val Leu Ile Ser Met Ser Lys Cys 305 310

- (2) INFORMATION FOR SEQ ID NO:1142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..307
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597001
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:
- Met Leu Phe Leu Asp Gly Ile Ser Thr Pro Arg Lys Ser Glu Asn Glu
- Thr Pro Ile Ala Lys Lys Leu Lys Arg Ser His Ile Leu Asp Leu Thr 20 25 30
- Glu Ile Ser Asn Tyr Gly Arg Ala Glu Ala Cys Val Asn Gln Gln Ile 35 40 45
- Arg Ser Pro Phe Ser Val Leu Ala Arg Asn Ala Thr Gly Ile Asp Ser 50 55 60
- Leu Glu Glu Gln Asn Gln Thr Ser Asn Val Asn Glu Ser Asp Gly Glu 65 70 75 80
- Gly Met Phe Leu Lys Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln 85 90 95
- Gln Ala Glu Leu Leu Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn 100 105 110
- Thr Glu Gln Ser Met Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu 115 120 125
- Asn Lys Gly Lys Glu Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile 130 135 140

```
Asp Phe Lys Ile Glu Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser
               150
                                155
Gly Tyr Glu Asp Asn Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp
      165
                   170
Ser Pro Ala Ser Ser Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp
                         185
        180
Gln Ser Gly Asp Lys Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu
                     200
                                      205
His Lys Gln Val Gly Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu
         215
                                  220
Asn Met Pro Ile Ser Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val
       230 235
Thr Pro Leu Phe Arg Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe
          245 250
Ser Glu Ser Val Ser Phe Ala Pro Ser Leu Phe Ile Ile Gln Tyr Leu
        260 265
Gly Phe Glu Lys Ser Met Ser Leu Lys Arg Leu Ile Ala Phe Val Gly
     275 280 285
Glu Glu Leu Pro Ala Lys Asn Thr Arg Asp Arg Val Leu Ile Ser Met
                  295
Ser Lys Cys
```

- (2) INFORMATION FOR SEQ ID NO:1143:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..226
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597002
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143: Met Phe Leu Lys Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln Gln 10 5 Ala Glu Leu Leu Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn Thr 25 20 Glu Gln Ser Met Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu Asn 4.0 Lys Gly Lys Glu Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile Asp 55 Phe Lys Ile Glu Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser Gly 70 75 Tyr Glu Asp Asn Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp Ser 90 85 Pro Ala Ser Ser Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp Gln 105 100 Ser Gly Asp Lys Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu His 120 Lys Gln Val Gly Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu Asn 140 135 Met Pro Ile Ser Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val Thr 155 150 Pro Leu Phe Arg Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe Ser 170 165 Glu Ser Val Ser Phe Ala Pro Ser Leu Phe Ile Ile Gln Tyr Leu Gly 185 180 Phe Glu Lys Ser Met Ser Leu Lys Arg Leu Ile Ala Phe Val Gly Glu 195 200 205

Glu Leu Pro Ala Lys Asn Thr Arg Asp Arg Val Leu Ile Ser Met Ser

210 215 220 Lys Cys

225

- (2) INFORMATION FOR SEQ ID NO:1144:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1098 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1098
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597003
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144: tcaagctcaa actctaaagg tgtaggtgaa gtcatcatta taagaccaga gtgaactgat 60 aatgctgtga agaacaggtt tacaacactt tgtaagaaga gagccaagca tgaagctatg 120 actaaagaca gcaactcaaa caccaaaaga atgttgttct tagacggtat cagtacaccg 180 240 cgaaaatccg agaatgaaac tcctattgct aagaaattga agagaagtca cattctagat ctcacagaga tcagtaacta tggaagggcc gaggcatgtg tgaatcagca gataaggtct 300 360 ccattttcgg ttttagctcg aaatgccact ggtattgata gcttggaaga acagaatcaa 420 acaagcaatg tgaatgagag tgatggtgaa gggatgtttc ttaagaagga tgatccaaaa gttacagctt tgatgcaaca agctgaactt ttaagctcct tggcgcagaa agttaatgca 480 540 gacaacacag aacagagtat ggagaatgct tggaaggttc ttcaggactt cttgaataaa 600 ggcaaggaga atgatttatt cagatatgga atacctgata tagattttaa gatcgaggaa tttaaggacc ttatagagga tttgaggagt ggttatgaag acaatcaatt atcttggagg 660 caacctgatc ttcatgactc accagctagc tctgagtata gttccggatc aaccatcatg 720 780 gtggatcagt ctggtgataa aacacaacca ttctcagcag atactcagac agaacataag 840 caagttggag aggagttgct cgtcccgaaa aatcctgatg agaatatgcc catctcgggc gaagaaaagt tcagctcgcc tattcaggtc acgccattgt tcagatcttt ggcagacggt 900 ataccaagtc cacagttctc cgaaagtgag aggagcttcc tgctaaaaac actagggatc 960 gagtcctcat ctccatgtcc aagtgctaat ccttcaaaac caccccttg caaaagagtc 1020 cttctccata gcttgaagcc atctacaaaa gaaggcacca gtgtgtcttt aagaaaaaat 1080
- (2) INFORMATION FOR SEQ ID NO:1145:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

tctttggttt gtctctaa

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597004
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

Met Thr Lys Asp Ser Asn Ser Asn Thr Lys Arg Met Leu Phe Leu Asp 1 5 10 15

Gly Ile Ser Thr Pro Arg Lys Ser Glu Asn Glu Thr Pro Ile Ala Lys 20 25 30

Lys Leu Lys Arg Ser His Ile Leu Asp Leu Thr Glu Ile Ser Asn Tyr 35 40 45

Gly Arg Ala Glu Ala Cys Val Asn Gln Gln Ile Arg Ser Pro Phe Ser 50 55 60

Val Leu Ala Arg Asn Ala Thr Gly Ile Asp Ser Leu Glu Glu Gln Asn 65 70 75 80

Gln Thr Ser Asn Val Asn Glu Ser Asp Gly Glu Gly Met Phe Leu Lys 85 90 95

Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln Gln Ala Glu Leu Leu 100 105 110

Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn Thr Glu Gln Ser Met

125 120 Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu Asn Lys Gly Lys Glu 130 135 140 Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile Asp Phe Lys Ile Glu 145 150 155 Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser Gly Tyr Glu Asp Asn 165 170 175 Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp Ser Pro Ala Ser Ser 180 185 190 Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp Gln Ser Gly Asp Lys 195 200 205 Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu His Lys Gln Val Gly 210 215 220 Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu Asn Met Pro Ile Ser 225 230 235 240 Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val Thr Pro Leu Phe Arg 245 250 255 Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe Ser Glu Ser Glu Arg 260 265 270 Ser Phe Leu Leu Lys Thr Leu Gly Ile Glu Ser Ser Pro Cys Pro 275 280 285 Ser Ala Asn Pro Ser Lys Pro Pro Pro Cys Lys Arg Val Leu Leu His 290 295 300 Ser Leu Lys Pro Ser Thr Lys Glu Gly Thr Ser Val Ser Leu Arg Lys 315 310 Asn Ser Leu Val Cys Leu 325

- (2) INFORMATION FOR SEQ ID NO:1146:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..315
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597005
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

Met Leu Phe Leu Asp Gly Ile Ser Thr Pro Arg Lys Ser Glu Asn Glu

10 15

10 15

Thr Pro Ile Ala Lys Lys Leu Lys Arg Ser His Ile Leu Asp Leu Thr 20 25 30

Glu Ile Ser Asn Tyr Gly Arg Ala Glu Ala Cys Val Asn Gln Gln Ile 35 40 45

Arg Ser Pro Phe Ser Val Leu Ala Arg Asn Ala Thr Gly Ile Asp Ser 50 55 60

Leu Glu Glu Gln Asn Gln Thr Ser Asn Val Asn Glu Ser Asp Gly Glu 65 70 75 80

Gly Met Phe Leu Lys Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln 85 90 95

Gln Ala Glu Leu Leu Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn 100 105 110

Thr Glu Gln Ser Met Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu 115 120 125

Asn Lys Gly Lys Glu Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile 130 135 140

Asp Phe Lys Ile Glu Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser 145 150 155 160

Gly Tyr Glu Asp Asn Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp 165 170 175

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
Ser Pro Ala Ser Ser Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp
                           185
Gln Ser Gly Asp Lys Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu
           200
                                        205
His Lys Gln Val Gly Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu
                          220
          215
Asn Met Pro Ile Ser Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val
225 230 235
Thr Pro Leu Phe Arg Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe
         245 250 255
Ser Glu Ser Glu Arg Ser Phe Leu Leu Lys Thr Leu Gly Ile Glu Ser
         260 265
Ser Ser Pro Cys Pro Ser Ala Asn Pro Ser Lys Pro Pro Pro Cys Lys
      275 280 285
Arg Val Leu Leu His Ser Leu Lys Pro Ser Thr Lys Glu Gly Thr Ser
  290 295 300
Val Ser Leu Arg Lys Asn Ser Leu Val Cys Leu
       310
(2) INFORMATION FOR SEQ ID NO:1147:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 234 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..234
        (D) OTHER INFORMATION: / Ceres Seq. ID 1597006
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:
Met Phe Leu Lys Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln Gln
                              10
Ala Glu Leu Leu Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn Thr
                          25
    20
Glu Gln Ser Met Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu Asn
                       40
  35
Lys Gly Lys Glu Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile Asp
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60 55 Phe Lys Ile Glu Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser Gly 75 70 Tyr Glu Asp Asn Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp Ser 90 8.5 Pro Ala Ser Ser Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp Gln 105 100 Ser Gly Asp Lys Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu His 120 Lys Gln Val Gly Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu Asn 140 135 Met Pro Ile Ser Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val Thr 155 150 Pro Leu Phe Arg Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe Ser 170 165 Glu Ser Glu Arg Ser Phe Leu Leu Lys Thr Leu Gly Ile Glu Ser Ser 185 180 Ser Pro Cys Pro Ser Ala Asn Pro Ser Lys Pro Pro Pro Cys Lys Arg 195 200 Val Leu Leu His Ser Leu Lys Pro Ser Thr Lys Glu Gly Thr Ser Val 215 Ser Leu Arg Lys Asn Ser Leu Val Cys Leu

225 230 (2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..3173
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148: 60 ctaatagaac taaaaactct ttgagatttt tggttgatga gaatggcaat gaacacactt tgaatagaga gaaaggcaat gaacacactt tgaatagaga gaaaggcaat attgcttctg 120 180 tttactttga gaatctgttc atgtcttctt atcctgctaa ctctcagtcg gctttggatg gttttaaaac tcgagtttca gaggagatga atcaagaatt aactcaagct gttactgaat 240 300 tggaaattca ttctgctaga gtgctcctgg tccagatggt tcactgcctt attcttccag 360 aaaaatggga atgttgtcaa ggatcagatt atatagagat tctgggtttt tttgagacgg 420 gggttctgcc tcaagactgg aatcatactc acctctgttt gattccaaaa tttactaacc 480 ctcagagaat gtccgatatt agaccaatta gtctatgctc agtcttatat aagattatct ccaaaatcct atctttcaga ttaaagaagc atctcccatc tatcgtttca ccttctcaat 540 600 ctgcgttttt tgctgaaagg ttaatctctc acaatattct cattgctcat gaaattgtgc 660 atagcttaag aactaatggc aggatctcca aagagtttat ggttttcaaa actgatatgg ctaaagccta tgatagggta gaatggtctt tcttacaaga aattttggtt gctttgggct 720 780 tcaatgataa atggaattct tggattatgg gctgtgtgac ttctgttacc tattcagttc tgataaatgg tcaacatttt gggcatatta ctcccgagag aggtatcaga caaggtgatc 840 ccatctctcc atttctgttt gtgctttgta cggaagctct tattcatatt ctacaacaag 900 ctgagaattc taagaaagtt agtggcattc agtttaatgg ttctgggcct tcagttaatc 960 atttattgtt tgttgatgac actcagttag tctgtcgagc aacaaaatcg gattgtgaac 1020 agatgatgct ttgtttatct cagtatgggc atatctcagg acaactgatt aatgtggaga 1080 aatcttcgat cacttttgga gttaaggtag atgaggatac taaacagtgg atcaagaatc 1140 gttctggtat tcatctagaa ggtgggacag ggaagtatct ggggttacct gagaacttga 1200 gtggttccaa acaggatttg tttggctata tcaaagaaaa attgcaatct catttgtctg 1260 1320 gttggtatga taaaactctc tcacaaggag gcaaggagat cttgttaaag tcaattgctt tggccttgcc tgtgtatatt atgacntgtt ttaggcttcc taaaggttta tgcactaagc 1380 ttacaagtgt aatgatggat ttttggtgga actctatgga attttcaaat aaaattcatt 1440 1500 ggataggtgg taagaagtta actctgccta agagcttagg gggttttggt ttcaaagact tncaatgttt taaccaggca ctattggcca aacaagcttg gagattattc agtgattcga 1560 agagcattgt ttctcaaata ttcaagagcc gagaattatt aaatggtggt ctgaagagac 1620 ttataggaaa tggtgagcaa accaatgtgt ggattgataa atggctgttt gatggacata 1680 gtcaacgacc tatgaatttg cattcattga tgaatattca tatgaaggtt agtcatttaa 1740 ttgatcctct ctctcggaat tggaacttga agaagctgac agagttattt catgagaaag 1800 1860 atgttcaatt aattatgcat cagagacctc tcatctctag cgaagactct tattgttggg ctgggactaa taatggttta tacacggtga agtctggata tgaaagaagt agcagggaga 1920 ctttcaagaa tctcttcaag gaggctgatg tttatccttc tgttaatctg ttgtttgaca 1980 2040 aggtttggtc tcttgaaacg gttccaaaaa ttaaagtctt catgtggaaa gctttaaaag 2100 gtgctcttgc agtagaagac atattaagat caagaggcat tcgaactgca gatggatgct 2160 tattttgtaa agaggaaatt gaaacaatta atcatctatt gtttcaatgt ccttttgcta 2220 gacaagtatg gacactttca cttattcagg cacctgcaac ggggtttggg acatctattt tctccaatat aaatcatgtg attcaaaatt ctcagaattt tggaatccct cgtcatatga 2280 gaactgtgag tccatggtta ttgtgggaga tatggaaaaa caggaataag actttgtttc 2340 2400 agggtactgg tttaacgagt agtgagattg tagctaaagc ttatgaagag tgcaatcttt 2460 ggategetaa gagtgteate actgagttea egggagaget ggatetettg tetgtgetae gaagggaacc ctggctttac aatagttggt ttgtcacggc tcatcgttgg gaggtaaact 2520 cggcttttga atacttgtct aacattgagt tgtgggttca aatgcgtggg attcctctcc 2580 2640 tctatgtttg tgaagccaca gtgacagaga tagctcttgg tttagggcaa attatatcat tggattttca tgatgctact acaacccaaa tagcttttat tagagtgaga atccgatttg 2700 agatcactga tcgtataagg ttcttccaaa gaattacctt tgattctggt gagactgcgc 2760 tgataagget gacteateat aggaattact geeettateg acaacetgag cetegtteta 2820 tcattcgtgg tcctaccaac aatctcacta ggtctagaag agaaggagtg tgtacccggg 2880 atgaatatca tcgttcttcc ctgaactccc aatcacagat gtctgagaac gcctttccag 2940 cacctattga acctcctcca agagtggcag ctcctccttt gaatcctgat gaatttaggg 3000 ctgcttattt tccagaaggc agagcaggtt ctttaccaaa tataggaaca ttaaatctta 3060 atcctccatc tcgcaggcaa gaggcgtcaa gaaactctga tgtacaaccg tttacgggtc 3120 ctgcatttgg tgcaaatgtt cctcgagtgg ttgaagtagg tgaatgttca tga

(2) INFORMATION FOR SEQ ID NO:1149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1056 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..1056
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597015
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:
- Asn Arg Thr Lys Asn Ser Leu Arg Phe Leu Val Asp Glu Asn Gly Asn 1 5 10 15
- Glu His Thr Leu Asn Arg Glu Lys Gly Asn Glu His Thr Leu Asn Arg 20 25 30
- Glu Lys Gly Asn Ile Ala Ser Val Tyr Phe Glu Asn Leu Phe Met Ser 35 40 45
- Ser Tyr Pro Ala Asn Ser Gln Ser Ala Leu Asp Gly Phe Lys Thr Arg 50 55 60
- Val Ser Glu Glu Met Asn Gln Glu Leu Thr Gln Ala Val Thr Glu Leu 65 70 75 80
- Glu Ile His Ser Ala Arg Val Leu Leu Val Gln Met Val His Cys Leu 85 90 95
- Ile Leu Pro Glu Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr Ile Glu 100 105 110
- Ile Leu Gly Phe Phe Glu Thr Gly Val Leu Pro Gln Asp Trp Asn His 115 120 125
- Thr His Leu Cys Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg Met Ser 130 135 140
- Asp Ile Arg Pro Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile Ile Ser 145 150 155 160
- Lys Ile Leu Ser Phe Arg Leu Lys Lys His Leu Pro Ser Ile Val Ser 165 170 175
- Pro Ser Gln Ser Ala Phe Phe Ala Glu Arg Leu Ile Ser His Asn Ile 180 185 190
- Leu Ile Ala His Glu Ile Val His Ser Leu Arg Thr Asn Gly Arg Ile 195 200 205
- Ser Lys Glu Phe Met Val Phe Lys Thr Asp Met Ala Lys Ala Tyr Asp 210 215 220
- Arg Val Glu Trp Ser Phe Leu Gln Glu Ile Leu Val Ala Leu Gly Phe 225 230 235 240
- Asn Asp Lys Trp Asn Ser Trp Ile Met Gly Cys Val Thr Ser Val Thr 245 250 255
- Tyr Ser Val Leu Ile Asn Gly Gln His Phe Gly His Ile Thr Pro Glu 260 265 270

 Arg Gly Ile Arg Gln Gly Asp Pro Ile Ser Pro Phe Leu Phe Val Leu
- 275 280 285

 Cys Thr Glu Ala Leu Ile His Ile Leu Gln Gln Ala Glu Asn Ser Lys
- Cys Thr Glu Ala Leu lle His lle Leu Gin Gin Ala Glu Ash Ser Lys
 290 295 300

 The Charles Ash Charles Ash Charles Charl
- Lys Val Ser Gly Ile Gln Phe Asn Gly Ser Gly Pro Ser Val Asn His 305 310 315
- Leu Leu Phe Val Asp Asp Thr Gln Leu Val Cys Arg Ala Thr Lys Ser 325 330 335 Asp Cys Glu Gln Met Met Leu Cys Leu Ser Gln Tyr Gly His Ile Ser
- 340 345 350 Gly Gln Leu Ile Asn Val Glu Lys Ser Ser Ile Thr Phe Gly Val Lys 355 360 365

Val Asp Glu Asp Thr Lys Gln Trp Ile Lys Asn Arg Ser Gly Ile His 375 Leu Glu Gly Gly Thr Gly Lys Tyr Leu Gly Leu Pro Glu Asn Leu Ser 395 390 Gly Ser Lys Gln Asp Leu Phe Gly Tyr Ile Lys Glu Lys Leu Gln Ser 410 405 His Leu Ser Gly Trp Tyr Asp Lys Thr Leu Ser Gln Gly Gly Lys Glu 425 Ile Leu Leu Lys Ser Ile Ala Leu Ala Leu Pro Val Tyr Ile Met Xaa 445 440 Cys Phe Arg Leu Pro Lys Gly Leu Cys Thr Lys Leu Thr Ser Val Met 460 455 Met Asp Phe Trp Trp Asn Ser Met Glu Phe Ser Asn Lys Ile His Trp 475 470 Ile Gly Gly Lys Lys Leu Thr Leu Pro Lys Ser Leu Gly Gly Phe Gly 490 485 Phe Lys Asp Xaa Gln Cys Phe Asn Gln Ala Leu Leu Ala Lys Gln Ala 510 505 Trp Arg Leu Phe Ser Asp Ser Lys Ser Ile Val Ser Gln Ile Phe Lys 520 Ser Arg Glu Leu Leu Asn Gly Gly Leu Lys Arg Leu Ile Gly Asn Gly 540 535 Glu Gln Thr Asn Val Trp Ile Asp Lys Trp Leu Phe Asp Gly His Ser 550 555 Gln Arg Pro Met Asn Leu His Ser Leu Met Asn Ile His Met Lys Val 570 575 565 Ser His Leu Ile Asp Pro Leu Ser Arg Asn Trp Asn Leu Lys Lys Leu 585 580 Thr Glu Leu Phe His Glu Lys Asp Val Gln Leu Ile Met His Gln Arg 600 595 Pro Leu Ile Ser Ser Glu Asp Ser Tyr Cys Trp Ala Gly Thr Asn Asn 615 Gly Leu Tyr Thr Val Lys Ser Gly Tyr Glu Arg Ser Ser Arg Glu Thr 635 630 Phe Lys Asn Leu Phe Lys Glu Ala Asp Val Tyr Pro Ser Val Asn Leu 650 645 Leu Phe Asp Lys Val Trp Ser Leu Glu Thr Val Pro Lys Ile Lys Val 665 660 Phe Met Trp Lys Ala Leu Lys Gly Ala Leu Ala Val Glu Asp Ile Leu 675 680 Arg Ser Arg Gly Ile Arg Thr Ala Asp Gly Cys Leu Phe Cys Lys Glu 695 Glu Ile Glu Thr Ile Asn His Leu Leu Phe Gln Cys Pro Phe Ala Arg 715 710 Gln Val Trp Thr Leu Ser Leu Ile Gln Ala Pro Ala Thr Gly Phe Gly 730 725 Thr Ser Ile Phe Ser Asn Ile Asn His Val Ile Gln Asn Ser Gln Asn 745 740 Phe Gly Ile Pro Arg His Met Arg Thr Val Ser Pro Trp Leu Leu Trp 760 Glu Ile Trp Lys Asn Arg Asn Lys Thr Leu Phe Gln Gly Thr Gly Leu 780 775 Thr Ser Ser Glu Ile Val Ala Lys Ala Tyr Glu Glu Cys Asn Leu Trp 795 790 Ile Ala Lys Ser Val Ile Thr Glu Phe Thr Gly Glu Leu Asp Leu Leu 810 Ser Val Leu Arg Arg Glu Pro Trp Leu Tyr Asn Ser Trp Phe Val Thr 830 825 Ala His Arg Trp Glu Val Asn Ser Ala Phe Glu Tyr Leu Ser Asn Ile 835 840 845 Glu Leu Trp Val Gln Met Arg Gly Ile Pro Leu Leu Tyr Val Cys Glu

860 855 850 Ala Thr Val Thr Glu Ile Ala Leu Gly Leu Gly Gln Ile Ile Ser Leu 865 870 875 Asp Phe His Asp Ala Thr Thr Thr Gln Ile Ala Phe Ile Arg Val Arg 885 890 Ile Arg Phe Glu Ile Thr Asp Arg Ile Arg Phe Phe Gln Arg Ile Thr 900 905 910 Phe Asp Ser Gly Glu Thr Ala Leu Ile Arg Leu Thr His His Arg Asn 915 920 925 Tyr Cys Pro Tyr Arg Gln Pro Glu Pro Arg Ser Ile Ile Arg Gly Pro 930 935 940 Thr Asn Asn Leu Thr Arg Ser Arg Arg Glu Gly Val Cys Thr Arg Asp 955 960 945 950 Glu Tyr His Arg Ser Ser Leu Asn Ser Gln Ser Gln Met Ser Glu Asn 965 970 975 Ala Phe Pro Ala Pro Ile Glu Pro Pro Pro Arg Val Ala Ala Pro Pro 980 985 990 Leu Asn Pro Asp Glu Phe Arg Ala Ala Tyr Phe Pro Glu Gly Arg Ala 1000 1005 Gly Ser Leu Pro Asn Ile Gly Thr Leu Asn Leu Asn Pro Pro Ser Arg 1010 1015 1020 Arg Gln Glu Ala Ser Arg Asn Ser Asp Val Gln Pro Phe Thr Gly Pro 1025 1030 1035 1040 Ala Phe Gly Ala Asn Val Pro Arg Val Val Glu Val Gly Glu Cys Ser 1045 1050

- (2) INFORMATION FOR SEQ 1D NO:1150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1010 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..1010
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150: Met Ser Ser Tyr Pro Ala Asn Ser Gln Ser Ala Leu Asp Gly Phe Lys

Glu Leu Glu Ile His Ser Ala Arg Val Leu Leu Val Gln Met Val His 35 40 45

Cys Leu Ile Leu Pro Glu Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr 50 55 60

Ile Glu Ile Leu Gly Phe Phe Glu Thr Gly Val Leu Pro Gln Asp Trp 65 70 75 80

Asn His Thr His Leu Cys Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg 85 90 95

Met Ser Asp Ile Arg Pro Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile 100 105 110

Ile Ser Lys Ile Leu Ser Phe Arg Leu Lys Lys His Leu Pro Ser Ile 115 120 125

Val Ser Pro Ser Gln Ser Ala Phe Phe Ala Glu Arg Leu Ile Ser His 130 135 140

Asn Ile Leu Ile Ala His Glu Ile Val His Ser Leu Arg Thr Asn Gly 145 150 155 160

Arg Ile Ser Lys Glu Phe Met Val Phe Lys Thr Asp Met Ala Lys Ala 165 170 175 Tyr Asp Arg Val Glu Trp Ser Phe Leu Gln Glu Ile Leu Val Ala Leu 185 Gly Phe Asn Asp Lys Trp Asn Ser Trp Ile Met Gly Cys Val Thr Ser 200 Val Thr Tyr Ser Val Leu Ile Asn Gly Gln His Phe Gly His Ile Thr 220 215 Pro Glu Arg Gly Ile Arg Gln Gly Asp Pro Ile Ser Pro Phe Leu Phe 230 235 Val Leu Cys Thr Glu Ala Leu Ile His Ile Leu Gln Gln Ala Glu Asn 250 245 Ser Lys Lys Val Ser Gly Ile Gln Phe Asn Gly Ser Gly Pro Ser Val 265 Asn His Leu Leu Phe Val Asp Asp Thr Gln Leu Val Cys Arg Ala Thr 280 Lys Ser Asp Cys Glu Gln Met Met Leu Cys Leu Ser Gln Tyr Gly His 300 295 Ile Ser Gly Gln Leu Ile Asn Val Glu Lys Ser Ser Ile Thr Phe Gly 315 310 Val Lys Val Asp Glu Asp Thr Lys Gln Trp Ile Lys Asn Arg Ser Gly 330 325 Ile His Leu Glu Gly Gly Thr Gly Lys Tyr Leu Gly Leu Pro Glu Asn 345 340 Leu Ser Gly Ser Lys Gln Asp Leu Phe Gly Tyr Ile Lys Glu Lys Leu 355 360 Gln Ser His Leu Ser Gly Trp Tyr Asp Lys Thr Leu Ser Gln Gly Gly 380 375 Lys Glu Ile Leu Leu Lys Ser Ile Ala Leu Ala Leu Pro Val Tyr Ile 385 390 395 Met Xaa Cys Phe Arg Leu Pro Lys Gly Leu Cys Thr Lys Leu Thr Ser 405 410 Val Met Met Asp Phe Trp Trp Asn Ser Met Glu Phe Ser Asn Lys Ile 420 425 His Trp Ile Gly Gly Lys Lys Leu Thr Leu Pro Lys Ser Leu Gly Gly 445 440 Phe Gly Phe Lys Asp Xaa Gln Cys Phe Asn Gln Ala Leu Leu Ala Lys 455 Gln Ala Trp Arg Leu Phe Ser Asp Ser Lys Ser Ile Val Ser Gln Ile 475 480 470 Phe Lys Ser Arg Glu Leu Leu Asn Gly Gly Leu Lys Arg Leu Ile Gly 490 495 485 Asn Gly Glu Gln Thr Asn Val Trp Ile Asp Lys Trp Leu Phe Asp Gly 505 500 His Ser Gln Arg Pro Met Asn Leu His Ser Leu Met Asn Ile His Met 520 Lys Val Ser His Leu Ile Asp Pro Leu Ser Arg Asn Trp Asn Leu Lys 535 540 Lys Leu Thr Glu Leu Phe His Glu Lys Asp Val Gln Leu Ile Met His 555 550 Gln Arg Pro Leu Ile Ser Ser Glu Asp Ser Tyr Cys Trp Ala Gly Thr 570 565 Asn Asn Gly Leu Tyr Thr Val Lys Ser Gly Tyr Glu Arg Ser Ser Arg 585 Glu Thr Phe Lys Asn Leu Phe Lys Glu Ala Asp Val Tyr Pro Ser Val 600 Asn Leu Leu Phe Asp Lys Val Trp Ser Leu Glu Thr Val Pro Lys Ile 620 615 Lys Val Phe Met Trp Lys Ala Leu Lys Gly Ala Leu Ala Val Glu Asp 635 630 Ile Leu Arg Ser Arg Gly Ile Arg Thr Ala Asp Gly Cys Leu Phe Cys 650 Lys Glu Glu Ile Glu Thr Ile Asn His Leu Leu Phe Gln Cys Pro Phe

665 670 660 Ala Arg Gln Val Trp Thr Leu Ser Leu Ile Gln Ala Pro Ala Thr Gly 675 680 685 Phe Gly Thr Ser Ile Phe Ser Asn Ile Asn His Val Ile Gln Asn Ser 695 700 Gln Asn Phe Gly Ile Pro Arg His Met Arg Thr Val Ser Pro Trp Leu 705 710 715 720 Leu Trp Glu Ile Trp Lys Asn Arg Asn Lys Thr Leu Phe Gln Gly Thr 725 730 735 Gly Leu Thr Ser Ser Glu Ile Val Ala Lys Ala Tyr Glu Glu Cys Asn 745 740 Leu Trp Ile Ala Lys Ser Val Ile Thr Glu Phe Thr Gly Glu Leu Asp 755 760 765 Leu Leu Ser Val Leu Arg Arg Glu Pro Trp Leu Tyr Asn Ser Trp Phe 770 775 780 Val Thr Ala His Arg Trp Glu Val Asn Ser Ala Phe Glu Tyr Leu Ser 795 800 785 790 Asn Ile Glu Leu Trp Val Gln Met Arg Gly Ile Pro Leu Leu Tyr Val 805 810 815 Cvs Glu Ala Thr Val Thr Glu Ile Ala Leu Gly Leu Gly Gln Ile Ile 820 825 830 Ser Leu Asp Phe His Asp Ala Thr Thr Gln Ile Ala Phe Ile Arg 835 840 845 Val Arg Ile Arg Phe Glu Ile Thr Asp Arg Ile Arg Phe Phe Gln Arg 850 855 860 Ile Thr Phe Asp Ser Gly Glu Thr Ala Leu Ile Arg Leu Thr His His 875 880 865 870 Arg Asn Tyr Cys Pro Tyr Arg Gln Pro Glu Pro Arg Ser Ile Ile Arg 890 885 Gly Pro Thr Asn Asn Leu Thr Arg Ser Arg Arg Glu Gly Val Cys Thr 900 905 Arg Asp Glu Tyr His Arg Ser Ser Leu Asn Ser Gln Ser Gln Met Ser 920 Glu Asn Ala Phe Pro Ala Pro Ile Glu Pro Pro Pro Arg Val Ala Ala 940 930 935 Pro Pro Leu Asn Pro Asp Glu Phe Arg Ala Ala Tyr Phe Pro Glu Gly 945 950 955 Arg Ala Gly Ser Leu Pro Asn Ile Gly Thr Leu Asn Leu Asn Pro Pro 970 975 965 Ser Arg Arg Gln Glu Ala Ser Arg Asn Ser Asp Val Gln Pro Phe Thr 985 Gly Pro Ala Phe Gly Ala Asn Val Pro Arg Val Val Glu Val Gly Glu 1000 Cys Ser

1010

- (2) INFORMATION FOR SEQ ID NO:1151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 988 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..988
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597017
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

Met Asn Gln Glu Leu Thr Gln Ala Val Thr Glu Leu Glu Ile His Ser 10 1 5

Ala Arg Val Leu Leu Val Gln Met Val His Cys Leu Ile Leu Pro Glu 20 25

Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr Ile Glu Ile Leu Gly Phe Phe Glu Thr Gly Val Leu Pro Gln Asp Trp Asn His Thr His Leu Cys 55 Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg Met Ser Asp Ile Arg Pro 75 70 Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile Ile Ser Lys Ile Leu Ser 90 Phe Arg Leu Lys Lys His Leu Pro Ser Ile Val Ser Pro Ser Gln Ser 105 Ala Phe Phe Ala Glu Arg Leu Ile Ser His Asn Ile Leu Ile Ala His 120 Glu Ile Val His Ser Leu Arg Thr Asn Gly Arg Ile Ser Lys Glu Phe 140 135 Met Val Phe Lys Thr Asp Met Ala Lys Ala Tyr Asp Arg Val Glu Trp 150 155 Ser Phe Leu Gln Glu Ile Leu Val Ala Leu Gly Phe Asn Asp Lys Trp 175 170 165 Asn Ser Trp Ile Met Gly Cys Val Thr Ser Val Thr Tyr Ser Val Leu 185 180 Ile Asn Gly Gln His Phe Gly His Ile Thr Pro Glu Arg Gly Ile Arg 200 195 Gln Gly Asp Pro Ile Ser Pro Phe Leu Phe Val Leu Cys Thr Glu Ala 220 215 Leu Ile His Ile Leu Gln Gln Ala Glu Asn Ser Lys Lys Val Ser Gly 235 230 Ile Gln Phe Asn Gly Ser Gly Pro Ser Val Asn His Leu Leu Phe Val 250 255 245 Asp Asp Thr Gln Leu Val Cys Arg Ala Thr Lys Ser Asp Cys Glu Gln 265 260 Met Met Leu Cys Leu Ser Gln Tyr Gly His Ile Ser Gly Gln Leu Ile 280 Asn Val Glu Lys Ser Ser Ile Thr Phe Gly Val Lys Val Asp Glu Asp 295 Thr Lys Gln Trp Ile Lys Asn Arg Ser Gly Ile His Leu Glu Gly Gly 315 310 Thr Gly Lys Tyr Leu Gly Leu Pro Glu Asn Leu Ser Gly Ser Lys Gln 330 325 Asp Leu Phe Gly Tyr Ile Lys Glu Lys Leu Gln Ser His Leu Ser Gly 345 340 Trp Tyr Asp Lys Thr Leu Ser Gln Gly Gly Lys Glu Ile Leu Leu Lys 360 Ser Ile Ala Leu Ala Leu Pro Val Tyr Ile Met Xaa Cys Phe Arg Leu 380 375 Pro Lys Gly Leu Cys Thr Lys Leu Thr Ser Val Met Met Asp Phe Trp 395 390 Trp Asn Ser Met Glu Phe Ser Asn Lys Ile His Trp Ile Gly Gly Lys 405 410 Lys Leu Thr Leu Pro Lys Ser Leu Gly Gly Phe Gly Phe Lys Asp Xaa 420 425 Gln Cys Phe Asn Gln Ala Leu Leu Ala Lys Gln Ala Trp Arg Leu Phe 445 440Ser Asp Ser Lys Ser Ile Val Ser Gln Ile Phe Lys Ser Arg Glu Leu 455 460 Leu Asn Gly Gly Leu Lys Arg Leu Ile Gly Asn Gly Glu Gln Thr Asn 475 470 Val Trp Ile Asp Lys Trp Leu Phe Asp Gly His Ser Gln Arg Pro Met 490 485 Asn Leu His Ser Leu Met Asn Ile His Met Lys Val Ser His Leu Ile 505 Asp Pro Leu Ser Arg Asn Trp Asn Leu Lys Lys Leu Thr Glu Leu Phe

							520					525			
II i o	Clu	515	Asp	Val	Gln			Met	His	Gln			Leu	Ile	Ser
	530					535					540				
545	Glu		Ser		550					555					200
Val	Lys	Ser	Gly	Tyr 565	Glu	Arg	Ser	Ser	Arg 570	Glu	Thr	Phe	Lys	Asn 575	Leu
Phe	Lys	Glu	Ala 580	Asp	Val	Tyr	Pro	Ser 585	Val	Asn	Leu	Leu	Phe 590	Asp	Lys
Val	Trp	Ser 595	Leu	Glu	Thr	Val	Pro 600	Lys	Ile	Lys	Val	Phe 605	Met	Trp	Lys
Ala	Leu 610	Lys	Gly	Ala	Leu	Ala 615		Glu	Asp	Ile	Leu 620	Arg	Ser	Arg	Gly
Ile 625	Arg	Thr	Ala	Asp	Gly 630		Leu	Phe	Cys	Lys 635	Glu	Glu	Ile	Glu	Thr 640
Ile	Asn	His	Leu	Leu 645	Phe	Gln	Cys	Pro	Phe 650	Ala	Arg	Gln	Val	Trp 655	Thr
Leu	Ser	Leu	Ile 660	Gln	Ala	Pro	Ala	Thr 665	Gly	Phe	Gly	Thr	Ser 670	Ile	Phe
Ser	Asn	Ile 675	Asn	His	Val	Ile	Gln 680	Asn	Ser	Gln	Asn	Phe 685	Gly	Ile	Pro
Arg	His 690	Met	Arg	Thr	Val	Ser 695		Trp	Leu	Leu	Trp 700	Glu	Ile	Trp	Lys
705	Arg		Lys		710					715					120
Ile			Lys	725					730					/35	
Val	Ile	Thr	Glu 740	Phe	Thr	Gly	Glu	Leu 745	Asp	Leu	Leu	Ser	Val 750	Leu	Arg
		755	Trp				760					765			
	770	Asn	Ser			775					780				
Gln 785	Met	Arg	Gly	Ile	Pro 790	Leu	Leu	Tyr	Val	Cys 795	Glu	Ala	Thr	Val	Thr 800
Glu	Ile	Ala	Leu	Gly 805	Leu	Gly	Gln	Ile	Ile 810	Ser	Leu	Asp	Phe	His 815	Asp
			820	Gln	Ile			825					830		Glu
		835	Arg	Ile			840					845			Gly
	850	Ala	a Leu			855					860				Tyr
Arg 865	Glr	n Pro	o Glu	ı Pro	Arg 870		Ile	Ile	Arg	g Gly 875	Pro	Thr	Asn	Asn	Leu 880
Thr	Arg			885	g Glu	ı Gly			890)				895	
			900)				905	,				910)	Ala
		91.	5				920)				925) Asp
	930	e Aro	g Ala			935	5				940)			ı Pro
	ı Ile	e Gl	y Th:	r Lei	Asr 950		ı Asr	n Pro	Pro	5 Sei 95	r Arg	y Ar	g Glr	n Glu	Ala 960
945 Sei	r Ar	g As:	n Se	r Ası 96	o Val	L Glr	n Pro) Phe	• Th:	r Gly) Ala	a Phe	e Gly 97	y Ala
Ası	n Va	l Pr	o Ar	g Va		l Glı	ı Val	l Gl <u>y</u> 985	/ Gl		s Sei	£ .			
						~ TD	NTO - 1	1150							

(2) INFORMATION FOR SEQ ID NO:1152: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2497 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2497

(D) OTHER INFORMATION: / Ceres Seq. ID 1597018 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152: taatagaact aaaaactctt tgagattttt ggttgatgag aatggcaatg aacacacttt 60 gaatagagag aaaggcaatg aacacacttt gaatagagag aaaggcaata ttgcttctgt 120 ttactttgag aatctgttca tgtcttctta tcctgctaac tctcagtcgg ctttggatgg 180 ttttaaaact cgagtttcag aggagatgaa tcaagaatta actcaagctg ttactgaatt 240 300 ggaaattcat tctgctagag tgctcctggt ccagatggtt cactgcctta ttcttccaga aaaatgggaa tgttgtcaag gatcagatta tatagagatt ctgggttttt ttgagacggg 360 ggttctgcct caagactgga atcatactca cctctgtttg attccaaaat ttactaaccc 420 tcagagaatg tccgatatta gaccaattag tctatgctca gtcttatata agattatctc 480 540 caaaatccta tctttcagat taaagaagca tctcccatct atcgtttcac cttctcaatc tgcgtttttt gctgaaaggt taatctctca caatattctc attgctcatg aaattgtgca 600 tagcttaaga actaatggca ggatctccaa agagtttatg gttttcaaaa ctgatatggc 660 720 taaagcctat gatagggtag aatggtcttt cttacaagaa attttggttg ctttgggctt caatgataaa tggaattctt ggattatggg ctgtgtgact tctgttacct attcagttct 780 gataaatggt caacattttg ggcatattac tcccgagaga ggtatcagac aaggtgatcc 840 catctctcca tttctgtttg tgctttgtac ggaagctctt attcatattc tacaacaagc 900 tgagaattct aagaaagtta gtggcattca gtttaatggt tctgggcctt cagttaatca 960 tttattgttt gttgatgaca ctcagttagt ctgtcgagca acaaaatcgg attgtgaaca 1020 1080 gatgatgctt tgtttatctc agtatgggca tatctcagga caactgatta atgtggagaa atcttcgatc acttttggag ttaaggtaga tgaggatact aaacagtgga tcaagaatcg 1140 ttctggtatt catctagaag gtgggacagg gaagtatctg gggttacctg agaacttgag 1200 tggttccaaa caggatttgt ttggctatat caaagaaaaa ttgcaatctc atttgtctgg 1260 ttggtatgat aaaactctct cacaaggagg caaggagatc ttgttaaagt caattgcttt 1320 1380 ggccttgcct gtgtatatta tgacntgttt taggcttcct aaaggtttat gcactaagct tacaagtgta atgatggatt tttggtggaa ctctatggaa ttttcaaata aaattcattg 1440 1500 gataggtggt aagaagttaa ctctgcctaa gagcttaggg ggttttggtt tcaaagactt ncaatgtttt aaccaggcac tattggccaa acaagcttgg agattattca gtgattcgaa 1560 gagcattgtt tctcaaatat tcaagagccg agaattatta aatggtggtc tgaagagact 1620 tataggaaat ggtgagcaaa ccaatgtgtg gattgataaa tggctgtttg atggacatag 1680 1740 tcaacgacct atgaatttgc attcattgat gaatattcat atgaagtcgt ggcagaaggt tgacaggtag ttcacgggag agctggatct cttgtctgtg ctacgaaggg aaccctggct 1800 ttacaatagt tggtttgtca cggctcatcg ttgggaggta aactcggctt ttgaatactt 1860 1920 gtctaacatt gagttgtggg ttcaaatgcg tgggattcct ctcctctatg tttgtgaagc cacagtgaca gagatagete ttggtttagg geaaattata teattggatt tteatgatge 1980 2040 tactacaacc caaatagctt ttattagagt gagaatccga tttgagatca ctgatcgtat 2100 aaggttette caaagaatta cetttgatte tggtgagaet gegetgataa ggetgaetea tcataggaat tactgccctt atcgacaacc tgagcctcgt tctatcattc gtggtcctac 2160 2220 caacaatctc actaggtcta gaagagaagg agtgtgtacc cgggatgaat atcatcgttc 2280 ttccctgaac tcccaatcac agatgtctga gaacgccttt ccagcaccta ttgaacctcc tccaagagtg gcagctcctc ctttgaatcc tgatgaattt agggctgctt attttccaga 2340 2400 aggcagagca ggttctttac caaatatagg aacattaaat cttaatcctc catctcgcag gcaagaggcg tcaagaaact ctgatgtaca accgtttacg ggtcctgcat ttggtgcaaa 2460

- (2) INFORMATION FOR SEQ ID NO:1153:
 - (i) SEQUENCE CHARACTERISTICS:

tgttcctcga gtggttgaag taggtgaatg ttcatga

- (A) LENGTH: 582 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..582

(D) OTHER INFORMATION: / Ceres Seq. ID 1597019 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153: Asn Arg Thr Lys Asn Ser Leu Arg Phe Leu Val Asp Glu Asn Gly Asn Glu His Thr Leu Asn Arg Glu Lys Gly Asn Glu His Thr Leu Asn Arg 25 Glu Lys Gly Asn Ile Ala Ser Val Tyr Phe Glu Asn Leu Phe Met Ser 40 Ser Tyr Pro Ala Asn Ser Gln Ser Ala Leu Asp Gly Phe Lys Thr Arg 55 Val Ser Glu Glu Met Asn Gln Glu Leu Thr Gln Ala Val Thr Glu Leu 70 75 Glu Ile His Ser Ala Arg Val Leu Leu Val Gln Met Val His Cys Leu 90 Ile Leu Pro Glu Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr Ile Glu 105 Ile Leu Gly Phe Phe Glu Thr Gly Val Leu Pro Gln Asp Trp Asn His 115 120 125 Thr His Leu Cys Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg Met Ser 135 140 Asp Ile Arg Pro Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile Ile Ser 145 150 155 160 Lys Ile Leu Ser Phe Arg Leu Lys Lys His Leu Pro Ser Ile Val Ser 165 170 175 Pro Ser Gln Ser Ala Phe Phe Ala Glu Arg Leu Ile Ser His Asn Ile 180 185 190 Leu Ile Ala His Glu Ile Val His Ser Leu Arg Thr Asn Gly Arg Ile 195 200 205 Ser Lys Glu Phe Met Val Phe Lys Thr Asp Met Ala Lys Ala Tyr Asp 210 215 220 Arg Val Glu Trp Ser Phe Leu Gln Glu Ile Leu Val Ala Leu Gly Phe 225 230 235 240 Asn Asp Lys Trp Asn Ser Trp Ile Met Gly Cys Val Thr Ser Val Thr 245 250 255 Tyr Ser Val Leu Ile Asn Gly Gln His Phe Gly His Ile Thr Pro Glu 265 270 Arg Gly Ile Arg Gln Gly Asp Pro Ile Ser Pro Phe Leu Phe Val Leu 275 280 285 Cys Thr Glu Ala Leu Ile His Ile Leu Gln Gln Ala Glu Asn Ser Lys 295 Lys Val Ser Gly Ile Gln Phe Asn Gly Ser Gly Pro Ser Val Asn His 305 310 315 320 Leu Leu Phe Val Asp Asp Thr Gln Leu Val Cys Arg Ala Thr Lys Ser 325 . 330 Asp Cys Glu Gln Met Met Leu Cys Leu Ser Gln Tyr Gly His Ile Ser 345 340 Gly Gln Leu Ile Asn Val Glu Lys Ser Ser Ile Thr Phe Gly Val Lys 360 365 Val Asp Glu Asp Thr Lys Gln Trp Ile Lys Asn Arg Ser Gly Ile His 375 Leu Glu Gly Gly Thr Gly Lys Tyr Leu Gly Leu Pro Glu Asn Leu Ser 390 395 Gly Ser Lys Gln Asp Leu Phe Gly Tyr Ile Lys Glu Lys Leu Gln Ser 405 410 His Leu Ser Gly Trp Tyr Asp Lys Thr Leu Ser Gln Gly Gly Lys Glu 425 Ile Leu Leu Lys Ser Ile Ala Leu Ala Leu Pro Val Tyr Ile Met Xaa 440 445 Cys Phe Arg Leu Pro Lys Gly Leu Cys Thr Lys Leu Thr Ser Val Met 455

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Met Asp Phe Trp Trp Asn Ser Met Glu Phe Ser Asn Lys Ile His Trp
                           475
Ile Gly Gly Lys Lys Leu Thr Leu Pro Lys Ser Leu Gly Gly Phe Gly
          485 490 495
Phe Lys Asp Xaa Gln Cys Phe Asn Gln Ala Leu Leu Ala Lys Gln Ala
        500 505 510
Trp Arg Leu Phe Ser Asp Ser Lys Ser Ile Val Ser Gln Ile Phe Lys
     515 520 525
Ser Arg Glu Leu Leu Asn Gly Gly Leu Lys Arg Leu Ile Gly Asn Gly
  530 535 540
Glu Gln Thr Asn Val Trp Ile Asp Lys Trp Leu Phe Asp Gly His Ser
   550 555 560
Gln Arg Pro Met Asn Leu His Ser Leu Met Asn Ile His Met Lys Ser
      565 570
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Trp Gln Lys Val Asp Arg 580

- (2) INFORMATION FOR SEQ ID NO:1154:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 amino acids
 - (B) TYPE: amino acid (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..536
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597020
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154: Met Ser Ser Tyr Pro Ala Asn Ser Gln Ser Ala Leu Asp Gly Phe Lys 10 Thr Arg Val Ser Glu Glu Met Asn Gln Glu Leu Thr Gln Ala Val Thr 25 20 Glu Leu Glu Ile His Ser Ala Arg Val Leu Leu Val Gln Met Val His 40 Cys Leu Ile Leu Pro Glu Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr 55 Ile Glu Ile Leu Gly Phe Phe Glu Thr Gly Val Leu Pro Gln Asp Trp 75 70 Asn His Thr His Leu Cys Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg 90 85 Met Ser Asp Ile Arg Pro Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile 100 105 Ile Ser Lys Ile Leu Ser Phe Arg Leu Lys Lys His Leu Pro Ser Ile 115 120 Val Ser Pro Ser Gln Ser Ala Phe Phe Ala Glu Arg Leu Ile Ser His 140 135 Asn Ile Leu Ile Ala His Glu Ile Val His Ser Leu Arg Thr Asn Gly 150 155 160 Arg Ile Ser Lys Glu Phe Met Val Phe Lys Thr Asp Met Ala Lys Ala 165 170 Tyr Asp Arg Val Glu Trp Ser Phe Leu Gln Glu Ile Leu Val Ala Leu 180 185 Gly Phe Asn Asp Lys Trp Asn Ser Trp Ile Met Gly Cys Val Thr Ser 200 Val Thr Tyr Ser Val Leu Ile Asn Gly Gln His Phe Gly His Ile Thr 220 215 Pro Glu Arg Gly Ile Arg Gln Gly Asp Pro Ile Ser Pro Phe Leu Phe 235 240 230 Val Leu Cys Thr Glu Ala Leu Ile His Ile Leu Gln Gln Ala Glu Asn 245 250 255 Ser Lys Lys Val Ser Gly Ile Gln Phe Asn Gly Ser Gly Pro Ser Val

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265
        260
Asn His Leu Leu Phe Val Asp Asp Thr Gln Leu Val Cys Arg Ala Thr
    275 280
Lys Ser Asp Cys Glu Gln Met Met Leu Cys Leu Ser Gln Tyr Gly His
       295
Ile Ser Gly Gln Leu Ile Asn Val Glu Lys Ser Ser Ile Thr Phe Gly
305 310 315 320
Val Lys Val Asp Glu Asp Thr Lys Gln Trp Ile Lys Asn Arg Ser Gly
           325 330
Ile His Leu Glu Gly Gly Thr Gly Lys Tyr Leu Gly Leu Pro Glu Asn
                       345 350
Leu Ser Gly Ser Lys Gln Asp Leu Phe Gly Tyr Ile Lys Glu Lys Leu
                   360 365
Gln Ser His Leu Ser Gly Trp Tyr Asp Lys Thr Leu Ser Gln Gly Gly
370 375
                     380
Lys Glu Ile Leu Leu Lys Ser Ile Ala Leu Ala Leu Pro Val Tyr Ile
385 390 395
Met Xaa Cys Phe Arg Leu Pro Lys Gly Leu Cys Thr Lys Leu Thr Ser
           405 410 415
Val Met Met Asp Phe Trp Trp Asn Ser Met Glu Phe Ser Asn Lys Ile
        420 425 430
His Trp Ile Gly Gly Lys Lys Leu Thr Leu Pro Lys Ser Leu Gly Gly
     435 440 445
Phe Gly Phe Lys Asp Xaa Gln Cys Phe Asn Gln Ala Leu Leu Ala Lys
 450 455
Gln Ala Trp Arg Leu Phe Ser Asp Ser Lys Ser Ile Val Ser Gln Ile
465 470 475 480
Phe Lys Ser Arg Glu Leu Leu Asn Gly Gly Leu Lys Arg Leu Ile Gly
           485 490 495
Asn Gly Glu Gln Thr Asn Val Trp Ile Asp Lys Trp Leu Phe Asp Gly
      500 505 510
His Ser Gln Arg Pro Met Asn Leu His Ser Leu Met Asn Ile His Met
  515 520
Lys Ser Trp Gln Lys Val Asp Arg
      535
(2) INFORMATION FOR SEQ ID NO:1155:
   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 514 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..514
        (D) OTHER INFORMATION: / Ceres Seq. ID 1597021
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:
Met Asn Gln Glu Leu Thr Gln Ala Val Thr Glu Leu Glu Ile His Ser
```

10

90

60

75

Ala Arg Val Leu Leu Val Gln Met Val His Cys Leu Ile Leu Pro Glu 25

Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr Ile Glu Ile Leu Gly Phe 40 Phe Glu Thr Gly Val Leu Pro Gln Asp Trp Asn His Thr His Leu Cys

Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg Met Ser Asp Ile Arg Pro

Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile Ile Ser Lys Ile Leu Ser

Phe Arg Leu Lys Lys His Leu Pro Ser Ile Val Ser Pro Ser Gln Ser 105

55

70

85

20

Ala Phe Phe Ala Glu Arg Leu Ile Ser His Asn Ile Leu Ile Ala His 120 115 Glu Ile Val His Ser Leu Arg Thr Asn Gly Arg Ile Ser Lys Glu Phe 130 135 Met Val Phe Lys Thr Asp Met Ala Lys Ala Tyr Asp Arg Val Glu Trp 150 155 Ser Phe Leu Gln Glu Ile Leu Val Ala Leu Gly Phe Asn Asp Lys Trp 165 175 170 Asn Ser Trp Ile Met Gly Cys Val Thr Ser Val Thr Tyr Ser Val Leu 180 185 Ile Asn Gly Gln His Phe Gly His Ile Thr Pro Glu Arg Gly Ile Arg 195 200 Gln Gly Asp Pro Ile Ser Pro Phe Leu Phe Val Leu Cys Thr Glu Ala 210 215 220 Leu Ile His Ile Leu Gln Gln Ala Glu Asn Ser Lys Lys Val Ser Gly 235 230 Ile Gln Phe Asn Gly Ser Gly Pro Ser Val Asn His Leu Leu Phe Val 250 245 Asp Asp Thr Gln Leu Val Cys Arg Ala Thr Lys Ser Asp Cys Glu Gln 270 260 265 Met Met Leu Cys Leu Ser Gln Tyr Gly His Ile Ser Gly Gln Leu Ile 285 275 280 Asn Val Glu Lys Ser Ser Ile Thr Phe Gly Val Lys Val Asp Glu Asp 300 295 Thr Lys Gln Trp Ile Lys Asn Arg Ser Gly Ile His Leu Glu Gly Gly 310 315 Thr Gly Lys Tyr Leu Gly Leu Pro Glu Asn Leu Ser Gly Ser Lys Gln 325 330 335 Asp Leu Phe Gly Tyr Ile Lys Glu Lys Leu Gln Ser His Leu Ser Gly 345 340 Trp Tyr Asp Lys Thr Leu Ser Gln Gly Gly Lys Glu Ile Leu Leu Lys 365 360 355 Ser Ile Ala Leu Ala Leu Pro Val Tyr Ile Met Xaa Cys Phe Arg Leu 370 375 380 Pro Lys Gly Leu Cys Thr Lys Leu Thr Ser Val Met Met Asp Phe Trp 395 390 Trp Asn Ser Met Glu Phe Ser Asn Lys Ile His Trp Ile Gly Gly Lys 405 410 Lys Leu Thr Leu Pro Lys Ser Leu Gly Gly Phe Gly Phe Lys Asp Xaa 425 420 Gln Cys Phe Asn Gln Ala Leu Leu Ala Lys Gln Ala Trp Arg Leu Phe 440 Ser Asp Ser Lys Ser Ile Val Ser Gln Ile Phe Lys Ser Arg Glu Leu 460 455 Leu Asn Gly Gly Leu Lys Arg Leu Ile Gly Asn Gly Glu Gln Thr Asn 475 470 Val Trp Ile Asp Lys Trp Leu Phe Asp Gly His Ser Gln Arg Pro Met 485 490 Asn Leu His Ser Leu Met Asn Ile His Met Lys Ser Trp Gln Lys Val 500 505

(2) INFORMATION FOR SEQ ID NO:1156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

Asp Arg

(A) NAME/KEY: -

- (B) LOCATION: 1..525
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597022
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

gtgagaatat tttcgttgat ggatgaacca atcttagatg caatccgtga gaggctgaaa cagaggacat acatagggag tagcacagtg ttgcaccgtg gaggactagt tgagaaaatg 120 gtattcatag tgagaggtga gatggagagc attggagaag atggttctgt tcttccatta 180 tatgaaggeg atgtttgtgg tgaagaacte eteaettggt geetegaaeg etettetgta 240 aaccccgatg ggacgaggat aaggatgcca tcaaagggat tgcttagtag cagaaatgta 300 aggtgtgtga caaatgtgga ggcgttttcg ctgagtgtag ccgatctgga agacgtaacg 360 agcttgtttt cgagattctt gaggagtcat agagtccaag gagccataag gtacgactct 420 ccatattgga ggctacgagc ggctaggcag attcaagtgg cgtggagata ccgtaggaga 480 cggcttcata gattatgcac tectcagtet agttatagee tttag

- (2) INFORMATION FOR SEQ ID NO:1157:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..174
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597023
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:
- Val Arg Ile Phe Ser Leu Met Asp Glu Pro Ile Leu Asp Ala Ile Arg
- Glu Arg Leu Lys Gln Arg Thr Tyr Ile Gly Ser Ser Thr Val Leu His 20 25 30
- Arg Gly Gly Leu Val Glu Lys Met Val Phe Ile Val Arg Gly Glu Met 35 40 45
- Glu Ser Ile Gly Glu Asp Gly Ser Val Leu Pro Leu Tyr Glu Gly Asp 50 55 60
- Val Cys Gly Glu Glu Leu Leu Thr Trp Cys Leu Glu Arg Ser Ser Val 65 70 75 80
- Asn Pro Asp Gly Thr Arg Ile Arg Met Pro Ser Lys Gly Leu Leu Ser 85 90 95
 Ser Arg Asn Val Arg Cys Val Thr Asn Val Glu Ala Phe Ser Leu Ser
- 100 105 110

 Val Ala Asp Leu Glu Asp Val Thr Ser Leu Phe Ser Arg Phe Leu Arg
- 115 120 125

 Ser His Arg Val Gln Gly Ala Ile Arg Tyr Asp Ser Pro Tyr Trp Arg
- Ser His Arg Val Gln Gly Ala He Arg Tyr Asp Ser Pro Tyr Hp Arg
 130
 140
- Leu Arg Ala Ala Arg Gln Ile Gln Val Ala Trp Arg Tyr Arg Arg Arg 145 150 155 160
- Arg Leu His Arg Leu Cys Thr Pro Gln Ser Ser Tyr Ser Leu 165 170
- (2) INFORMATION FOR SEQ ID NO:1158:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..168
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597024
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:
- Met Asp Glu Pro Ile Leu Asp Ala Ile Arg Glu Arg Leu Lys Gln Arg 1 5 10 15 Thr Tyr Ile Gly Ser Ser Thr Val Leu His Arg Gly Gly Leu Val Glu

25 Lys Met Val Phe Ile Val Arg Gly Glu Met Glu Ser Ile Gly Glu Asp 35 40 Gly Ser Val Leu Pro Leu Tyr Glu Gly Asp Val Cys Gly Glu Glu Leu 55 Leu Thr Trp Cys Leu Glu Arg Ser Ser Val Asn Pro Asp Gly Thr Arg 75 Ile Arg Met Pro Ser Lys Gly Leu Leu Ser Ser Arg Asn Val Arg Cys 90 Val Thr Asn Val Glu Ala Phe Ser Leu Ser Val Ala Asp Leu Glu Asp 100 105 110 Val Thr Ser Leu Phe Ser Arg Phe Leu Arg Ser His Arg Val Gln Gly 115 120 125 Ala Ile Arg Tyr Asp Ser Pro Tyr Trp Arg Leu Arg Ala Ala Arg Gln 130 135 140 Ile Gln Val Ala Trp Arg Tyr Arg Arg Arg Leu His Arg Leu Cys 150 155 Thr Pro Gln Ser Ser Tyr Ser Leu 165

- (2) INFORMATION FOR SEQ ID NO:1159:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597025
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:
- Met Val Phe Ile Val Arg Gly Glu Met Glu Ser Ile Gly Glu Asp Gly 1 5 10 15

Ser Val Leu Pro Leu Tyr Glu Gly Asp Val Cys Gly Glu Glu Leu Leu 20 25 30

Thr Trp Cys Leu Glu Arg Ser Ser Val Asn Pro Asp Gly Thr Arg Ile 35 40 45

Arg Met Pro Ser Lys Gly Leu Leu Ser Ser Arg Asn Val Arg Cys Val
50 55 60

Thr Asn Val Glu Ala Phe Ser Leu Ser Val Ala Asp Leu Glu Asp Val 65 70 75 80

Thr Ser Leu Phe Ser Arg Phe Leu Arg Ser His Arg Val Gln Gly Ala 85 90 95

Ile Arg Tyr Asp Ser Pro Tyr Trp Arg Leu Arg Ala Ala Arg Gln Ile 100 105 110 Gln Val Ala Trp Arg Tyr Arg Arg Arg Arg Leu His Arg Leu Cys Thr

115 120 125

Pro Gln Ser Ser Tyr Ser Leu 130 135

- (2) INFORMATION FOR SEQ ID NO:1160:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..669
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597076
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

a+~~~~~~~~	aagtgatcct	tctcaatttc	taaccaaaca	tattcagaat	gaggacgatg	60
alggeageeg	aggagaaagg	agtasagtat	ggtegage	aagaggatgt	gatcaataac	120
ategegttag	tgctactaga	agtgaagtat	attacasas	caatccccct	tctcatccac	180
aagagtccct	tgetaetaga	gatgaateeg	acceacaaga	atatagaga	aatttaatat	240
aatggtaaac	cggttcttga	atcccttatc	CadalCCadl	atacayacya	atttaggee	300
gacaacaact	catttctccc	ttctgatcct	taccatagag	ClCaagettt	accetgggee	360
gatttcatcg	acaagaagga	acagttgtat	gtttgtggga	ggaagactag	ggcaacgaaa	420
ggtgaggagc	tagaagcagc	caataaagag	tttattgaaa	tactcaagac	tetteaatgt	12.0
gagctcggag	aaaaacctta	ctttggcggc	gataaattcg	ggtttgtaga	cattgtcctg	480
attggattct	atagttggtt	tccagcatac	cagaagtttg	gtaacttcag	catcgaacca	540
gagtgtttga	agctgattgc	ttggggaaaa	agatgtatgc	aaagagagag	tgtggctaaa	600
actttaccta	attctgagaa	agttgttgga	tacgttttac	agcttaagaa	gttatatgga	660
attgagtaa						

- (2) INFORMATION FOR SEQ ID NO:1161:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..222
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597077
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161: Met Ala Ala Glu Val Ile Leu Leu Gly Phe Trp Pro Ser Met Phe Gly 10 Met Arg Thr Met Ile Ala Leu Glu Glu Lys Gly Val Lys Tyr Glu Tyr 30 25 20 Arg Glu Glu Asp Val Ile Asn Asn Lys Ser Pro Leu Leu Glu Met 40 Asn Pro Ile His Lys Thr Ile Pro Val Leu Ile His Asn Gly Lys Pro 55 Val Leu Glu Ser Leu Ile Gln Ile Gln Tyr Ile Asp Glu Val Trp Ser 75 70 Asp Asn Asn Ser Phe Leu Pro Ser Asp Pro Tyr His Arg Ala Gln Ala 90 85 Leu Phe Trp Ala Asp Phe Ile Asp Lys Lys Glu Gln Leu Tyr Val Cys 100 105 Gly Arg Lys Thr Arg Ala Thr Lys Gly Glu Glu Leu Glu Ala Ala Asn 125 120 115 Lys Glu Phe Ile Glu Ile Leu Lys Thr Leu Gln Cys Glu Leu Gly Glu 140 135 Lys Pro Tyr Phe Gly Gly Asp Lys Phe Gly Phe Val Asp Ile Val Leu 155 150 Ile Gly Phe Tyr Ser Trp Phe Pro Ala Tyr Gln Lys Phe Gly Asn Phe 165 170 Ser Ile Glu Pro Glu Cys Leu Lys Leu Ile Ala Trp Gly Lys Arg Cys 190 180 185 Met Gln Arg Glu Ser Val Ala Lys Ala Leu Pro Asp Ser Glu Lys Val 200 205 Val Gly Tyr Val Leu Gln Leu Lys Lys Leu Tyr Gly Ile Glu 220 215 210
- (2) INFORMATION FOR SEQ ID NO:1162:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1597079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162: Met Phe Gly Met Arg Thr Met Ile Ala Leu Glu Glu Lys Gly Val Lys 10 Tyr Glu Tyr Arg Glu Glu Asp Val Ile Asn Asn Lys Ser Pro Leu Leu 30 25 Leu Glu Met Asn Pro Ile His Lys Thr Ile Pro Val Leu Ile His Asn 4.5 40 Gly Lys Pro Val Leu Glu Ser Leu Ile Gln Ile Gln Tyr Ile Asp Glu 55 Val Trp Ser Asp Asn Asn Ser Phe Leu Pro Ser Asp Pro Tyr His Arg 75 70 Ala Gln Ala Leu Phe Trp Ala Asp Phe Ile Asp Lys Lys Glu Gln Leu 90 Tyr Val Cys Gly Arg Lys Thr Arg Ala Thr Lys Gly Glu Glu Leu Glu 110 105 100 Ala Ala Asn Lys Glu Phe Ile Glu Ile Leu Lys Thr Leu Gln Cys Glu 125 Leu Gly Glu Lys Pro Tyr Phe Gly Gly Asp Lys Phe Gly Phe Val Asp 140 135 130 Ile Val Leu Ile Gly Phe Tyr Ser Trp Phe Pro Ala Tyr Gln Lys Phe 155 150 Gly Asn Phe Ser Ile Glu Pro Glu Cys Leu Lys Leu Ile Ala Trp Gly 175 170 165 Lys Arg Cys Met Gln Arg Glu Ser Val Ala Lys Ala Leu Pro Asp Ser 190 185 180 Glu Lys Val Val Gly Tyr Val Leu Gln Leu Lys Lys Leu Tyr Gly Ile 200 Glu

- (2) INFORMATION FOR SEQ ID NO:1163:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1786
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597092
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

60 tctacagagg ctgatttttg atagacctcc agaaggaatt aggaaaatag tactggccac caatatggct gagacaagta tcaccatcaa tgatgttgta tatgtgattg attgtgggaa 120 agcaaaagaa acatettatg atgegettaa caataceeet tgtetgette catettggat 180 ttcaaaggca gctgctcgcc aaagaagagg aagagctggt cgtgttatgc ctggagaatg 240 ttatcacctc tatcctagat gtgtctacga agcttttgct gactaccagc agccggaact 300 360 tctaaggacg ccgttgcagt ctctgtgttt acaaattaaa agcctaggac ttggaagcat ttcggagttc ctctccaggg cattgcaacc tcctgaagca ttatcggtcc aaaatgctgt 420 480 tgagtatota aaaatcattg gggctottga tgacgatgaa aatttaacac otttaggaac tcataatatg ctctatgcag ggaaaaatct gtcaatgctt cctgtggagc ctaaacttgg 540 aaaaatgott attttagggg ctatottcaa ctgtotagat ccagtaatga cagttgttgc 600 tggtcttagt gtcagagacc cattccttat gccatttgac aaaaaagatc tagcagaaac 660 agcaaggtcc aagttctctg gccgtgatta cagtgatcat ttgacattgg ttcgagcata 720 caatggttgg aaagatgctg aaagaacaca ttctggttac gactattgct ggaagaactt 780 tctctcttct caaactctta aggccatgga ctctatgcgg aaacaattct tcaatctcct 840 caaggaggct tctctgattg ataacattga aggttgcagt aagctgagtc atgatgaaca 900 tcttgtacgc gcaatcattt gtgctggcat gttccctgga gtctgttctg ttgttttta 960 ccctacaata aacaattctc cctcgcagaa taaggaaaag tcaattacgc tcaagacaat 1020 ggaagatgga caagtgcttc tatacncgag ttctgtgaat ggcaatgtac caatgattcc 1080 cttcccttgg ctagtcttca acgacaaagt gaaagttaat tctgtgtttc tgcgagactc tactgctgta tctgactctg ttcttctttt gtttggagat aaaatctctt ccggtggatt tgatggtcat ctcaaaatgc ttggaggata tctggagttt ttcatgaaac ctactttagc 1320 atatacatac ctttcgttaa aaagagagct cgacgaactt attcagaata agcttgtgaa tccaaaactt gatattcaac tatacgacaa acttatgact gccattagat tacttgtgtc agaggaccaa tgtgagggca gattcgtcta tggccggaaa gctctaagcc ctacaccaac aaagaagtta aaagatgtag gggctcagct tcagaacagc ggtggtgaaa acaacaagaa 1560 1620 gccatgtggt agtaagaaaa atgcagagaa ggatgcagct catgaggctt tgttgtggtt 1680 acaaggcgag tccaagtcaa gcctgaatga tcttaaccac atgtcaatgc tcttaaagaa 1740 gaacaaaagt aaaaaccacg ccaaggcatc aactaaatgg ggttaa

- (2) INFORMATION FOR SEQ ID NO:1164:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..594
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164: Leu Gln Arg Leu Ile Phe Asp Arg Pro Pro Glu Gly Ile Arg Lys Ile 10 Val Leu Ala Thr Asn Met Ala Glu Thr Ser Ile Thr Ile Asn Asp Val 25 Val Tyr Val Ile Asp Cys Gly Lys Ala Lys Glu Thr Ser Tyr Asp Ala 40 Leu Asn Asn Thr Pro Cys Leu Leu Pro Ser Trp Ile Ser Lys Ala Ala 60 55 Ala Arg Gln Arg Arg Gly Arg Ala Gly Arg Val Met Pro Gly Glu Cys 75 70 Tyr His Leu Tyr Pro Arg Cys Val Tyr Glu Ala Phe Ala Asp Tyr Gln 90 8.5 Gln Pro Glu Leu Leu Arg Thr Pro Leu Gln Ser Leu Cys Leu Gln Ile 110 105 100 Lys Ser Leu Gly Leu Gly Ser Ile Ser Glu Phe Leu Ser Arg Ala Leu 120 125 115 Gln Pro Pro Glu Ala Leu Ser Val Gln Asn Ala Val Glu Tyr Leu Lys 135 140 Ile Ile Gly Ala Leu Asp Asp Asp Glu Asn Leu Thr Pro Leu Gly Thr 155 150 His Asn Met Leu Tyr Ala Gly Lys Asn Leu Ser Met Leu Pro Val Glu 170 175 165 Pro Lys Leu Gly Lys Met Leu Ile Leu Gly Ala Ile Phe Asn Cys Leu 185 180 Asp Pro Val Met Thr Val Val Ala Gly Leu Ser Val Arg Asp Pro Phe 200 Leu Met Pro Phe Asp Lys Lys Asp Leu Ala Glu Thr Ala Arg Ser Lys 220 215 Phe Ser Gly Arg Asp Tyr Ser Asp His Leu Thr Leu Val Arg Ala Tyr 235 230 Asn Gly Trp Lys Asp Ala Glu Arg Thr His Ser Gly Tyr Asp Tyr Cys 250 245 Trp Lys Asn Phe Leu Ser Ser Gln Thr Leu Lys Ala Met Asp Ser Met 265 2.60 Arg Lys Gln Phe Phe Asn Leu Leu Lys Glu Ala Ser Leu Ile Asp Asn 280 Ile Glu Gly Cys Ser Lys Leu Ser His Asp Glu His Leu Val Arg Ala

300 295 290 Ile Ile Cys Ala Gly Met Phe Pro Gly Val Cys Ser Val Val Phe Tyr 310 315 Pro Thr Ile Asn Asn Ser Pro Ser Gln Asn Lys Glu Lys Ser Ile Thr 325 330 Leu Lys Thr Met Glu Asp Gly Gln Val Leu Leu Tyr Xaa Ser Ser Val 340 345 350 Asn Gly Asn Val Pro Met Ile Pro Phe Pro Trp Leu Val Phe Asn Asp 355 360 365 Lys Val Lys Val Asn Ser Val Phe Leu Arg Asp Ser Thr Ala Val Ser 370 375 380 Asp Ser Val Leu Leu Phe Gly Asp Lys Ile Ser Ser Gly Gly Phe 385 390 395 Asp Gly His Leu Lys Met Leu Gly Gly Tyr Leu Glu Phe Phe Met Lys 405 410 415 Pro Thr Leu Ala Tyr Thr Tyr Leu Ser Leu Lys Arg Glu Leu Asp Glu 425 430 420 Leu Ile Gln Asn Lys Leu Val Asn Pro Lys Leu Asp Ile Gln Leu Tyr 440 445 Asp Lys Leu Met Thr Ala Ile Arg Leu Leu Val Ser Glu Asp Gln Cys 455 460 Glu Gly Arg Phe Val Tyr Gly Arg Lys Ala Leu Ser Pro Thr Pro Thr 465 470 475 480 Lys Lys Leu Lys Asp Val Gly Ala Gln Leu Gln Asn Ser Gly Gly Glu 490 485 Asn Asn Lys Asn Gln Leu Gln Thr Leu Leu Ala Arg Ala Gly His Gly 505 500 Ser Pro Val Tyr Lys Thr Arg Gln Leu Lys Asn Asn Gln Phe Arg Ser 520 525 Met Val Thr Phe Asn Gly Leu Asp Phe Met Gly Lys Pro Cys Gly Ser 530 535 540 Lys Lys Asn Ala Glu Lys Asp Ala Ala His Glu Ala Leu Leu Trp Leu 550 555 560 Gln Gly Glu Ser Lys Ser Ser Leu Asn Asp Leu Asn His Met Ser Met 565 570 575 Leu Leu Lys Lys Asn Lys Ser Lys Asn His Ala Lys Ala Ser Thr Lys 585 580 Trp Gly

- (2) INFORMATION FOR SEQ ID NO:1165:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..573
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

Met Ala Glu Thr Ser Ile Thr Ile Asn Asp Val Val Tyr Val Ile Asp

1 10 15

15 The Grant Thr Bro

Cys Gly Lys Ala Lys Glu Thr Ser Tyr Asp Ala Leu Asn Asn Thr Pro 20 25 30

Cys Leu Leu Pro Ser Trp Ile Ser Lys Ala Ala Ala Arg Gln Arg Arg

Gly Arg Ala Gly Arg Val Met Pro Gly Glu Cys Tyr His Leu Tyr Pro 50 55 60

Arg Cys Val Tyr Glu Ala Phe Ala Asp Tyr Gln Gln Pro Glu Leu Leu 65 70 75 80

Arg Thr Pro Leu Gln Ser Leu Cys Leu Gln Ile Lys Ser Leu Gly Leu 90 85 Gly Ser Ile Ser Glu Phe Leu Ser Arg Ala Leu Gln Pro Pro Glu Ala 100 105 Leu Ser Val Gln Asn Ala Val Glu Tyr Leu Lys Ile Ile Gly Ala Leu 120 115 Asp Asp Asp Glu Asn Leu Thr Pro Leu Gly Thr His Asn Met Leu Tyr 135 Ala Gly Lys Asn Leu Ser Met Leu Pro Val Glu Pro Lys Leu Gly Lys 150 155 Met Leu Ile Leu Gly Ala Ile Phe Asn Cys Leu Asp Pro Val Met Thr 165 170 175 Val Val Ala Gly Leu Ser Val Arg Asp Pro Phe Leu Met Pro Phe Asp 180 185 Lys Lys Asp Leu Ala Glu Thr Ala Arg Ser Lys Phe Ser Gly Arg Asp 200 Tyr Ser Asp His Leu Thr Leu Val Arg Ala Tyr Asn Gly Trp Lys Asp 220 215 Ala Glu Arg Thr His Ser Gly Tyr Asp Tyr Cys Trp Lys Asn Phe Leu 235 230 Ser Ser Gln Thr Leu Lys Ala Met Asp Ser Met Arg Lys Gln Phe Phe 245 250 Asn Leu Leu Lys Glu Ala Ser Leu Ile Asp Asn Ile Glu Gly Cys Ser 260 265 Lys Leu Ser His Asp Glu His Leu Val Arg Ala Ile Ile Cys Ala Gly 280 285 Met Phe Pro Gly Val Cys Ser Val Val Phe Tyr Pro Thr Ile Asn Asn 300 295 Ser Pro Ser Gln Asn Lys Glu Lys Ser Ile Thr Leu Lys Thr Met Glu 310 315 Asp Gly Gln Val Leu Leu Tyr Xaa Ser Ser Val Asn Gly Asn Val Pro 325 330 Met Ile Pro Phe Pro Trp Leu Val Phe Asn Asp Lys Val Lys Val Asn 350 340 345 Ser Val Phe Leu Arg Asp Ser Thr Ala Val Ser Asp Ser Val Leu Leu 360 355 Leu Phe Gly Asp Lys Ile Ser Ser Gly Gly Phe Asp Gly His Leu Lys 375 380 Met Leu Gly Gly Tyr Leu Glu Phe Phe Met Lys Pro Thr Leu Ala Tyr 390 395 Thr Tyr Leu Ser Leu Lys Arg Glu Leu Asp Glu Leu Ile Gln Asn Lys 410 415 405 Leu Val Asn Pro Lys Leu Asp Ile Gln Leu Tyr Asp Lys Leu Met Thr 425 430 420 Ala Ile Arg Leu Leu Val Ser Glu Asp Gln Cys Glu Gly Arg Phe Val 435 440 Tyr Gly Arg Lys Ala Leu Ser Pro Thr Pro Thr Lys Lys Leu Lys Asp 455 Val Gly Ala Gln Leu Gln Asn Ser Gly Gly Glu Asn Asn Lys Asn Gln 470 475 Leu Gln Thr Leu Leu Ala Arg Ala Gly His Gly Ser Pro Val Tyr Lys 490 495 485 Thr Arg Gln Leu Lys Asn Asn Gln Phe Arg Ser Met Val Thr Phe Asn 505 500 Gly Leu Asp Phe Met Gly Lys Pro Cys Gly Ser Lys Lys Asn Ala Glu 515 520 Lys Asp Ala Ala His Glu Ala Leu Leu Trp Leu Gln Gly Glu Ser Lys 535 Ser Ser Leu Asn Asp Leu Asn His Met Ser Met Leu Leu Lys Lys Asn 550 555 Lys Ser Lys Asn His Ala Lys Ala Ser Thr Lys Trp Gly

570 565 (2) INFORMATION FOR SEQ ID NO:1166: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 519 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..519 (D) OTHER INFORMATION: / Ceres Seq. ID 1597095 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166: Met Pro Gly Glu Cys Tyr His Leu Tyr Pro Arg Cys Val Tyr Glu Ala 5 Phe Ala Asp Tyr Gln Gln Pro Glu Leu Leu Arg Thr Pro Leu Gln Ser Leu Cys Leu Gln Ile Lys Ser Leu Gly Leu Gly Ser Ile Ser Glu Phe 40 Leu Ser Arg Ala Leu Gln Pro Pro Glu Ala Leu Ser Val Gln Asn Ala 55 Val Glu Tyr Leu Lys Ile Ile Gly Ala Leu Asp Asp Asp Glu Asn Leu 70 75 80 Thr Pro Leu Gly Thr His Asn Met Leu Tyr Ala Gly Lys Asn Leu Ser 85 90 95 Met Leu Pro Val Glu Pro Lys Leu Gly Lys Met Leu Ile Leu Gly Ala 100 105 Ile Phe Asn Cys Leu Asp Pro Val Met Thr Val Val Ala Gly Leu Ser 115 120 Val Arg Asp Pro Phe Leu Met Pro Phe Asp Lys Lys Asp Leu Ala Glu 130 135 140 Thr Ala Arg Ser Lys Phe Ser Gly Arg Asp Tyr Ser Asp His Leu Thr 150 155 160 Leu Val Arg Ala Tyr Asn Gly Trp Lys Asp Ala Glu Arg Thr His Ser 165 170 175 Gly Tyr Asp Tyr Cys Trp Lys Asn Phe Leu Ser Ser Gln Thr Leu Lys 180 185 Ala Met Asp Ser Met Arg Lys Gln Phe Phe Asn Leu Leu Lys Glu Ala 195 200 Ser Leu Ile Asp Asn Ile Glu Gly Cys Ser Lys Leu Ser His Asp Glu 215 220 His Leu Val Arg Ala Ile Ile Cys Ala Gly Met Phe Pro Gly Val Cys 230 235 240 Ser Val Val Phe Tyr Pro Thr Ile Asn Asn Ser Pro Ser Gln Asn Lys 245 250 Glu Lys Ser Ile Thr Leu Lys Thr Met Glu Asp Gly Gln Val Leu Leu 260 265 270 Tyr Xaa Ser Ser Val Asn Gly Asn Val Pro Met Ile Pro Phe Pro Trp 280 285 Leu Val Phe Asn Asp Lys Val Lys Val Asn Ser Val Phe Leu Arg Asp 295 300 Ser Thr Ala Val Ser Asp Ser Val Leu Leu Leu Phe Gly Asp Lys Ile 310 315 Ser Ser Gly Gly Phe Asp Gly His Leu Lys Met Leu Gly Gly Tyr Leu 325 330 335 Glu Phe Phe Met Lys Pro Thr Leu Ala Tyr Thr Tyr Leu Ser Leu Lys 345 350 Arg Glu Leu Asp Glu Leu Ile Gln Asn Lys Leu Val Asn Pro Lys Leu

355 360 365

375

Asp Ile Gln Leu Tyr Asp Lys Leu Met Thr Ala Ile Arg Leu Leu Val

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Ser Glu Asp Gln Cys Glu Gly Arg Phe Val Tyr Gly Arg Lys Ala Leu
                                        395
                    390
Ser Pro Thr Pro Thr Lys Lys Leu Lys Asp Val Gly Ala Gln Leu Gln
                                    410
                405
Asn Ser Gly Gly Glu Asn Asn Lys Asn Gln Leu Gln Thr Leu Leu Ala
                                425
            420
Arg Ala Gly His Gly Ser Pro Val Tyr Lys Thr Arg Gln Leu Lys Asn
                            440
        435
Asn Gln Phe Arg Ser Met Val Thr Phe Asn Gly Leu Asp Phe Met Gly
                                            460
                        455
Lys Pro Cys Gly Ser Lys Lys Asn Ala Glu Lys Asp Ala Ala His Glu
                                        475
                   470
Ala Leu Leu Trp Leu Gln Gly Glu Ser Lys Ser Ser Leu Asn Asp Leu
                                    490
                485
Asn His Met Ser Met Leu Leu Lys Lys Asn Lys Ser Lys Asn His Ala
                                505
            500
Lys Ala Ser Thr Lys Trp Gly
        515
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- (2) INFORMATION FOR SEQ ID NO:1167:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 780 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..780
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597129
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167: 60 atgcaaacaa taataatttc tccacttgtt tctcatcgtc tctgtcttgc tcgtgctgtt cettgcaacc gtettetcaa caaccaccac egtgeteete ettegateeg eetetcaaac 120 caccgttcaa ccacctcact ccgcctcttc tcctccgccg ggtctctctg tgtttgcaaa 180 240 tctgacgccg agtattttgc taaagcagca gccagtcggg acagtgaaat ggcgactgaa 300 gatgtgcaag atcccagaat cgctaagatt gcctcttcca ttagagtcat ccccgacttc 360 cctaaaccag gaatcatgtt tcaggacata acgacgcttc ttctcgacac tgaggccttt aaggatacta ttgctttgtt tgttgataga tacaaagata aaggcatatc tgttgttgca 420 ggtgttgaag ctagaggttt catttttggc cctcctattg cgttggctat tggtgccaaa 480 tttgttccca tgaggacgcc caagaagcta cctgggaagg ttatttcgga ggagtattcg 540 ttggagtatg gaccagatac gattgagatg cacgtaggtg cagtagagcc tggtgagcgt 600 gctattatta ttgatgncct cattgccacg ggtgggactc tcgctgctgc aatccgacta 660 cttgaacgag taggagtgna gattgttgaa tgtgcttgcg taattgagtt accagagctt 720 aagggaaagg agaaactagg agagacgtcg ctatttgttc ttgtaaagtc ggctgcttaa 780
- (2) INFORMATION FOR SEQ ID NO:1168:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..259
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597130
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

Met Gln Thr Ile Ile Ile Ser Pro Leu Val Ser His Arg Leu Cys Leu 1 5 5 5 10 10 15 Ala Arg Ala Val Pro Cys Asn Arg Leu Leu Asn Asn His His Arg Ala 20 25 30 30 Pro Pro Ser Ile Arg Leu Ser Asn His Arg Ser Thr Thr Ser Leu Arg

40 35 Leu Phe Ser Ser Ala Gly Ser Leu Cys Val Cys Lys Ser Asp Ala Glu 55 Tyr Phe Ala Lys Ala Ala Ala Ser Arg Asp Ser Glu Met Ala Thr Glu 75 Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser Ser Ile Arg Val 85 Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln Asp Ile Thr Thr 100 105 110 Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile Ala Leu Phe Val 115 120 125 Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala Gly Val Glu Ala 130 135 140 Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala Ile Gly Ala Lys 145 150 155 Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly Lys Val Ile Ser 165 170 Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile Glu Met His Val 180 185 190 Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile Asp Xaa Leu Ile 195 200 205 Ala Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu Leu Glu Arg Val 210 215 220 Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu Leu Pro Glu Leu 225 230 235 240 Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe Val Leu Val Lys 250 Ser Ala Ala

- (2) INFORMATION FOR SEQ ID NO:1169:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..183
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:
- Met Ala Thr Glu Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser 1 5 10 15
 Ser Ile Arg Val Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln
- 20 25 30
 Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile
- 35 40 45 Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala
- 50 55 60

 Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala
 65 70 75 80
- Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly 85 90 95
- Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile
 100 105 110
- Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile 115 120 125
- Asp Xaa Leu Ile Ala Thr Gly Gly Thr Leu Ala Ala Ile Arg Leu 130 135 140
- Leu Glu Arg Val Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu
 145 150 155 160

Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe 165 170 175

Val Leu Val Lys Ser Ala Ala 180

- (2) INFORMATION FOR SEQ ID NO:1170:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..870
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170: atggcgactc tcttcactgc gacggttcct tctcaccacc gtttcgtctc tccatcccaa 60 catccgaaac agagtcttct atcgcagtcg ctaagcgtca cattcacgga gaatccacaa 120 ccaacggcgg tggtcacatt gcaggagcag caattgacgg attggattac ttctccggtg 180 acgcgacggt tcggaatcgg cgccgggttt acctgggctg ggtttttagc tttcggtgtt 240 gtctccgagc agatgaagaa gtcacgactc gatgtgtttc aggaagagga taacacaaga 300 ggtttagaaa agcaagaaga gatcatctta ccaaacggca taaggtacta tgatctacaa 360 gttggaagtg gagctactcc aagctcagga tacttggtag tgtttgatgt aaagggacaa 420 gtacatggca ctgaacaagt gttcgtggac acatttggag gcaaaggcaa gtcactagcg 480 atggtaatgg actcaagacc gtatagcaag ggactatgcc aaggtataga gcatgttctc 540 aggtcaatga aggctggagg taaacgtaga gtgataattc caccgtcctt aggatttgga 600 gacagaaatg tcgaatttgg acagggtttg gagattcctc catctgcaac acttgactat 660 720 atcatcgagg ttgatacagt ttattgtttc caaactattg tggtttacca gttcatattc 780 ttcgtaatca cggctctttt caaatttgat caagtcactg actttgctgg tagcacaaac 840 ttcgttatac ttgctgtgtt aacacttgtt ctcaaagcct cttggcattt tcgacaggat
- cttgcaatgg ggggaagatc gtcgctttga (2) INFORMATION FOR SEQ ID NO:1171:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..289
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597163
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:
- Met Ala Thr Leu Phe Thr Ala Thr Val Pro Ser His His Arg Phe Val 1 5 10 15
- Ser Pro Ser Gln His Pro Lys Gln Ser Leu Leu Ser Gln Ser Leu Ser 20 25 30
- Val Thr Phe Thr Glu Asn Pro Gln Pro Thr Ala Val Val Thr Leu Gln 35 40 45
- Glu Gln Gln Leu Thr Asp Trp Ile Thr Ser Pro Val Thr Arg Arg Phe
 50
 60
- Gly Ile Gly Ala Gly Phe Thr Trp Ala Gly Phe Leu Ala Phe Gly Val 65 70 75 80 Val Ser Glu Gln Met Lys Lys Ser Arg Leu Asp Val Phe Gln Glu Glu
- 85 90 95 Asp Asn Thr Arg Gly Leu Glu Lys Gln Glu Glu Ile Ile Leu Pro Asn
- Gly Ile Arg Tyr Tyr Asp Leu Gln Val Gly Ser Gly Ala Thr Pro Ser
- Ser Gly Tyr Leu Val Val Phe Asp Val Lys Gly Gln Val His Gly Thr

Glu Gln Val Phe Val Asp Thr Phe Gly Gly Lys Gly Lys Ser Leu Ala 150 155 Met Val Met Asp Ser Arg Pro Tyr Ser Lys Gly Leu Cys Gln Gly Ile 170 165 175 Glu His Val Leu Arg Ser Met Lys Ala Gly Gly Lys Arg Arg Val Ile 185 180 Ile Pro Pro Ser Leu Gly Phe Gly Asp Arg Asn Val Glu Phe Gly Gln 200 Gly Leu Glu Ile Pro Pro Ser Ala Thr Leu Asp Tyr Ile Ile Glu Val 215 220 Asp Thr Val Tyr Cys Phe Gln Thr Ile Val Val Tyr Gln Phe Ile Phe 230 235 Phe Val Ile Thr Ala Leu Phe Lys Phe Asp Gln Val Thr Asp Phe Ala 245 250 Gly Ser Thr Asn Phe Val Ile Leu Ala Val Leu Thr Leu Val Leu Lys 260 265 Ala Ser Trp His Phe Arg Gln Asp Leu Ala Met Gly Gly Arg Ser Ser 280

Leu

- (2) INFORMATION FOR SEQ ID NO:1172:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..205
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597165
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172: Met Lys Lys Ser Arg Leu Asp Val Phe Gln Glu Glu Asp Asn Thr Arg 10 Gly Leu Glu Lys Gln Glu Glu Ile Ile Leu Pro Asn Gly Ile Arg Tyr 25 20 Tyr Asp Leu Gln Val Gly Ser Gly Ala Thr Pro Ser Ser Gly Tyr Leu 40 Val Val Phe Asp Val Lys Gly Gln Val His Gly Thr Glu Gln Val Phe 60 Val Asp Thr Phe Gly Gly Lys Gly Lys Ser Leu Ala Met Val Met Asp 70 75 Ser Arg Pro Tyr Ser Lys Gly Leu Cys Gln Gly Ile Glu His Val Leu 85 Arg Ser Met Lys Ala Gly Gly Lys Arg Arg Val Ile Ile Pro Pro Ser 105 100 Leu Gly Phe Gly Asp Arg Asn Val Glu Phe Gly Gln Gly Leu Glu Ile 125 120 115 Pro Pro Ser Ala Thr Leu Asp Tyr Ile Ile Glu Val Asp Thr Val Tyr 135 Cys Phe Gln Thr Ile Val Val Tyr Gln Phe Ile Phe Phe Val Ile Thr 150 155 Ala Leu Phe Lys Phe Asp Gln Val Thr Asp Phe Ala Gly Ser Thr Asn 170 165 Phe Val Ile Leu Ala Val Leu Thr Leu Val Leu Lys Ala Ser Trp His 180 185 190 Phe Arg Gln Asp Leu Ala Met Gly Gly Arg Ser Ser Leu 200
- (2) INFORMATION FOR SEQ ID NO:1173:

195

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..600
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173: atggggaagg gtaaccagtt ggaagaagtc agctacatca acaaccaagggtggctac 60 aaaggataca acaacttcaa aaccaacaat cccaacctct cctaccgtag caccagcgtt 120 gctaatcctc aggatcaggt gtatcccgtg caacaacaac aaggtcagaa caaacctttt 180 gttctctaca accaaggttt cgttcctaag cagcaatttn tggggaacta ccagccgcca 240 ccaccacctg gatttgcaca tcagcaaaac catgatggaa acactgaata ccaaagtccg 300 atacttagag ggacattctg catcttcttc agctccaaca caaacaagcc aaactaccca 360 ggcaaagcag ttcagaatct aaaagaatat gctcatgcta ttacactgcg tagtggaaaa 420 gcacttccaa ctagggagga accaaagacg gtcactgagg acagtgaaga tcaagatgga 480 gaggatttaa gtctcgagca accactcgac ntgtcactcg agcanccact cgaccaacca 540 ctcgagcaac cactcgaccg tgctactcaa cctatcttcc cagcagtatc atcaacgtag 600

(2) INFORMATION FOR SEQ ID NO:1174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..199
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174: Met Gly Lys Gly Asn Gln Leu Glu Glu Val Ser Tyr Ile Asn Asn Asn 10 Gln Gly Gly Tyr Lys Gly Tyr Asn Asn Phe Lys Thr Asn Asn Pro Asn 30 25 20 Leu Ser Tyr Arg Ser Thr Ser Val Ala Asn Pro Gln Asp Gln Val Tyr 40 Pro Val Gln Gln Gln Gly Gln Asn Lys Pro Phe Val Leu Tyr Asn 60 5.5 Gln Gly Phe Val Pro Lys Gln Gln Phe Xaa Gly Asn Tyr Gln Pro Pro 75 70 Pro Pro Pro Gly Phe Ala His Gln Gln Asn His Asp Gly Asn Thr Glu 90 85 Tyr Gln Ser Pro Ile Leu Arg Gly Thr Phe Cys Ile Phe Phe Ser Ser 110 105 100 Asn Thr Asn Lys Pro Asn Tyr Pro Gly Lys Ala Val Gln Asn Leu Lys 120 Glu Tyr Ala His Ala Ile Thr Leu Arg Ser Gly Lys Ala Leu Pro Thr 135 Arg Glu Glu Pro Lys Thr Val Thr Glu Asp Ser Glu Asp Gln Asp Gly 155 150
- Glu Asp Leu Ser Leu Glu Gln Pro Leu Asp Xaa Ser Leu Glu Xaa Pro
- 170 165 Leu Asp Gln Pro Leu Glu Gln Pro Leu Asp Arg Ala Thr Gln Pro Ile 185 180
- Phe Pro Ala Val Ser Ser Thr 195
- (2) INFORMATION FOR SEQ ID NO:1175:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..126
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Trp Gly Arg Val Thr Ser Trp Lys Lys Ser Ala Thr Ser Thr Thr 10 10 15

Arg Val Ala Thr Lys Asp Thr Thr Thr Ser Lys Pro Thr Ile Pro Thr 20 25 30

Ser Pro Thr Val Ala Pro Ala Leu Leu Ile Leu Arg Ile Arg Cys Ile 35 40 45

Pro Cys Asn Asn Asn Lys Val Arg Thr Asn Leu Leu Phe Ser Thr Thr 50 60

Lys Val Ser Phe Leu Ser Ser Asn Xaa Trp Gly Thr Thr Ser Arg His 65 70 75 80

His His Leu Asp Leu His Ile Ser Lys Thr Met Met Glu Thr Leu Asn 85 90 95

Thr Lys Val Arg Tyr Leu Glu Gly His Ser Ala Ser Ser Ser Ala Pro 100 105 110

Thr Gln Thr Ser Gln Thr Thr Gln Ala Lys Gln Phe Arg Ile 115 120 125

- (2) INFORMATION FOR SEQ ID NO:1176:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1026 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1026
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176: gaagaacccc gtaacgttta tctcgggttg tgtrctgatg ggttcaatcc atttggcatg 60 120 totogtaato attogttgtg gootgtgato otaactoott ataatttaco cootggtatg 180 tgcatgaata cagagtactt atttcttacc attctgaatt ctggtccaaa tcatcctcga gctagtcttg atgtcttcct ccaacctctt attgaggagt taaaagagtt gtggtctact 240 ggagtcgatg cgtacgatgt ttcattgagt cagaatttta atctaaaagc agtactacta 300 360 tggacgatta gcgactttcc ggcgtatagc atgttatcag gatggactac tcagttttgt aaatgtagta tgttcgaaga ttatctttct gcgaaatatc catgcttgcc cgaaaaagaa 420 ctctacgcga gaagagcgaa agaatatcat ctatgggtta aagaatatgt aacatactgg 480 540 aacactactt ctccatttcc tacttgggtt caagagattg tgcaaggacc tttgaacaag gttaaaactt ggccaatgta tttcacaaga ggatatttgt ttcatacgca aaatcacggc 600 gctggacgaa agacatgtaa ctatggggtc tgtgttaaag gtggaaatta cgctgattca 660 tctgatgaag cggatttcta cggtacctta actgataata tagaactcga gtatgaggat 720 caagtttgtt atattccgta tccatatacg aagaaaccaa agaacatttg gctcaatgtt 780 ctaaaagtca atccgagggg aaatatttct ggagaatatg aaaacaatga tccaactctt 840 ttgcaaacag aaaatgatga tgatgttttg ctcactacaa ttgaagatct tgttcttgaa 900 actocggtag ccaacttaaa cccaataatc cttgattacg atgtcgggga tgctgaacca 960 gaagacgaat toogatgtaa tttatogtoo toggacgaag atgaagtaga agatgaagat 1020 gtataa
- (2) INFORMATION FOR SEQ ID NO:1177:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..341
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys Xaa Asp Gly Phe Asn 1 10 15

Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu Thr 20 25 30

Pro Tyr Asn Leu Pro Pro Gly Met Cys Met Asn Thr Glu Tyr Leu Phe 35 40 45

Leu Thr Ile Leu Asn Ser Gly Pro Asn His Pro Arg Ala Ser Leu Asp 50 55 60

Val Phe Leu Gln Pro Leu Ile Glu Glu Leu Lys Glu Leu Trp Ser Thr 65 70 75 80

Gly Val Asp Ala Tyr Asp Val Ser Leu Ser Gln Asn Phe Asn Leu Lys 85 90 95

Ala Val Leu Leu Trp Thr Ile Ser Asp Phe Pro Ala Tyr Ser Met Leu 100 105 110

Ser Gly Trp Thr Thr Gln Phe Cys Lys Cys Ser Met Phe Glu Asp Tyr 115 120 125

Leu Ser Ala Lys Tyr Pro Cys Leu Pro Glu Lys Glu Leu Tyr Ala Arg 130 135 140

Arg Ala Lys Glu Tyr His Leu Trp Val Lys Glu Tyr Val Thr Tyr Trp 145 150 155 160

Asn Thr Thr Ser Pro Phe Pro Thr Trp Val Gln Glu Ile Val Gln Gly
165 170 175

Pro Leu Asn Lys Val Lys Thr Trp Pro Met Tyr Phe Thr Arg Gly Tyr 180 185 190

Leu Phe His Thr Gln Asn His Gly Ala Gly Arg Lys Thr Cys Asn Tyr
195 200 205

Gly Val Cys Val Lys Gly Gly Asn Tyr Ala Asp Ser Ser Asp Glu Ala 210 215 220

Asp Phe Tyr Gly Thr Leu Thr Asp Asn Ile Glu Leu Glu Tyr Glu Asp 225 230 235 240

Gln Val Cys Tyr Ile Pro Tyr Pro Tyr Thr Lys Lys Pro Lys Asn Ile
245 250 255

Trp Leu Asn Val Leu Lys Val Asn Pro Arg Gly Asn Ile Ser Gly Glu 260 265 270

Tyr Glu Asn Asp Pro Thr Leu Leu Gln Thr Glu Asn Asp Asp Asp 275 280 285

Val Leu Leu Thr Thr Ile Glu Asp Leu Val Leu Glu Thr Pro Val Ala 290 295 300

Asn Leu Asn Pro Ile Ile Leu Asp Tyr Asp Val Gly Asp Ala Glu Pro 305 310 315 320

Glu Asp Glu Phe Arg Cys Asn Leu Ser Ser Ser Asp Glu Asp Glu Val 325 330 335

Glu Asp Glu Asp Val

340

- (2) INFORMATION FOR SEQ ID NO:1178:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..322
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178: Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu Thr Pro Tyr Asn 10 15 Leu Pro Pro Gly Met Cys Met Asn Thr Glu Tyr Leu Phe Leu Thr Ile 25 Leu Asn Ser Gly Pro Asn His Pro Arg Ala Ser Leu Asp Val Phe Leu 40 Gln Pro Leu Ile Glu Glu Leu Lys Glu Leu Trp Ser Thr Gly Val Asp 55 Ala Tyr Asp Val Ser Leu Ser Gln Asn Phe Asn Leu Lys Ala Val Leu 70 Leu Trp Thr Ile Ser Asp Phe Pro Ala Tyr Ser Met Leu Ser Gly Trp 85 90 Thr Thr Gln Phe Cys Lys Cys Ser Met Phe Glu Asp Tyr Leu Ser Ala 105 Lys Tyr Pro Cys Leu Pro Glu Lys Glu Leu Tyr Ala Arg Arg Ala Lys 120 115 Glu Tyr His Leu Trp Val Lys Glu Tyr Val Thr Tyr Trp Asn Thr Thr 140 135 Ser Pro Phe Pro Thr Trp Val Gln Glu Ile Val Gln Gly Pro Leu Asn 150 155 Lys Val Lys Thr Trp Pro Met Tyr Phe Thr Arg Gly Tyr Leu Phe His 170 165 Thr Gln Asn His Gly Ala Gly Arg Lys Thr Cys Asn Tyr Gly Val Cys 185 180 Val Lys Gly Gly Asn Tyr Ala Asp Ser Ser Asp Glu Ala Asp Phe Tyr 200 195 Gly Thr Leu Thr Asp Asn Ile Glu Leu Glu Tyr Glu Asp Gln Val Cys 220 215 Tyr Ile Pro Tyr Pro Tyr Thr Lys Lys Pro Lys Asn Ile Trp Leu Asn 235 240 230 Val Leu Lys Val Asn Pro Arg Gly Asn Ile Ser Gly Glu Tyr Glu Asn 250 245 Asn Asp Pro Thr Leu Leu Gln Thr Glu Asn Asp Asp Asp Val Leu Leu 260 265 270 Thr Thr Ile Glu Asp Leu Val Leu Glu Thr Pro Val Ala Asn Leu Asn 275 280 Pro Ile Ile Leu Asp Tyr Asp Val Gly Asp Ala Glu Pro Glu Asp Glu 290 295 300 Phe Arg Cys Asn Leu Ser Ser Ser Asp Glu Asp Glu Val Glu Asp Glu 315 310 Asp Val

- (2) INFORMATION FOR SEQ ID NO:1179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..302
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:
- Met Cys Met Asn Thr Glu Tyr Leu Phe Leu Thr Ile Leu Asn Ser Gly
 1 10 15
- Pro Asn His Pro Arg Ala Ser Leu Asp Val Phe Leu Gln Pro Leu Ile 20 25 30
- Glu Glu Leu Lys Glu Leu Trp Ser Thr Gly Val Asp Ala Tyr Asp Val

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Ser Leu Ser Gln Asn Phe Asn Leu Lys Ala Val Leu Leu Trp Thr Ile
                    55
Ser Asp Phe Pro Ala Tyr Ser Met Leu Ser Gly Trp Thr Thr Gln Phe
                                 75
                70
Cys Lys Cys Ser Met Phe Glu Asp Tyr Leu Ser Ala Lys Tyr Pro Cys
                              90
Leu Pro Glu Lys Glu Leu Tyr Ala Arg Arg Ala Lys Glu Tyr His Leu
                          105
                               110
         100
Trp Val Lys Glu Tyr Val Thr Tyr Trp Asn Thr Thr Ser Pro Phe Pro
                    120
                                        125
 115
Thr Trp Val Gln Glu Ile Val Gln Gly Pro Leu Asn Lys Val Lys Thr
                   135
Trp Pro Met Tyr Phe Thr Arg Gly Tyr Leu Phe His Thr Gln Asn His
               150
                                 155
Gly Ala Gly Arg Lys Thr Cys Asn Tyr Gly Val Cys Val Lys Gly Gly
            165
                             170
                                    175
Asn Tyr Ala Asp Ser Ser Asp Glu Ala Asp Phe Tyr Gly Thr Leu Thr
         180
                                           190
                          185
Asp Asn Ile Glu Leu Glu Tyr Glu Asp Gln Val Cys Tyr Ile Pro Tyr
 195 200
                                        205
Pro Tyr Thr Lys Lys Pro Lys Asn Ile Trp Leu Asn Val Leu Lys Val
                                    220
  210 215
Asn Pro Arg Gly Asn Ile Ser Gly Glu Tyr Glu Asn Asn Asp Pro Thr
        230 235
Leu Leu Gln Thr Glu Asn Asp Asp Asp Val Leu Leu Thr Thr Ile Glu
                             250
            245
Asp Leu Val Leu Glu Thr Pro Val Ala Asn Leu Asn Pro Ile Ile Leu
         260 265
Asp Tyr Asp Val Gly Asp Ala Glu Pro Glu Asp Glu Phe Arg Cys Asn
    275 280
Leu Ser Ser Ser Asp Glu Asp Glu Val Glu Asp Glu Asp Val
          295
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- (2) INFORMATION FOR SEQ ID NO:1180:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..240
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597208
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

, ,	_				and the second s	~ ^
tccagtgagg	tatctcctat	tgtcttgatg	ggcaatcggt	taacacagtt	gcttgatgcg	60
atggaggtaa	atcaacaac	catgaagacc	gtgaagcaaa	acctttggtg	ggcgttcgga	120
tagaagatta	taggatage	aattacaact	adagtattac	taccattgac	tggaaccatg	180
Lacadacatty	Laggaalccc	aaccgcggcc	9949696696	tatataaata	tantanactan	240
ttgactccat	caatqqcqqq	ggctctcatg	ggntgtaage	receiving	tcatgactaa	240

- (2) INFORMATION FOR SEQ ID NO:1181:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597209
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

Client Docket No. 80146.003 Ser Ser Glu Val Ser Pro Val Val Leu Met Gly Asn Arg Leu Thr Gln 10 Leu Leu Asp Ala Met Glu Leu Ser Arg Gln Thr Met Lys Thr Val Lys 2.5 Gln Asn Leu Trp Trp Ala Phe Gly Tyr Asn Ile Val Gly Ile Pro Ile 45 40 Ala Ala Gly Val Leu Leu Pro Leu Thr Gly Thr Met Leu Thr Pro Ser 60 55 Met Ala Gly Ala Leu Met Xaa Cys Lys Leu Ser Arg Cys His Asp 70 (2) INFORMATION FOR SEQ ID NO:1182: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..70 (D) OTHER INFORMATION: / Ceres Seq. ID 1597210 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182: Met Gly Asn Arg Leu Thr Gln Leu Leu Asp Ala Met Glu Leu Ser Arg 10 Gln Thr Met Lys Thr Val Lys Gln Asn Leu Trp Trp Ala Phe Gly Tyr 25 20 Asn Ile Val Gly Ile Pro Ile Ala Ala Gly Val Leu Leu Pro Leu Thr 40 Gly Thr Met Leu Thr Pro Ser Met Ala Gly Ala Leu Met Xaa Cys Lys Leu Ser Arg Cys His Asp 7.0 (2) INFORMATION FOR SEQ ID NO:1183: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..59 (D) OTHER INFORMATION: / Ceres Seq. ID 1597211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183: Met Glu Leu Ser Arg Gln Thr Met Lys Thr Val Lys Gln Asn Leu Trp 10 5 Trp Ala Phe Gly Tyr Asn Ile Val Gly Ile Pro Ile Ala Ala Gly Val 20 25 Leu Leu Pro Leu Thr Gly Thr Met Leu Thr Pro Ser Met Ala Gly Ala 40 Leu Met Xaa Cys Lys Leu Ser Arg Cys His Asp 55 (2) INFORMATION FOR SEQ ID NO:1184: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 982 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1597224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184: aacacaattt gatacgcgtc agtttgacca gaggctgaat gaagttctcg atggacagga 60 tgagttcttc acctcatatg atgaggtcca tgagagcttt gatgccatgg gtttgcaaga 120 gaatcttctt aggggtatct atgcttacgg tttcgaaaag ccttctgcta ttcagcaaag 180 aggaattgta cccttttgca agggtcttga tgtgatccag caggcacagt ctggtactgg 240 aaaaaccgcc actttctgct ctggtgtctt gcagcagctt gactatgccc ttctccagtg 300 ccaggetete gttttggete ccaccagaga gettgeteag cagattgaga aggteatgeg 360 tgcccttggt gactaccaag gtgtcaaggt tcatgcctgt gttggtggaa ccagtgtccg 420 tnaggatcag cgcattctcc aggctggtgt tcatgttgtc gttggaactc ctggtcgtgt 480 ttttgacatg cttagaagac aatctctccg ccctgactgc atcaagatgt ttgtccttga 540 tgaagctgat gaaatgctct cocgtggttt caaggatcag atctatgaca tattccagct 600 tctcccacca aagattcagg ttggagtgtt ctctgcgaca atgcctccgg aagctttgga 660 gatcacaagg aaattcatga gcaaaccagt gagaatcttg gtgaaacgtg atgagctcac 720 780 acttgaaggn tatcaagcaa ttctacgtga ancgtggaga aagaagactg gaangcttga 840 gactctctgc gatctctacg nagactctag ccatcactca gagtgtcatc tttgtcaaca 900 ctcgtcgcaa ggtcganctg gctncacaga caaaatgaga agccgtgacc acacagtctc 960 agennnetca tggagacatg gaccaaaaca ccagagacat catcatgaga gagttcaggt cntggctcgt ctcgtgttct aa

- (2) INFORMATION FOR SEQ ID NO:1185:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

210

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185: Thr Gln Phe Asp Thr Arg Gln Phe Asp Gln Arg Leu Asn Glu Val Leu 10 Asp Gly Gln Asp Glu Phe Phe Thr Ser Tyr Asp Glu Val His Glu Ser 25 20 Phe Asp Ala Met Gly Leu Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala 40 Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly Ile Val Pro 55 Phe Cys Lys Gly Leu Asp Val Ile Gln Gln Ala Gln Ser Gly Thr Gly 75 7.0 Lys Thr Ala Thr Phe Cys Ser Gly Val Leu Gln Gln Leu Asp Tyr Ala 90 Leu Leu Gln Cys Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Leu Ala 110 105 Gln Gln Ile Glu Lys Val Met Arg Ala Leu Gly Asp Tyr Gln Gly Val 125 120 115 Lys Val His Ala Cys Val Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg 140 135 Ile Leu Gln Ala Gly Val His Val Val Val Gly Thr Pro Gly Arg Val 150 155 Phe Asp Met Leu Arg Arg Gln Ser Leu Arg Pro Asp Cys Ile Lys Met 175 170 165 Phe Val Leu Asp Glu Ala Asp Glu Met Leu Ser Arg Gly Phe Lys Asp 190 185 180 Gln Ile Tyr Asp Ile Phe Gln Leu Leu Pro Pro Lys Ile Gln Val Gly 205 200 195 Val Phe Ser Ala Thr Met Pro Pro Glu Ala Leu Glu Ile Thr Arg Lys

Phe Met Ser Lys Pro Val Arg Ile Leu Val Lys Arg Asp Glu Leu Thr

220

215

235 230 225 Leu Glu Xaa Tyr Gln Ala Ile Leu Arg Glu Xaa Trp Arg Lys Lys Thr 245 250 255 Gly Xaa Leu Glu Thr Leu Cys Asp Leu Tyr Xaa Asp Ser Ser His His 265 Ser Glu Cys His Leu Cys Gln His Ser Ser Gln Gly Arg Xaa Gly Xaa 285 275 280 Thr Asp Lys Met Arg Ser Arg Asp His Thr Val Ser Xaa Xaa Ser Trp 290 295 300 Arg His Gly Pro Lys His Gln Arg His His His Glu Arg Val Gln Val 305 310 315 Xaa Ala Arg Leu Val Phe 325

- (2) INFORMATION FOR SEQ ID NO:1186:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..291
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met Gly Leu Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe 1 5 10 15 Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys

20 25 30
Gly Leu Asp Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala

35 40 45 Thr Phe Cys Ser Gly Val Leu Gln Gln Leu Asp Tyr Ala Leu Leu Gln

50 55 60 Cys Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile 65 70 75 80

Glu Lys Val Met Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys Val His 85 90 95

Ala Cys Val Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg Ile Leu Gln
100 105 110

Ala Gly Val His Val Val Val Gly Thr Pro Gly Arg Val Phe Asp Met 115 120 125

Leu Arg Arg Gln Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu 130 135 140

Asp Glu Ala Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr 145 150 155 160

Asp Ile Phe Gln Leu Leu Pro Pro Lys Ile Gln Val Gly Val Phe Ser 165 170 175

Ala Thr Met Pro Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Ser 180 185 190

Lys Pro Val Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Xaa 195 200 205

Tyr Gln Ala Ile Leu Arg Glu Xaa Trp Arg Lys Lys Thr Gly Xaa Leu 210 215 220

Glu Thr Leu Cys Asp Leu Tyr Xaa Asp Ser Ser His His Ser Glu Cys 225 230 235 240

His Leu Cys Gln His Ser Ser Gln Gly Arg Xaa Gly Xaa Thr Asp Lys 245 250 255

Met Arg Ser Arg Asp His Thr Val Ser Xaa Xaa Ser Trp Arg His Gly 260 265 270

Pro Lys His Gln Arg His His His Glu Arg Val Gln Val Xaa Ala Arg 275 280 285 Leu Val Phe 290

- (2) INFORMATION FOR SEQ ID NO:1187:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..208
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597227
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys Val His Ala Cys Val 1 10 15

Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg Ile Leu Gln Ala Gly Val 20 25 30

His Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Arg Arg

Gln Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu Asp Glu Ala 50 55 60

Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile Phe
65 70 75 80

Gln Leu Leu Pro Pro Lys Ile Gln Val Gly Val Phe Ser Ala Thr Met
85 90 95

Pro Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Ser Lys Pro Val 100 105 110

Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Xaa Tyr Gln Ala 115 120 125

Ile Leu Arg Glu Xaa Trp Arg Lys Lys Thr Gly Xaa Leu Glu Thr Leu 130 135 140

Cys Asp Leu Tyr Xaa Asp Ser Ser His His Ser Glu Cys His Leu Cys 145 150 155 160

Gln His Ser Ser Gln Gly Arg Xaa Gly Xaa Thr Asp Lys Met Arg Ser 165 170 175

Arg Asp His Thr Val Ser Xaa Xaa Ser Trp Arg His Gly Pro Lys His

180
185
190
Cla Arg His His Cla Arg Val Gla Val Xaa Ala Arg Jeu Val Phe

Gln Arg His His Glu Arg Val Gln Val Xaa Ala Arg Leu Val Phe 195 200 205

- (2) INFORMATION FOR SEQ ID NO:1188:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..342
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597228
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

atgaagtttg acatcagaga agcttcaggg aaatcaacaa caggagttca gaacatnaat 60 attgatgaag nngcagaagc tggaacccca ccaagagtta actatacttc tcaacttagc 120 aagctgaaga ggacttttga ccacaagaag agagcaacag aaaggctagc tcagactgga gatcctacaa aagatgactg ctctgtaaga gtcaagctta gtgaattaaa acaagctcac 240 ttgggaggaa gtcccatgtc tatccaggnt tgtctcattg atcattataa agtcaatggt 300

cgagtnaact caaaccaagt caagaaagat ctcagccgtt ga (2) INFORMATION FOR SEQ ID NO:1189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597229
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

Met Lys Phe Asp Ile Arg Glu Ala Ser Gly Lys Ser Thr Thr Gly Val 1 10 15

Gln Asn Xaa Asn Ile Asp Glu Xaa Ala Glu Ala Gly Thr Pro Pro Arg 20 25 30

Val Asn Tyr Thr Ser Gln Leu Ser Lys Leu Lys Arg Thr Phe Asp His 35 40 45

Lys Lys Arg Ala Thr Glu Arg Leu Ala Gln Thr Gly Asp Pro Thr Lys 50 55 60

Asp Asp Cys Ser Val Arg Val Lys Leu Ser Glu Leu Lys Gln Ala His 65 70 75 80

Leu Gly Gly Ser Pro Met Ser Ile Gln Xaa Cys Leu Ile Asp His Tyr 85 90 95

Lys Val Asn Gly Arg Xaa Asn Ser Asn Gln Val Lys Lys Asp Leu Ser 100 105 110

Arg

- (2) INFORMATION FOR SEQ ID NO:1190:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1032 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1032
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597257
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190: atngcntgtn atcattnctg cttngtcatn cactngcctg ctatngccat ttctgctttt 60 120 agtttcattt catttcggtt attgcatact aggactgtta gaaccaacca actttctact tggcttgact tagagctttc tgatcatatc tcatctgttt gcgtcacact gaattggatt 180 gacatcctaa aatactacaa cgacaggata gtaccttgca acctgcttta cagacgcatc 240 300 tctgattcgt ctgttatagc ccnggctgct atctgttgca tgcatacacg gtcagaagga 360 aatcagaacc tcctattcaa cgataacatc gaccgtattg ctcgccaact aagagaacag acagaaaccg acacaatggc tgacgttgta gatgagcaag agcaacctac caacattggt 420 gctggtgact tccctcacaa ccacaaccag cgtcatggaa ttgttccacc tccagtacag 480 aacaacaact ttgagatcaa aagcggtctc attgctatgg ttcaagggaa caagtttcat 540 600 ggcctgccaa tggaggatcc gctagatcat ctngacgagt tngaaagnct ctgtgncctn 660 actaaaatca atggagttag tgaagatggt ttnnnanttc gcttgtttcc attctcactt ggagataaag cccatctgtg ggaaaagacg ctaccccaga attcaatcac aacctgggat 720 gactgcaaaa aggccttctt ggcaaaattc ttttccaact ccagaactgc aagactccgg 780 840 aatgagatat ccggatttac tcagaagcaa aatgaaagct tctgtgaagc ttgggagcgc 900 tttaagggtt atcaaaccaa atgccctcat cacggattta agcangctnc tctnctcagc 960 acactctata gagncgtctn gcctaagata aggatactgc ttgacaccgc ttcaaatggg aattttttga agaaggatgt tgaagaagga tggnagctag tngaaaanct ttgctcagtc 1020 gnatggcaat na
- (2) INFORMATION FOR SEQ ID NO:1191:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..343
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:
- Xaa Xaa Cys Xaa His Xaa Cys Xaa Val Xaa His Xaa Pro Ala Xaa Ala 1 5 10
- Ile Ser Ala Phe Ser Phe Ile Ser Phe Arg Leu Leu His Thr Arg Thr 20 25 30
- Val Arg Thr Asn Gln Leu Ser Thr Trp Leu Asp Leu Glu Leu Ser Asp 35 40 45
- His Ile Ser Ser Val Cys Val Thr Leu Asn Trp Ile Asp Ile Leu Lys 50 55
- Tyr Tyr Asn Asp Arg Ile Val Pro Cys Asn Leu Leu Tyr Arg Arg Ile 65 70 75 80
- Ser Asp Ser Ser Val Ile Ala Xaa Ala Ala Ile Cys Cys Met His Thr 85 90 95
- Arg Ser Glu Gly Asn Gln Asn Leu Leu Phe Asn Asp Asn Ile Asp Arg 100 105 110
- Ile Ala Arg Gln Leu Arg Glu Gln Thr Glu Thr Asp Thr Met Ala Asp 115 120 125
- Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala Gly Asp Phe 130 135 140
- Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro Pro Val Gln 145 150 155 160
- Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met Val Gln Gly
 165 170 175
- Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp His Xaa Asp 180 185 190
- Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly Val Ser Glu 195 200 205
- Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly Asp Lys Ala 210 215 220
- His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr Thr Trp Asp 225 230 230 235 240
- Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn Ser Arg Thr 245 250 255
- Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys Gln Asn Glu
 260 265 270
- Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln Thr Lys Cys 275 280 285
- 305 Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu Xaa Glu Xaa 335 320

Leu Cys Ser Val Xaa Trp Gln

340

- (2) INFORMATION FOR SEQ ID NO:1192:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1597259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192: Met His Thr Arg Ser Glu Gly Asn Gln Asn Leu Leu Phe Asn Asp Asn 10 Ile Asp Arg Ile Ala Arg Gln Leu Arg Glu Gln Thr Glu Thr Asp Thr 25 Met Ala Asp Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala 40 Gly Asp Phe Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro 55 Pro Val Gln Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met 70 75 Val Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp 85 90 His Xaa Asp Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly 100 105 110 Val Ser Glu Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly 120 125 Asp Lys Ala His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr 130 135 140 Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn 150 155 Ser Arg Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys 165 170 Gln Asn Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln 185 190 Thr Lys Cys Pro His His Gly Phe Lys Xaa Ala Xaa Xaa Leu Ser Thr 195 200 205

Leu Tyr Arg Xaa Val Xaa Pro Lys Ile Arg Ile Leu Leu Asp Thr Ala 210 215 220

Ser Asn Gly Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu 230 235

Xaa Glu Xaa Leu Cys Ser Val Xaa Trp Gln 245 250

- (2) INFORMATION FOR SEQ ID NO:1193:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..218
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193: Met Ala Asp Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala

10 Gly Asp Phe Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro

25 20

Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met 40

Val Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp 60 55

His Xaa Asp Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly 75 70

Val Ser Glu Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly 90 8.5

Asp Lys Ala His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr 105 100

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Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn
                            120
        115
Ser Arg Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys
                        135
                                            140
   130
Gln Asn Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln
                                        155
                    150
Thr Lys Cys Pro His His Gly Phe Lys Xaa Ala Xaa Xaa Leu Ser Thr
                                    170
                165
Leu Tyr Arg Xaa Val Xaa Pro Lys Ile Arg Ile Leu Leu Asp Thr Ala
                               185
                                                     190
            180
Ser Asn Gly Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu
                            200
Xaa Glu Xaa Leu Cys Ser Val Xaa Trp Gln
                        215
(2) INFORMATION FOR SEQ ID NO:1194:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 591 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
```

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..591
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194: 60 atgtcaacaa gatcgccact cgcaaggatt caacctacaa gaacgttggt tggacttccc 120 ngtggctaca aaggtcgcga ctttnctcat cgcngaggac ctagttccat ctctcccngc aattctcaag attctttgaa caaagatgtt tgctttcacc ntggagtgaa catactcgca 180 gctacttctc caaatgatac attttatgac ggaggatttc ctatgaaatc aggaacatca 240 atgtcgactc cttttgttgc aggaattgta gcactcctta agtctttgca ccctcattgg 300 tctccggccg ccattagatc tgctattgtt actacagctt ggagaacaga tccatccgag 360 aaagccgcga aacccggtct tgtttacgat atgggagtta acgattatgt tctntatttg 420 480 tgctccgttg gttacacaga ttcatccatt actagacttg tccgcaagaa gacggtttgt gcaaacccta aaccttcagt tottgacctc aaattgcctt caatcacaat cccaaacctt 540 gcaaaannga agttattatc actagaaccg ttaccaacgt tggaccagta g
- (2) INFORMATION FOR SEQ ID NO:1195:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..196
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597262
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

Met Ser Thr Arg Ser Pro Leu Ala Arg Ile Gln Pro Thr Arg Thr Leu 10

Val Gly Leu Pro Xaa Gly Tyr Lys Gly Arg Asp Phe Xaa His Arg Xaa 25

Gly Pro Ser Ser Ile Ser Pro Xaa Asn Ser Gln Asp Ser Leu Asn Lys 40

Asp Val Cys Phe His Xaa Gly Val Asn Ile Leu Ala Ala Thr Ser Pro 55

Asn Asp Thr Phe Tyr Asp Gly Gly Phe Pro Met Lys Ser Gly Thr Ser 75 70 Met Ser Thr Pro Phe Val Ala Gly Ile Val Ala Leu Leu Lys Ser Leu

90 His Pro His Trp Ser Pro Ala Ala Ile Arg Ser Ala Ile Val Thr Thr

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110
                                105
            100
Ala Trp Arg Thr Asp Pro Ser Glu Lys Ala Ala Lys Pro Gly Leu Val
                                            125
                           120
        115
Tyr Asp Met Gly Val Asn Asp Tyr Val Xaa Tyr Leu Cys Ser Val Gly
                        135
    130
Tyr Thr Asp Ser Ser Ile Thr Arg Leu Val Arg Lys Lys Thr Val Cys
                                       155
                   150
Ala Asn Pro Lys Pro Ser Val Leu Asp Leu Lys Leu Pro Ser Ile Thr
                                170
                165
Ile Pro Asn Leu Ala Lys Xaa Lys Leu Leu Ser Leu Glu Pro Leu Pro
                               185
            180
Thr Leu Asp Gln
        195
(2) INFORMATION FOR SEQ ID NO:1196:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 122 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..122
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597264
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:
Met Lys Ser Gly Thr Ser Met Ser Thr Pro Phe Val Ala Gly Ile Val
                                    10
Ala Leu Leu Lys Ser Leu His Pro His Trp Ser Pro Ala Ala Ile Arg
                                25
Ser Ala Ile Val Thr Thr Ala Trp Arg Thr Asp Pro Ser Glu Lys Ala
                            40
Ala Lys Pro Gly Leu Val Tyr Asp Met Gly Val Asn Asp Tyr Val Xaa
                        55
Tyr Leu Cys Ser Val Gly Tyr Thr Asp Ser Ser Ile Thr Arg Leu Val
                    70
                                         75
Arg Lys Lys Thr Val Cys Ala Asn Pro Lys Pro Ser Val Leu Asp Leu
                                     90
Lys Leu Pro Ser Ile Thr Ile Pro Asn Leu Ala Lys Xaa Lys Leu Leu
            100
                                 105
Ser Leu Glu Pro Leu Pro Thr Leu Asp Gln
                             120
        115
 (2) INFORMATION FOR SEQ ID NO:1197:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 714 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..714
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597281
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:
                                                                        60
 tctqtctgtc tcgtcactca ggatcagatc ttagctaaat tgagacaagc tcaaaatgag
 taagcttcag agtgaggccg ttcgtgaagc catcactact atcacaggga aatccgaggc
                                                                        120
 aaagaaacgt aactttgtcg agactattga gctccagatc ggtctgaaga actatgaccc
                                                                        180
 tcaaaaggac aagcgtttca gtggatctgt caagttacca catatccccc gtcctaaaat
                                                                        240
 gaagatetge atgeteggag atgeceagea tgttgaagag gaaaatteee aactettgtg
                                                                        300
 agccaccagg aatccttgga gtcaaaggtg aatgaaacaa aggcaacagt gaagttccag
                                                                        360
 ctgaagaagg ttctgtgcat gggagttgca gttggtaacc tttcaatgga agagaagcag
                                                                        420
 atctttcaga atgtgcagat gagcgtcaac ttcctcgtct cgctattgaa gaagaactgg
```

caaaatgtca ggtgtttgta cctcaagagc acaatgggac caccacaaag aatcttctga 540 gctttcacct acttaaaatt ggtggctata agacacttct tcttaccctt tcgtttttgt 600 ttcagacata tctgttaaac agtgtaagag ttgtgctgct actctcctct ttagcttttg 660 gtttggataa tttgaaataa ctgcagtgat tttggttaat ggattttgta gctt

- (2) INFORMATION FOR SEQ ID NO:1198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (B) TYPE: amino acid

(A) LENGTH: 81 amino acids

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

Met Ser Lys Leu Gln Ser Glu Ala Val Arg Glu Ala Ile Thr Thr Ile 1 5 10 15

Thr Gly Lys Ser Glu Ala Lys Lys Arg Asn Phe Val Glu Thr Ile Glu 20 25 30

Leu Gln Ile Gly Leu Lys Asn Tyr Asp Pro Gln Lys Asp Lys Arg Phe

Ser Gly Ser Val Lys Leu Pro His Ile Pro Arg Pro Lys Met Lys Ile
50 60

Cys Met Leu Gly Asp Ala Gln His Val Glu Glu Glu Asn Ser Gln Leu 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:1199:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..53
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597283
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

Met Gly Val Ala Val Gly Asn Leu Ser Met Glu Glu Lys Gln Ile Phe 1 5 10 15

Gln Asn Val Gln Met Ser Val Asn Phe Leu Val Ser Leu Leu Lys Lys 20 25 30

Asn Trp Gln Asn Val Arg Cys Leu Tyr Leu Lys Ser Thr Met Gly Pro 35 40 45

Pro Gln Arg Ile Phe 50

- (2) INFORMATION FOR SEQ ID NO:1200:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..44
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597284
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

Met Glu Glu Lys Gln Ile Phe Gln Asn Val Gln Met Ser Val Asn Phe

10 1 5 Leu Val Ser Leu Leu Lys Lys Asn Trp Gln Asn Val Arg Cys Leu Tyr 30 25 Leu Lys Ser Thr Met Gly Pro Pro Gln Arg Ile Phe

40

- (2) INFORMATION FOR SEQ ID NO:1201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 821 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..821
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597285
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201: attgagtett tagggtetet etgtgtttge aaatetgaeg eegagtattt tgetaaagea 60 120 gcagccagtc gggacagtga aatggcgact gaagatgtgc aagatcccag aatcgctaag attgcctctt ccattagagt catccccgac ttccctaaac caggaatcat gtttcaggac 180 240 ataacgacgc ttcttctcga cactgaggcc tttaaggata ctattgcttt gtttgttgat 300 agatacaaag ataaaggcat atctgttgtt gcaggtgttg aagctagagg tttcattttt 360 ggccctccta ttgcgttggc tattggtgcc aaatttgttc ccatgaggac gcccaagaag 420 ctacctggga aggttatttc ggaggagtat tcgttggagt atggaccaga tacgattgag atgcacgtag gtgcagtaga gcctggtgag cgtgctatta ttattgatgn cctcattgcc 480 acgggtggga ctctcgctgc tgcaatccga ctacttgaac gagtaggagt gnagattgtt 540 600 gaatgtgctt gcgtaattga gttaccagag cttaagggaa aggagaaact aggagagacg tcgctatttg ttcttgtaaa gtcggctgct taacaagaaa ctggaagtga aggttattgg 660 720 atcgagtgtt gatgctattt ttcatgtatg gtgagacatt ttgcgtggga tttgatcctt 780 gttgnttcaa cttttatcat anttggttca gnctagaaaa tggcatttga atgtcaggat togattgcag tttcctattg ttccacttaa aatccccgat t
- (2) INFORMATION FOR SEQ ID NO:1202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..210
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202: Ile Glu Ser Leu Gly Ser Leu Cys Val Cys Lys Ser Asp Ala Glu Tyr

1.0 Phe Ala Lys Ala Ala Ala Ser Arg Asp Ser Glu Met Ala Thr Glu Asp 25

Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser Ser Ile Arg Val Ile 40

Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln Asp Ile Thr Thr Leu 60 55

Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile Ala Leu Phe Val Asp 75 70

Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala Gly Val Glu Ala Arg 90

Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala Ile Gly Ala Lys Phe 105

Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly Lys Val Ile Ser Glu 125 120 115

Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile Glu Met His Val Gly 140 130 135

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile Asp Xaa Leu Ile Ala 155 150 Thr Gly Gly Thr Leu Ala Ala Ile Arg Leu Leu Glu Arg Val Gly 165 170 Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu Leu Pro Glu Leu Lys 180 185 Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe Val Leu Val Lys Ser 200 Ala Ala 210 (2) INFORMATION FOR SEQ ID NO:1203: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 183 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..183 (D) OTHER INFORMATION: / Ceres Seq. ID 1597287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203: Met Ala Thr Glu Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser 10 Ser Ile Arg Val Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln 25 20 Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile 45 40 Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala 60 55 Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala 75 Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly 90 95 85 Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile 110 105 Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile

- (2) INFORMATION FOR SEQ ID NO:1204:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597288
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met Phe Gln Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys 1 5 10 15
Asp Thr Ile Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser

120

180

240

300

360

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
            20
Val Val Ala Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile
                            40
Ala Leu Ala Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys
                        55
Leu Pro Gly Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro
                                        75
                    70
Asp Thr Ile Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala
                                    90
                85
Ile Ile Ile Asp Xaa Leu Ile Ala Thr Gly Gly Thr Leu Ala Ala Ala
                                105
            100
Ile Arg Leu Leu Glu Arg Val Gly Val Xaa Ile Val Glu Cys Ala Cys
                                                125
                           120
Val Ile Glu Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr
                       135
Ser Leu Phe Val Leu Val Lys Ser Ala Ala
                150
(2) INFORMATION FOR SEQ ID NO:1205:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 365 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..365
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597313
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:
taagcttcag agtgaggccg ttcgtgaagc catcactact atcacaggga aatccgaggc
aaagaaacgt aactttgtcg agactattga gctccagatc ggtctgaaga actatgaccc
tcaaaaggac aagcgtttca gtggatctgt caagttacca catatccccc gtcctaaaat
gaagatetge atgeteggag atgeceagea tgttgaagag aacatggatg ttgagtetet
aaaaaagctt aacaagaaca agaaactcgt caagaagctt gcaaagaaat accatqcttt
cttggcctct gagtctgtca ttaagcagat tcctcgtctt cttggtcctg gtcttaacaa
ggcag
```

- (2) INFORMATION FOR SEQ ID NO:1206:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..121
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597314
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

Lys Leu Gln Ser Glu Ala Val Arg Glu Ala Ile Thr Thr Ile Thr Gly 10

Lys Ser Glu Ala Lys Lys Arg Asn Phe Val Glu Thr Ile Glu Leu Gln 25

Ile Gly Leu Lys Asn Tyr Asp Pro Gln Lys Asp Lys Arg Phe Ser Gly 40

Ser Val Lys Leu Pro His Ile Pro Arg Pro Lys Met Lys Ile Cys Met

Leu Gly Asp Ala Gln His Val Glu Glu Asn Met Asp Val Glu Ser Leu 75

Lys Lys Leu Asn Lys Asn Lys Lys Leu Val Lys Lys Leu Ala Lys Lys 90

Tyr His Ala Phe Leu Ala Ser Glu Ser Val Ile Lys Gln Ile Pro Arg

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

110 105 100 Leu Leu Gly Pro Gly Leu Asn Lys Ala 120 115 (2) INFORMATION FOR SEQ ID NO:1207: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..62 (D) OTHER INFORMATION: / Ceres Seq. ID 1597315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207: Met Lys Ile Cys Met Leu Gly Asp Ala Gln His Val Glu Glu Asn Met 5 10 Asp Val Glu Ser Leu Lys Lys Leu Asn Lys Asn Lys Lys Leu Val Lys 30 25 Lys Leu Ala Lys Lys Tyr His Ala Phe Leu Ala Ser Glu Ser Val Ile 40 Lys Gln Ile Pro Arg Leu Leu Gly Pro Gly Leu Asn Lys Ala 55 (2) INFORMATION FOR SEQ ID NO:1208: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1036 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..1036 (D) OTHER INFORMATION: / Ceres Seq. ID 1597316 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208: acaatggatg agttataggt ttggttaaga cttgaaaagt cattgatcac ggcttttgtc 60 cattattccg tgtttaaagt aatttacatt ctcttttaag atctctcagt ccaaagacaa 120 tgcaaacaat aataatttct ccacttgttt ctcatcgtct ctgtcttgct cgtgctgttc 180 cttgcaaccg tcttctcaac aaccaccacc gtgctcctcc ttcgatccgc ctctcaaacc 240 accettcaac cacctcactc cectettet ceteceece agecagtege gacagteaaa 300 tggcgactga agatgtgcaa gatcccagaa tcgctaagat tgcctcttcc attagagtca 360 tccccgactt ccctaaacca ggaatcatgt ttcaggacat aacgacgett cttctcgaca 420 ctgaggcctt taaggatact attgctttgt ttgttgatag atacaaagat aaaggcatat 480 ctgttgttgc aggtgttgaa gctagaggtt tcatttttgg ccctcctatt gcgttgqcta 540 ttggtgccaa atttgttccc atgaggacgc ccaagaagct acctgggaag gttatttcgg 600 660 aggagtattc gttggagtat ggaccagata cgattgagat gcacgtaggt gcagtagagc 720 ctggtgagcg tgctattatt attgatgncc tcattgccac gggtgggact ctcgctgctg caatccgact acttgaacga gtaggagtgn agattgttga atgtgcttgc gtaattgagt 780 taccagaget taagggaaag gagaaactag gagagaegte getatttgtt ettgtaaagt 840 900 cggctgctta acaagaaact ggaagtgaag gttattggat cgagtgttga tgctattttt catgtatggt gagacatttt gcgtgggatt tgatccttgt tgnttcaact tttatcatan 960 1020 ttggttcagn ctagaaaatg gcatttgaat gtcaggattc gattgcagtt tcctattgtt ccacttaaaa tccccg (2) INFORMATION FOR SEQ ID NO:1209: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 amino acids (B) TYPE: amino acid

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:
Met Gln Thr Ile Ile Ile Ser Pro Leu Val Ser His Arg Leu Cys Leu
10 10 15

1 5 10 15 Ala Arg Ala Val Pro Cys Asn Arg Leu Leu Asn Asn His His Arg Ala 20 25 30

Pro Pro Ser Ile Arg Leu Ser Asn His Arg Ser Thr Thr Ser Leu Arg

Leu Phe Ser Ser Ala Ala Ala Ser Arg Asp Ser Glu Met Ala Thr Glu 50 55 60

Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser Ser Ile Arg Val 65 70 75 80

Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln Asp Ile Thr Thr 85 90 95

Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile Ala Leu Phe Val 100 105 110

Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala Gly Val Glu Ala 115 120 125

Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala Ile Gly Ala Lys 130 135 140

Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly Lys Val Ile Ser 145 150 155 160

Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile Glu Met His Val

Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile Asp Xaa Leu Ile 180 185 190

Ala Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu Leu Glu Arg Val 195 200 205

Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu Leu Pro Glu Leu 210 215 220

Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe Val Leu Val Lys 225 230 235 240

Ser Ala Ala

- (2) INFORMATION FOR SEQ ID NO:1210:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..183
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

Met Ala Thr Glu Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser 1 5 5 10 15 Ser Ile Arg Val Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln

20 25 30
Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile

35 40 45
Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala

Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly 11e 3er val val Ala
50 55 60
Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala

Gly Val Glu Ala Arg Gly Phe lie Phe Gly Flo 110 116 Ala 264 Ala 65 70 75 80

Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly 95

Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile

240

360

110 100 105 Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile 125 120 Asp Xaa Leu Ile Ala Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu 140 135 Leu Glu Arg Val Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu 150 155 Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe 170 165 Val Leu Val Lys Ser Ala Ala 180 (2) INFORMATION FOR SEQ ID NO:1211: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..154 (D) OTHER INFORMATION: / Ceres Seq. ID 1597319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211: Met Phe Gln Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys 5 10 Asp Thr Ile Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser 25 20 Val Val Ala Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile 40 Ala Leu Ala Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys 55 Leu Pro Gly Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro 75 70 Asp Thr Ile Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala 90 85 Ile Ile Ile Asp Xaa Leu Ile Ala Thr Gly Gly Thr Leu Ala Ala Ala 105 100 Ile Arg Leu Leu Glu Arg Val Gly Val Xaa Ile Val Glu Cys Ala Cys 125 120 Val Ile Glu Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr 135 Ser Leu Phe Val Leu Val Lys Ser Ala Ala 150 (2) INFORMATION FOR SEQ ID NO:1212: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1097 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..1097 (D) OTHER INFORMATION: / Ceres Seq. ID 1597344 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212: cacaatttga tacgcgtcag tttgaccaga ggctgaatga agttctcgat ggacaggatg agttcttcac ctcatatgat gaggtccatg agagctttga tgccatgggt ttgcaagaga atcttcttag gggtatctat gcttacggtt tcgaaaagcc ttctgctatt cagcaaagag gaattgtacc cttttgcaag ggtcttgatg tgatccagca ggcacagtct ggtactggaa aaaccgccac tttctgctct ggtgtcttgc agcagcttga ctatgccctt ctccagtgcc

aggetetegt tttggeteec accagagage ttgeteagea gattgagaag gteatgegtg

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cccttggtga ctaccaaggt gtcaaggttc atgcctgtgt tggtggaacc agtgtccgtn
                                                                       420
aggatcageg cattetecag getggtgtte atgttgtegt tggaacteet ggtegtgttt
                                                                       480
ttgacatgct tagaagacaa tctctccgcc ctgactgcat caagatgttt gtccttgatg
                                                                       540
aagctgatga aatgctctcc cgtggtttca aggatcagct catggagaca tggaccaaaa
                                                                       600
caccagagac atcatcatga gagagttcag gtcntggctc gtctcgtgtt ctaatcacaa
ccgatctctt ggctcgtggt atcgatgtgc agcaagtctc tctagtcata aanctttgac
                                                                       720
ctcccaactc agccagagaa ttaccttcac cgtatcggaa gaagtggaag gttcgggaga
aagggtgtgg cgattaactt tgtgancnnt tgangatcag agaatgctgt ttgatattca
                                                                       840
gaaantetne aatginggit gitgagnage tieceneaaa egiggeigat tingeigtga
agaagaagaa gaagaagaan gaagaaaggt tngcttgttn cgcnnntttc ttatttngat
                                                                       960
                                                                      1020
ttttgacccg tctnnnnntc tctgaatcat cgatacatct ttttcattct ctagtattct
tcatcaactc tatcgaacat atatatgtct cttctgacca tatttctttn ttatcaaatg
                                                                      1080
caatatttat ttcttct
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- (2) INFORMATION FOR SEQ ID NO:1213:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..205
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597345
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:
- Gln Phe Asp Thr Arg Gln Phe Asp Gln Arg Leu Asn Glu Val Leu Asp 1 5 10 15
- Gly Gln Asp Glu Phe Phe Thr Ser Tyr Asp Glu Val His Glu Ser Phe 20 25 30
- Asp Ala Met Gly Leu Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr 35 40 45
- Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe 50 55 60
- Cys Lys Gly Leu Asp Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys 65 70 75 80
- Thr Ala Thr Phe Cys Ser Gly Val Leu Gln Gln Leu Asp Tyr Ala Leu 85 90 95
 Leu Gln Cys Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Gln
- 100 105 110 Gln Ile Glu Lys Val Met Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys
- 115 120 125

 Well the Ale Con Val Cly The See Val Arg Yaa Asp Gln Arg Tle
- Val His Ala Cys Val Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg Ile
 130 135 140
- Leu Gln Ala Gly Val His Val Val Val Gly Thr Pro Gly Arg Val Phe
 145 150 155 160
- Leu Met Glu Thr Trp Thr Lys Thr Pro Glu Thr Ser Ser
 195 200 205
- (2) INFORMATION FOR SEQ ID NO:1214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..171

(ix) FEATURE:

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1597346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214: Met Gly Leu Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe 10 Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys 25 20 Gly Leu Asp Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala 4.5 40 Thr Phe Cys Ser Gly Val Leu Gln Gln Leu Asp Tyr Ala Leu Leu Gln 60 Cys Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile 75 Glu Lys Val Met Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys Val His 90 Ala Cys Val Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg Ile Leu Gln 110 105 100 Ala Gly Val His Val Val Val Gly Thr Pro Gly Arg Val Phe Asp Met 125 120 115 Leu Arg Arg Gln Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu 135 140 Asp Glu Ala Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Leu Met 150 155 Glu Thr Trp Thr Lys Thr Pro Glu Thr Ser Ser 165 (2) INFORMATION FOR SEQ ID NO:1215: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..123 (D) OTHER INFORMATION: / Ceres Seq. ID 1597347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215: Met Pro Phe Ser Ser Ala Arg Leu Ser Phe Trp Leu Pro Pro Glu Ser 10 5 Leu Leu Ser Arg Leu Arg Arg Ser Cys Val Pro Leu Val Thr Thr Lys 25 20 Val Ser Arg Phe Met Pro Val Leu Val Glu Pro Val Ser Xaa Arg Ile 40 Ser Ala Phe Ser Arg Leu Val Phe Met Leu Ser Leu Glu Leu Leu Val 55 Val Phe Leu Thr Cys Leu Glu Asp Asn Leu Ser Ala Leu Thr Ala Ser 75 70 Arg Cys Leu Ser Leu Met Lys Leu Met Lys Cys Ser Pro Val Val Ser 90 Arg Ile Ser Ser Trp Arg His Gly Pro Lys His Gln Arg His His His 105 100 Glu Arg Val Gln Val Xaa Ala Arg Leu Val Phe 120 115 (2) INFORMATION FOR SEQ ID NO:1216: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1156 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

(B) LOCATION: 1..1156

(D) OTHER INFORMATION: / Ceres Seq. ID 1597360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216: 60 tgtgcggctc gaagaaggaa cggtgaagtc tttaatagaa gaaaaaggag tgatcaaagg agtgacatac aaaaataaag caggcgaaga aacaacagcc ttggcacctc tcactgtagt 120 180 atgcgacggt tgctactcaa accttcgtcg gtctctaaac gataacaatg ctgaggttct gtottaccaa gttgottaca totogaagaa ttgtoggott gatgatocca aaaacottoa 240 tttgataatg tccaaaccct cctacatcat gttgtaccaa ttaagcagca ctgatgttcg 300 ttgtggtttt gaacttttct ccgccaattt tccttccatt gcaaaaggtg aaatggctac 360 ttttgcgaag aacactctag ctcctcaggt acctccaaaa cttcgcaaaa tattcttgaa 420 aggtctagat gaaggagcac acataaaagc ggtgccagca aagcgcatga cagcttcttt 480 aaccaagaaa aatggagtga ttgtgttggg agatgcattc aacatgcgtc atcnttcggt 540 cgcggctggt atgatggttt tattgtctga cattctcatt ctacgtcgtc ttctccagcc 600 660 actaagcaac cttggtgatg caaacaaagt ctcagaagtc attaagtcct ttaatattat 720 ccgcaagcca atgtcagcga cggtgaacac attaggaaat gcattttctc aagttctaat 780 tgcatcaact gacgaagcaa aagaggcaat gagacaaggt tgctatgatt acctctctag 840 tggtggtttt tgcacgtcgg ggatgatggc tctactaggt ggcatgaatc ctcgtccgct 900 ctctctcata tatcatctat gtgctatcac tttacattca attggccatc ttctatctcc 960 gttggttccc catctcaagg ctgagggagt tagcgaaatg ttttttccag caaacgcagc 1020 cgcatatcgc aaaagctata tggccgcatc tggtctttaa acattgatgc tctaaacagc 1080 aacatacgta agcttgtaaa ctcgttgaaa tgttattgta atgcttagct tacataatat 1140 tacttaatga gtttct

- (2) INFORMATION FOR SEQ ID NO:1217:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

195

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597361
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217: Val Arg Leu Glu Glu Gly Thr Val Lys Ser Leu Ile Glu Glu Lys Gly 15 10 Val Ile Lys Gly Val Thr Tyr Lys Asn Lys Ala Gly Glu Glu Thr Thr 30 25 2.0 Ala Leu Ala Pro Leu Thr Val Val Cys Asp Gly Cys Tyr Ser Asn Leu 45 40 Arg Arg Ser Leu Asn Asp Asn Asn Ala Glu Val Leu Ser Tyr Gln Val 55 Ala Tyr Ile Ser Lys Asn Cys Arg Leu Asp Asp Pro Lys Asn Leu His 75 70 Leu Ile Met Ser Lys Pro Ser Tyr Ile Met Leu Tyr Gln Leu Ser Ser 90 Thr Asp Val Arg Cys Gly Phe Glu Leu Phe Ser Ala Asn Phe Pro Ser 110 105 100 Ile Ala Lys Gly Glu Met Ala Thr Phe Ala Lys Asn Thr Leu Ala Pro 125 120 Gln Val Pro Pro Lys Leu Arg Lys Ile Phe Leu Lys Gly Leu Asp Glu 140 135 Gly Ala His Ile Lys Ala Val Pro Ala Lys Arg Met Thr Ala Ser Leu 155 150 Thr Lys Lys Asn Gly Val Ile Val Leu Gly Asp Ala Phe Asn Met Arg 170 165 His Xaa Ser Val Ala Ala Gly Met Met Val Leu Leu Ser Asp Ile Leu 190 185 Ile Leu Arg Arg Leu Leu Gln Pro Leu Ser Asn Leu Gly Asp Ala Asn

200

205

Lys Val Ser Glu Val Ile Lys Ser Phe Asn Ile Ile Arg Lys Pro Met 220 215 Ser Ala Thr Val Asn Thr Leu Gly Asn Ala Phe Ser Gln Val Leu Ile 230 235 Ala Ser Thr Asp Glu Ala Lys Glu Ala Met Arg Gln Gly Cys Tyr Asp 250 245 Tyr Leu Ser Ser Gly Gly Phe Cys Thr Ser Gly Met Met Ala Leu Leu 265 270 260 Gly Gly Met Asn Pro Arg Pro Leu Ser Leu Ile Tyr His Leu Cys Ala 275 280 Ile Thr Leu His Ser Ile Gly His Leu Leu Ser Pro Phe Pro Ser Pro 295 300 Leu Ser Ile Trp His Ser Leu Arg Leu Phe Gly Leu Ala Leu Lys Met 310 315 Leu Val Pro His Leu Lys Ala Glu Gly Val Ser Glu Met Phe Pro 325 330 335 Ala Asn Ala Ala Ala Tyr Arg Lys Ser Tyr Met Ala Ala Ser Gly Leu 345 340

(2) INFORMATION FOR SEQ ID NO:1218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..270
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597362
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218: Met Ser Lys Pro Ser Tyr Ile Met Leu Tyr Gln Leu Ser Ser Thr Asp 10 5 Val Arg Cys Gly Phe Glu Leu Phe Ser Ala Asn Phe Pro Ser Ile Ala 25 20 Lys Gly Glu Met Ala Thr Phe Ala Lys Asn Thr Leu Ala Pro Gln Val 40 Pro Pro Lys Leu Arg Lys Ile Phe Leu Lys Gly Leu Asp Glu Gly Ala 55 His Ile Lys Ala Val Pro Ala Lys Arg Met Thr Ala Ser Leu Thr Lys 75 70 Lys Asn Gly Val Ile Val Leu Gly Asp Ala Phe Asn Met Arg His Xaa 90 85 Ser Val Ala Ala Gly Met Met Val Leu Leu Ser Asp Ile Leu Ile Leu 105 Arg Arg Leu Gln Pro Leu Ser Asn Leu Gly Asp Ala Asn Lys Val 125 120 115 Ser Glu Val Ile Lys Ser Phe Asn Ile Ile Arg Lys Pro Met Ser Ala 135 Thr Val Asn Thr Leu Gly Asn Ala Phe Ser Gln Val Leu Ile Ala Ser 150 155 Thr Asp Glu Ala Lys Glu Ala Met Arg Gln Gly Cys Tyr Asp Tyr Leu 170 175 165 Ser Ser Gly Gly Phe Cys Thr Ser Gly Met Met Ala Leu Leu Gly Gly 185 180 Met Asn Pro Arg Pro Leu Ser Leu Ile Tyr His Leu Cys Ala Ile Thr 205 200 Leu His Ser Ile Gly His Leu Leu Ser Pro Phe Pro Ser Pro Leu Ser 210 215 220 Ile Trp His Ser Leu Arg Leu Phe Gly Leu Ala Leu Lys Met Leu Val

235 225 230 Pro His Leu Lys Ala Glu Gly Val Ser Glu Met Phe Pro Ala Asn 245 250 Ala Ala Ala Tyr Arg Lys Ser Tyr Met Ala Ala Ser Gly Leu 260 265 (2) INFORMATION FOR SEQ ID NO:1219: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..263 (D) OTHER INFORMATION: / Ceres Seq. ID 1597363 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219: Met Leu Tyr Gln Leu Ser Ser Thr Asp Val Arg Cys Gly Phe Glu Leu 5 10 Phe Ser Ala Asn Phe Pro Ser Ile Ala Lys Gly Glu Met Ala Thr Phe 20 25 Ala Lys Asn Thr Leu Ala Pro Gln Val Pro Pro Lys Leu Arg Lys Ile 40 Phe Leu Lys Gly Leu Asp Glu Gly Ala His Ile Lys Ala Val Pro Ala 55 Lys Arg Met Thr Ala Ser Leu Thr Lys Lys Asn Gly Val Ile Val Leu 65 70 75 Gly Asp Ala Phe Asn Met Arg His Xaa Ser Val Ala Ala Gly Met Met 85 90 Val Leu Leu Ser Asp Ile Leu Ile Leu Arg Arg Leu Leu Gln Pro Leu 100 105 110 Ser Asn Leu Gly Asp Ala Asn Lys Val Ser Glu Val Ile Lys Ser Phe 115 120 125 Asn Ile Ile Arg Lys Pro Met Ser Ala Thr Val Asn Thr Leu Gly Asn 130 135 140 Ala Phe Ser Gln Val Leu Ile Ala Ser Thr Asp Glu Ala Lys Glu Ala 150 155 160 Met Arg Gln Gly Cys Tyr Asp Tyr Leu Ser Ser Gly Gly Phe Cys Thr 165 170 175 Ser Gly Met Met Ala Leu Leu Gly Gly Met Asn Pro Arg Pro Leu Ser 180 185 190 Leu Ile Tyr His Leu Cys Ala Ile Thr Leu His Ser Ile Gly His Leu 195 200 205 Leu Ser Pro Phe Pro Ser Pro Leu Ser Ile Trp His Ser Leu Arg Leu 210 215 Phe Gly Leu Ala Leu Lys Met Leu Val Pro His Leu Lys Ala Glu Gly 225 230 235 Val Ser Glu Met Phe Phe Pro Ala Asn Ala Ala Ala Tyr Arg Lys Ser 245 250 Tyr Met Ala Ala Ser Gly Leu 260 (2) INFORMATION FOR SEQ ID NO:1220: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 504 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..504

(D) OTHER INFORMATION: / Ceres Seq. ID 1597376 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:
aatcacggcg gcggcggcgg aagagtagca gcagcaggcg gcgccgagta gcgtctcccc acctcgagct tgccaccatg gctagaggat tgaagaagca tttgaagagg ctcaatgcgc ccaagcattg gatgctggac aagcttggcg gasttttgct cccaaaccat cttctggacc tcacaagtct agggagtgcc tgccactgat cctcatcatc aggaacaggc tcaagtatgc tcttacatac cgtgagtcat ttccatcctg atgcaacgcc atgtacttgt tgatggcaag gtcaggacag acaagaccta ccctgctggg ttcatggatg tcatttccat ccccaagacc aacgagaact acaggctgct gtatgacact aagggceget tccgccttca cccaaatcagg gatgaggatg ctaagttcaa gctttgcaag gttaggtctg ttcagtttgg gcagaagggc atcccgtacc tgaacacgta tgac (2) INFORMATION FOR SEQ ID NO:1221: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 amino acids
(B) TYPE: amino acid (C) STRANDEDNESS:
(C) SIRANDEDNESS: (D) TOPOLOGY: linear
<pre>(ii) MOLECULE TYPE: peptide (ix) FEATURE:</pre>
(A) NAME/KEY: peptide
(B) LOCATION: 168 (D) OTHER INFORMATION: / Ceres Seq. ID 1597377
(xi) SEQUENCE DESCRIPTION: SEQ ID No:1221:
Ser Arg Arg Arg Arg Lys Ser Ser Ser Arg Arg Arg Val 1 5 10 15
Ala Ser Pro His Leu Glu Leu Ala Thr Met Ala Arg Gly Leu Lys Lys 20 25 30
His Leu Lys Arg Leu Asn Ala Pro Lys His Trp Met Leu Asp Lys Leu 35 40 45
Gly Gly Xaa Leu Leu Pro Asn His Leu Leu Asp Leu Thr Ser Leu Gly 50 60
Ser Ala Cys His
(2) INFORMATION FOR SEQ ID NO:1222:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
<pre>(ix) FEATURE: (A) NAME/KEY: peptide</pre>
(B) LOCATION: 178
(D) OTHER INFORMATION: / Ceres Seq. ID 1597378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:
Met Gln Arg His Val Leu Val Asp Gly Lys Val Arg Thr Asp Lys Thr 1 5 10 15
Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Pro Lys Thr Asn Glu 20 25 30
Asn Tyr Arg Leu Leu Tyr Asp Thr Lys Gly Arg Phe Arg Leu His Pro 35 40 45
Ile Arg Asp Glu Asp Ala Lys Phe Lys Leu Cys Lys Val Arg Ser Val 50 55 60
Gln Phe Gly Gln Lys Gly Ile Pro Tyr Leu Asn Thr Tyr Asp 65 70 75
(2) INFORMATION FOR SEQ ID NO:1223:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..70 (D) OTHER INFORMATION: / Ceres Seq. ID 1597379 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223: Met Tyr Leu Leu Met Ala Arg Ser Gly Gln Thr Arg Pro Thr Leu Leu 10 5 Gly Ser Trp Met Ser Phe Pro Ser Pro Arg Pro Thr Arg Thr Thr Gly 2.5 2.0 Cys Cys Met Thr Leu Arg Ala Ala Ser Ala Phe Thr Gln Ser Gly Met 40 Arg Met Leu Ser Ser Ser Phe Ala Arg Leu Gly Leu Phe Ser Leu Gly 55 Arg Arg Ala Ser Arg Thr 70 (2) INFORMATION FOR SEQ ID NO:1224: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..466 (D) OTHER INFORMATION: / Ceres Seq. ID 1597392 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224: aatagcetce geeteteett ecagtgteeg eegtegtgeg etegetaeee eteteeeteg 60 aggcctttgc cggcgaagag cgcccagtcg cccaccagga tgaagtttgt tgctgcctac 120 etgettgetg teetegetgg gaactecage ceetetgeeg aggaettgae agecattetg 180 gagtcagttg gctgtgaagt tgacaatgaa aagatggaac tccttctgtc ccaactgagc 240 ggtaaggaca ttaccgagct cattgctgct ggcagggaga agtttgcttc agtcccatgt 300 ggeggtggge ggtgtggetg ttgtggcage tgcccetget getggeggeg etectgcage 360 tgaggcgaag aaagaagaga aggtggagga gaaggaagaa agtgatgacg acatgggctt 420 cagoctotto gactaagoot gtgcatagto aagagtattg tttttg (2) INFORMATION FOR SEQ ID NO:1225: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..120 (D) OTHER INFORMATION: / Ceres Seq. ID 1597393 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225: Asn Ser Leu Arg Leu Ser Phe Gln Cys Pro Pro Ser Cys Ala Arg Tyr 10 Pro Ser Pro Ser Arg Pro Leu Pro Ala Lys Ser Ala Gln Ser Pro Thr 30 25 Arg Met Lys Phe Val Ala Ala Tyr Leu Leu Ala Val Leu Ala Gly Asn 45 40 Ser Ser Pro Ser Ala Glu Asp Leu Thr Ala Ile Leu Glu Ser Val Gly Cys Glu Val Asp Asn Glu Lys Met Glu Leu Leu Leu Ser Gln Leu Ser

75

90

Gly Lys Asp Ile Thr Glu Leu Ile Ala Ala Gly Arg Glu Lys Phe Ala

Ser Val Pro Cys Gly Gly Gly Arg Cys Gly Cys Gly Ser Cys Pro

70

110 105 100 Cys Cys Trp Arg Arg Ser Cys Ser 115 120 (2) INFORMATION FOR SEQ ID NO:1226: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..87 (D) OTHER INFORMATION: / Ceres Seq. ID 1597394 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226: Met Lys Phe Val Ala Ala Tyr Leu Leu Ala Val Leu Ala Gly Asn Ser 10 Ser Pro Ser Ala Glu Asp Leu Thr Ala Ile Leu Glu Ser Val Gly Cys Glu Val Asp Asn Glu Lys Met Glu Leu Leu Leu Ser Gln Leu Ser Gly 40 Lys Asp Ile Thr Glu Leu Ile Ala Ala Gly Arg Glu Lys Phe Ala Ser 55 Val Pro Cys Gly Gly Gly Arg Cys Gly Cys Cys Gly Ser Cys Pro Cys 75 70 Cys Trp Arg Arg Ser Cys Ser 85 (2) INFORMATION FOR SEQ ID NO:1227: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 502 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..502 (D) OTHER INFORMATION: / Ceres Seq. ID 1597396 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227: aatagcetee geeteteett eeagtgteeg eegtegtgeg etegetaeee eteteeeteg 60 aggcetttge egegaagage geceagtege ceaecaggat gaagtttgtt getgeetate 120 tgettgetgt cetegetggg aactecagee cetetgeega ggaettgaca teeattetgg 180 agtcagttgg ctgtgaagtt gacaatgaaa agatggaact ccttctgtcc cagctgagcg 240 300 gtaaggacat taccgagctc attgccgccg gcagggagaa gtttgcttca gtcccatgtg geggtggegg tgtggetgte geggeastge ceetgetget ggeggeggeg gegeteetge 360 agctgaggcg aagaaagaag agaaggtgga ggagaaggaa gaaagtgatg acgacatggg 420 cttcagctct tcgactaagt ctgtgcaata gccaagggta ttgtttttga gtcgaggaag 480 cagagggaa gaaaaatagt ag (2) INFORMATION FOR SEQ ID NO:1228: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..64 (D) OTHER INFORMATION: / Ceres Seq. ID 1597397 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228: Ile Ala Ser Ala Ser Pro Ser Ser Val Arg Arg Arg Ala Leu Ala Thr

- (2) INFORMATION FOR SEQ ID NO:1229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597398
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

Met Lys Phe Val Ala Ala Tyr Leu Leu Ala Val Leu Ala Gly Asn Ser 1 10 15

Ser Pro Ser Ala Glu Asp Leu Thr Ser Ile Leu Glu Ser Val Gly Cys 20 25 30

Glu Val Asp Asn Glu Lys Met Glu Leu Leu Leu Ser Gln Leu Ser Gly

Lys Asp Ile Thr Glu Leu Ile Ala Ala Gly Arg Glu Lys Phe Ala Ser 50 55 60

Val Pro Cys Gly Gly Gly Val Ala Val Ala Ala Xaa Pro Leu Leu 65 70 75 80

Leu Ala Ala Ala Leu Leu Gln Leu Arg Arg Arg Lys Lys Arg Arg 85 90 95

Trp Arg Arg Lys Lys Val Met Thr Thr Trp Ala Ser Ala Leu Arg
100 105 110

Leu Ser Leu Cys Asn Ser Gln Gly Tyr Cys Phe 115 120

- (2) INFORMATION FOR SEQ ID NO:1230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

Met Glu Leu Leu Ser Gln Leu Ser Gly Lys Asp Ile Thr Glu Leu

1 15

Ile Ala Ala Gly Arg Glu Lys Phe Ala Ser Val Pro Cys Gly Gly Gly 20 25 30

Gly Val Ala Val Ala Ala Xaa Pro Leu Leu Leu Ala Ala Ala Leu 35 40 45

Leu Gln Leu Arg Arg Arg Lys Lys Arg Arg Trp Arg Arg Arg Lys Lys 50 55 60

Val Met Thr Trp Ala Ser Ala Leu Arg Leu Ser Leu Cys Asn Ser 65 70 75 80

Gln Gly Tyr Cys Phe

- (2) INFORMATION FOR SEQ ID NO:1231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..509
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597412
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231: cacccaagte caagcacedn teccaaaaaa ateceecatt ttettegagg egaggagage 60 gtgaaagaca gggcaccgnc agcgacgatg tcggggcgcg gcaagggcgg caaaggtctg 120 ggcaagggcg gasaaagcgc caccgtaagt ctccgtgaca acatccaggr gcatcaccaa 180 gecegegate egtagetgge teggagggge ggegtgaage satttteggg gettatetae 240 gaggagaccc gcggcgtcct caagatcttc ctcgagaacg tcatccgcga cgccgtcacc 300 tacaccgage acgcacgccg caagactgtt accgccatgg acgtcgtcta cgcgctcaag 360 cscagggccg aaccetetac ggetteggag getaggetgg atgeetette teettgetgt 420 cgtggatgcc tgtttgttgt tagggttact tcgtttagtt ccttgtctgt gacgtgttgg 480
- (2) INFORMATION FOR SEQ ID NO:1232:

actattgtta gtagtattct tgaagttgt

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597413
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

 His Pro
 Ser
 Pro
 Ser
 Thr
 Xaa
 Pro
 Lys
 Lys
 Ile
 Pro
 His
 Phe
 Leu
 Arg

 1
 Ser
 Val
 Lys
 Asp
 Arg
 Ala
 Pro
 Xaa
 Ala
 Thr
 Met
 Ser
 Gly

 20
 Ser
 25
 Ser
 Ser
 30
 Ser
 Se

Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Xaa Ser Ala Thr 35 40

Val Ser Leu Arg Asp Asn Ile Gln Xaa His His Gln Ala Arg Asp Pro 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1233:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..51
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

Pro Lys Ser Lys His Xaa Ser Gln Lys Asn Pro Pro Phe Ser Ser Arg 1 5 10 15

Arg Gly Glu Arg Glu Arg Gln Gly Thr Xaa Ser Asp Asp Val Gly Ala 20 25 30

Arg Gln Gly Arg Gln Arg Ser Gly Gln Gly Arg Xaa Lys Arg His Arg 35 40 45

Lys Ser Pro 50 (2) INFORMATION FOR SEQ ID NO:1234: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..57 (D) OTHER INFORMATION: / Ceres Seq. ID 1597415 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234: Met Asp Val Val Tyr Ala Leu Lys Xaa Arg Ala Glu Pro Ser Thr Ala 5 10 Ser Glu Ala Arg Leu Asp Ala Ser Ser Pro Cys Cys Arg Gly Cys Leu 30 25 Phe Val Val Arg Val Thr Ser Phe Ser Ser Leu Ser Val Thr Cys Trp 40 35 Thr Ile Val Ser Ser Ile Leu Glu Val 55 (2) INFORMATION FOR SEQ ID NO:1235: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 509 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..509 (D) OTHER INFORMATION: / Ceres Seq. ID 1597416 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235: 60 tngctctcaa atatctctca ccacctctss sctcagcttn tcsscacctt tggtcaggca ggctcaggca aagggggggg msaacaagga cgagsgatgg sgaccaaggt catctgcttc 120 cttgtgctcg catccctgct cctcgccgtc gcctttcccg tgtctgctct gcgncagcrg 180 ttcgaagaag ggcggcggcg gcggtggtgg cggaggcagt gttagcggaa sgcaggcgcc 240 aacctgaatc cctgggagtg ctcgcccaag tgcgggtcgc ggtgctccaa gacgcagtac 300 aggaaggeet geeteacett atgeaacaag tgetgegeea agtgeetetg egtgeeaeeg 360 gggttctacg gcaacaaggg cgcctgccct gctacaacaa ctggaaaacc aaggaaggag 420 ggeccaagtg eccetagaat aagateeace geageteeeg teegecattg tesemeette 480 tccgaatctg ggaacgtgtt gttcatctt (2) INFORMATION FOR SEQ ID NO:1236: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..74 (D) OTHER INFORMATION: / Ceres Seq. ID 1597417 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236: Xaa Leu Ser Asn Ile Ser His His Leu Xaa Xaa Gln Leu Xaa Xaa Thr 10 Phe Gly Gln Ala Gly Ser Gly Lys Gly Gly Xaa Xaa Gln Gly Arg Xaa 25 Met Xaa Thr Lys Val Ile Cys Phe Leu Val Leu Ala Ser Leu Leu

40

Ala Val Ala Phe Pro Val Ser Ala Leu Xaa Gln Xaa Phe Glu Glu Gly 50 55 60

Arg Arg Arg Trp Trp Arg Arg Gln Cys 65 70

- (2) INFORMATION FOR SEQ ID NO:1237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597418
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

Xaa Ser Gln Ile Ser Leu Thr Thr Ser Xaa Leu Ser Xaa Xaa Pro 1 5 10 15

Leu Val Arg Gln Ala Gln Ala Lys Gly Ala Xaa Asn Lys Asp Glu Xaa 20 25 30

Trp Xaa Pro Arg Ser Ser Ala Ser Leu Cys Ser His Pro Cys Ser Ser 35 40 45

Pro Ser Pro Phe Pro Cys Leu Leu Cys Xaa Ser Xaa Ser Lys Lys Gly 50 60

Gly Gly Gly Gly Gly Gly Gly Ser Val Ser Gly Xaa Gln Ala Pro
65 70 75 80
Thr

- (2) INFORMATION FOR SEQ ID NO:1238:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597419
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

Ala Leu Lys Tyr Leu Ser Pro Pro Xaa Xaa Ser Ala Xaa Xaa His Leu 1 5 10 15

Trp Ser Gly Arg Leu Arg Gln Arg Gly Arg Xaa Thr Arg Thr Xaa Asp 20 25 30

Xaa Asp Gln Gly His Leu Leu Pro Cys Ala Arg Ile Pro Ala Pro Arg 35 40 45

Arg Arg Leu Ser Arg Val Cys Ser Ala Xaa Xaa Val Arg Arg Ala 50 55 60

Ala Ala Val Val Ala Glu Ala Val Leu Ala Glu Xaa Arg Arg Gln 65 70 75 80

Pro Glu Ser Leu Gly Val Leu Ala Gln Val Arg Val Ala Val Leu Gln 85 90 95

Asp Ala Val Gln Glu Gly Leu Pro His Leu Met Gln Gln Val Leu Arg $100 \hspace{1.5cm} 105 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Gln Val Pro Leu Arg Ala Thr Gly Val Leu Arg Gln Gln Gly Arg Leu 115 120 125

Pro Cys Tyr Asn Asn Trp Lys Thr Lys Glu Gly Gly Pro Lys Cys Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:1239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..492
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597426
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

aattttagga cctaattata agastctctc ttggagatgc tctaaggcac cgactcgccg 60 gggacagaga gagagaccga cgcgccggca gatcccaagc tcaccctaga gggggaagag 120 ggcgaccgaa gcggcgatgg gtttcatcat ggacttcgcg gagaatctga tcctccgtct 180 gatggaggac ccggacaagc gcgaccaggt tcggcgggag catgtctaca agatgaagga 240 gcggtgcgag cgcactaagg cggcgtggag cctccctctg cgcccctacg gcttctggac 300 cttcgaccgc ttcaactcgc agctctcctg ggatccccag atcagccagg ccgccggcgt 360 negggaccce tacgacgacc teategcacg ceactetgge tegeogccgt ettectgaac 420 accepttecg atetttgece agaaggteta ettgggeate aataagaaac tettteeeet 480 caaactgatt gt

- (2) INFORMATION FOR SEQ ID NO:1240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597427
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met Gly Phe Ile Met Asp Phe Ala Glu Asn Leu Ile Leu Arg Leu Met 1 5 10 15

Glu Asp Pro Asp Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr Lys
20 25 30

Met Lys Glu Arg Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro Leu 35 40 45

Arg Pro Tyr Gly Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser 50 55 60

Trp Asp Pro Gln Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr Asp 65 70 75 80

Asp Leu Ile Ala Arg His Ser Gly Ser Pro Pro Ser Ser 85 90

- (2) INFORMATION FOR SEQ ID NO:1241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597428
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

Met Asp Phe Ala Glu Asn Leu Ile Leu Arg Leu Met Glu Asp Pro Asp

1 5 10 15

15 10 15

Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr Lys Met Lys Glu Arg 20 25 30

Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro Leu Arg Pro Tyr Gly

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                            40
                                                 45
        35
Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser Trp Asp Pro Gln
                        55
Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr Asp Asp Leu Ile Ala
                    70
                                         75
Arg His Ser Gly Ser Pro Pro Ser Ser
                85
(2) INFORMATION FOR SEQ ID NO:1242:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 78 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
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- - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597429
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

Met Glu Asp Pro Asp Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr 10

Lys Met Lys Glu Arg Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro 25 20

Leu Arg Pro Tyr Gly Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu 40

Ser Trp Asp Pro Gln Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr 55

Asp Asp Leu Ile Ala Arg His Ser Gly Ser Pro Pro Ser Ser 70

- (2) INFORMATION FOR SEQ ID NO:1243:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..868
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597430
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

agaagcttat cgcttatcat ccgcgcctct acatttcttc tctctctgct cctccgcctc 60 cgcctccgsc tggwtccsat ccaagacagg gatcgccatg tcggactcgg aggagcacca 120 180 cttcgaatcg aaggccgacg ctggggcgtc caagacctac ccgcagcagg ctggcaccgt ccgtaagaac ggcttcatcg tcatcaagaa ccgtccctgc aaggttgtgg aggtttctac 240 300 ctccaagact ggtaagcatg gccacgccaa atgccacttt gtcgccatag acatattcaa 360 tgggaaaaag cttgaagata ttgttccttc atcacacaac tgtgacattc cgcatgtgaa 420 ccgtactgag tatcagctga ttgatatttc tgaggatgga tttgtgagcc ttcttacttc agatggcaac actaaggatg atcttagact cccaactgat gagactcttg tggcccagat 480 540 taaggaaggg ttcgaaagcg ggaaggatct tgttgtgact gtccagtctg cgatgggga ggagcagatc tgcgcgctga aggatgttgg ccccaagtaa cttccttggc tttggagacg 600 660 gaaccctact ctatctcaac ttaaatcgga aaagaagtgt atcaccaaaa ggattgctac cgagacattc acctggcttg agctbgcttt tgctatagcg tgcaaggggt tgctgggtgt 720 cgtacctacc tgacttatca ttatctgtgg ttacattctg gaccctgtat tttctatgct 780 840 ttcatgtctc tctactttct agtattaatt atcaataagt tggtttggaa tggttgaatt gcatccaatg catgaagttt ctttggct

- (2) INFORMATION FOR SEQ ID NO:1244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..192
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597431
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:
 Glu Ala Tyr Arg Leu Ser Ser Ala Pro Leu His Phe Phe Ser Leu Cys
 1 5 10 15
- Ser Ser Ala Ser Ala Ser Xaa Trp Xaa Xaa Ser Lys Thr Gly Ile Ala 20 25 30
- Met Ser Asp Ser Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly
- Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Val Arg Lys Asn Gly 50 55 60
- Phe Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr 65 70 75 80
- Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile 85 90 95
- Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His
- Asn Cys Asp Ile Pro His Val Asn Arg Thr Glu Tyr Gln Leu Ile Asp 115 120 125
- Ile Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Ser Asp Gly Asn Thr
 130 135 140
- Lys Asp Asp Leu Arg Leu Pro Thr Asp Glu Thr Leu Val Ala Gln Ile 145 150 155 160
- Lys Glu Gly Phe Glu Ser Gly Lys Asp Leu Val Val Thr Val Gln Ser 165 170 175
- Ala Met Gly Glu Glu Gln Ile Cys Ala Leu Lys Asp Val Gly Pro Lys 180 185 190
- (2) INFORMATION FOR SEQ ID NO:1245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597432
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:
- Met Ser Asp Ser Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly
 1 5 10 15
- Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Val Arg Lys Asn Gly 20 25 30
- Phe Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr 35 40 45
- Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile
 50 55 60
- Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His 65 70 75 80
- Asn Cys Asp Ile Pro His Val Asn Arg Thr Glu Tyr Gln Leu Ile Asp 85 90 95
- Ile Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Ser Asp Gly Asn Thr 100 105 110
- Lys Asp Asp Leu Arg Leu Pro Thr Asp Glu Thr Leu Val Ala Gln Ile

120

180

- (2) INFORMATION FOR SEQ ID NO:1246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..239
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597437
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246: acagcatcte aagtetteae actectegee ateacataaa accagtgeaa geagaageag egeaatggeg ageageacea tggeeetete eteeacagee ttegeeggea akgeagtgaa egtgeegteg tetetewteg gegangeeeg egtgaegatg egeaagangg eggegaakge aaageeggeg geageteeg geageeegtg gtaeggeee gamegegtge tetacetgg (2) INFORMATION FOR SEQ ID NO:1247:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597438
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Gln His Leu Lys Ser Ser His Ser Ser Pro Ser His Lys Thr Ser Ala 1 5 10 15

Ser Arg Ser Ser Ala Met Ala Ser Ser Thr Met Ala Leu Ser Ser Thr 20 25 30

Ala Phe Ala Gly Xaa Ala Val Asn Val Pro Ser Ser Leu Xaa Gly Xaa

Ala Arg Val Thr Met Arg Lys Xaa Ala Ala Xaa Ala Lys Pro Ala Ala 50 55 60

Ser Ser Gly Ser Pro Trp Tyr Gly Pro Xaa Arg Val Leu Tyr Leu 65 70 75

- (2) INFORMATION FOR SEQ ID NO:1248:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..58
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597439
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

Met Ala Ser Ser Thr Met Ala Leu Ser Ser Thr Ala Phe Ala Gly Xaa

Ala Val Asn Val Pro Ser Ser Leu Xaa Gly Xaa Ala Arg Val Thr Met 20 25 30

Arg Lys Xaa Ala Ala Xaa Ala Lys Pro Ala Ala Ser Ser Gly Ser Pro

45 40 Trp Tyr Gly Pro Xaa Arg Val Leu Tyr Leu 55 50 (2) INFORMATION FOR SEQ ID NO:1249: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..53 (D) OTHER INFORMATION: / Ceres Seq. ID 1597440 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249: Met Ala Leu Ser Ser Thr Ala Phe Ala Gly Xaa Ala Val Asn Val Pro 10 5 Ser Ser Leu Xaa Gly Xaa Ala Arg Val Thr Met Arg Lys Xaa Ala Ala 25 Xaa Ala Lys Pro Ala Ala Ser Ser Gly Ser Pro Trp Tyr Gly Pro Xaa 40 35 Arg Val Leu Tyr Leu 50 (2) INFORMATION FOR SEQ ID NO:1250: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..130 (D) OTHER INFORMATION: / Ceres Seq. ID 1597452 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250: tctcccaaag ccatcttcct tccgcggact agttttttct gaagattcgg cgatggcggc 60 gacgatccaa tccgtgaagg cgcgccagat ctttgacagc cgcggcaacc ctacagtcga 120 ggtcgacgtg (2) INFORMATION FOR SEQ ID NO:1251: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1597453 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251: Leu Pro Lys Pro Ser Ser Phe Arg Gly Leu Val Phe Ser Glu Asp Ser 1.0 Ala Met Ala Ala Thr Ile Gln Ser Val Lys Ala Arg Gln Ile Phe Asp 25 20 Ser Arg Gly Asn Pro Thr Val Glu Val Asp Val 4.0 35 (2) INFORMATION FOR SEQ ID NO:1252: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 446 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..446
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

aagctcetcg tcaccagtca gaaaacagtg ggatcgagtt gtttcactgc acgagcacat 60 cctccggcga ccaccggcct ccctctcgt cctctagcga ccgaccaacg cgtcgagcga 120 agatgtcgtg gcagacgtac gtggacgagc aaccctggat gtgcgagatc gagggccacc gccgagttca agcccgagga gatggctgcc atcatgaagg atttcgacga gccggggcac cgagggcacc cggcccgacc cggcccgacc cggcccgacc cggcccgacc cggcccgacc cggcccgacc cggcccgacc cggcccgacc cggcccgacc cgaggagcac ccaagtacat ggtcatccaa gccggggcac 300 gagctgtcat ccgtggcaag aagggatccg ggggcatcac tgtgaagaaa acagggcagt 420 cactcatcat tggcatctac gacgag

- (2) INFORMATION FOR SEQ ID NO:1253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597457
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

Lys Leu Leu Val Thr Ser Gln Lys Thr Val Gly Ser Ser Cys Phe Thr 1 10 15

Ala Arg Ala His Pro Pro Ala Thr Thr Gly Leu Pro Leu Arg Pro Leu 20 25 30

Ala Thr Asp Gln Arg Val Glu Arg Arg Cys Arg Gly Arg Arg Thr Trp 35 40 45

Thr Ser Asn Pro Gly Cys Ala Arg Ser Arg Ala Thr Thr Ser Arg Arg 50 55 60

Arg Pro Ser Ser Ala Thr Xaa Ala Thr Trp Ala Gln Ser Thr Ala Phe 65 70 75 80

Pro Glu Phe Lys Pro Glu Glu Met Ala Ala Ile Met Lys Asp Phe Asp 85 90 95

Glu Pro Gly His Ser Pro Arg Pro Ala 100 105

- (2) INFORMATION FOR SEQ ID NO:1254:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597458
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:
- Ala Pro Arg His Gln Ser Glu Asn Ser Gly Ile Glu Leu Phe His Cys 1 10 15

Thr Ser Thr Ser Ser Gly Asp His Arg Pro Pro Ser Pro Ser Ser Ser 20 25 30

Asp Arg Pro Thr Arg Arg Ala Lys Met Ser Trp Gln Thr Tyr Val Asp 35 40 45

Glu Gln Pro Trp Met Cys Glu Ile Glu Gly His His Leu Thr Ser Ala

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Ala Ile Val Gly His Xaa Arg His Leu Gly Ser Glu His Arg Ile Pro
                                        75
Arg Val Gln Ala Arg Gly Asp Gly Cys His His Glu Gly Phe Arg Arg
                85
                                    90
Ala Gly Ala Leu Ala Pro Thr Gly Leu Ile Leu Gly Gly Thr Lys Tyr
                                105
            100
Met Val Ile Gln Val Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly
                                                 125
                            120
       115
Ser Gly Gly Ile Thr Val Lys Lys Thr Gly Gln Ser Leu Ile Ile Gly
                        135
    130
Ile Tyr Asp Glu
145
(2) INFORMATION FOR SEQ ID NO:1255:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 108 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..108
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597459
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:
Met Ser Trp Gln Thr Tyr Val Asp Glu Gln Pro Trp Met Cys Glu Ile
                                    10
                5
Glu Gly His His Leu Thr Ser Ala Ala Ile Val Gly His Xaa Arg His
                                25
Leu Gly Ser Glu His Arg Ile Pro Arg Val Gln Ala Arg Gly Asp Gly
                                                 45
                            40
Cys His His Glu Gly Phe Arg Arg Ala Gly Ala Leu Ala Pro Thr Gly
                                             60
                        55
Leu Ile Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Val Glu Pro Gly
                                         75
                    70
Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly Ile Thr Val Lys Lys
                                     90
                85
Thr Gly Gln Ser Leu Ile Ile Gly Ile Tyr Asp Glu
            100
(2) INFORMATION FOR SEQ ID NO:1256:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 472 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..472
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597476
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:
 atctcagcag tgacgaactc gaagcttgck ttcttgtagt agaggtcggc agcaagcggt
 ggtagagcga gaggtcgaga agatgaagag cagcactctg ttggcgatcc tagttctcca
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- 60 120 ggcccttctg gtctctgcgg ccgtggcaaa ggacctgcag ggccgacgac gaagaagcag 180 240 tgctggttgc ggcgagtgca ccasctggtc gggcgtgtgg acctgcgacg acctcctcac caagtgegee gecaectgea agaactgegt eeeegtgtee aeggaeaagg gggeeateaa 300 gtacaggtgc cgcgacttcc tccccgaaaa ctgcggctgc aagatccact agagactcat 360 ccaattccac catggccgcg cgccacagcg gcacagccga ttggatcctt ccatgttcct 420 ccgtccgtcc gccttgctac aagcaggcag ccacaccaat aagctagctc tt
- (2) INFORMATION FOR SEQ ID NO:1257:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

Met Lys Ser Ser Thr Leu Leu Ala Ile Leu Val Leu Gln Ala Leu Leu 1 5 10 15

Val Ser Ala Ala Val Ala Lys Asp Leu Gln Gly Arg Arg Arg Ser 20 25 30

Ser Ala Gly Cys Gly Glu Cys Thr Xaa Trp Ser Gly Val Trp Thr Cys 35 40 45

Asp Asp Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro 50 55 60

Val Ser Thr Asp Lys Gly Ala Ile Lys Tyr Arg Cys Arg Asp Phe Leu 65 70 75 80

Pro Glu Asn Cys Gly Cys Lys Ile His 85

- (2) INFORMATION FOR SEQ ID NO:1258:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..406
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597478
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

 accaaggaaa ttcacaaagc gcctagcaaa agcatacttc ccgaagcact cttgcaatcc 60

 actgagttct gtttgttgag acgcatagag ctagctgcta gcgtcgacaa tgtcgctcgt 120

 gaggcgcacg aacgtgttcg accccttctc gatggacctc tgggatccct tcgacaccat 180

 gttccgctcc atcgtccgt cggcgacctc caccaactcc gagactgccg ccttcgccag cgccgcatc gactggaagg agacgcccga ggsgcacgtc ttcaaggccg acctcccgg 300

 cgtcaagaag gaggaggtca aggtcgaggt cgaagmggnc aacgtgctgg tcatcagcgg 360

 ccagcgcasa gggagaagga ggacaaggac gacaagtgc accgcg
- (2) INFORMATION FOR SEQ ID NO:1259:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597479
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Thr Lys Glu Ile His Lys Ala Pro Ser Lys Ser Ile Leu Pro Glu Ala 1 5 10 15

Leu Leu Gln Ser Thr Glu Phe Cys Leu Leu Arg Arg Ile Glu Leu Ala 20 25 30

Ala Ser Val Asp Asn Val Ala Arg Glu Ala His Glu Arg Val Arg Pro 35 40 45

Leu Leu Asp Gly Pro Leu Gly Ser Leu Arg His His Val Pro Leu His 50 55 60
Arg Pro Val Gly Asp Leu His Gln Leu Arg Asp Cys Arg Leu Arg Gln

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 65 70 Arg Pro His Arg Leu Glu Gly Asp Ala Arg Xaa Ala Arg Leu Gln Gly 85 90 Arg Pro Pro Arg Arg Gln Glu Gly Gly Gln Gly Arg Gly Arg Xaa 100 105 Xaa Gln Arg Ala Gly His Gln Arg Pro Ala Xaa Arg Glu Lys Glu Asp 120 115 Lys Asp Asp Lys Trp His Arg 135 (2) INFORMATION FOR SEQ ID NO:1260: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..99 (D) OTHER INFORMATION: / Ceres Seq. ID 1597480 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260: Met Ser Leu Val Arg Arg Thr Asn Val Phe Asp Pro Phe Ser Met Asp 10 Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro Ser Ala 25 20 Thr Ser Thr Asn Ser Glu Thr Ala Ala Phe Ala Ser Ala Arg Ile Asp 4.0 Trp Lys Glu Thr Pro Glu Xaa His Val Phe Lys Ala Asp Leu Pro Gly 55 Val Lys Lys Glu Glu Val Lys Val Glu Val Glu Xaa Xaa Asn Val Leu 75 70 Val Ile Ser Gly Gln Arg Xaa Gly Arg Arg Arg Thr Arg Thr Thr Ser 90 Gly Thr Ala (2) INFORMATION FOR SEQ ID NO:1261:

- - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597481
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro 10

Ser Ala Thr Ser Thr Asn Ser Glu Thr Ala Ala Phe Ala Ser Ala Arg 25 20

Ile Asp Trp Lys Glu Thr Pro Glu Xaa His Val Phe Lys Ala Asp Leu 40

Pro Gly Val Lys Lys Glu Glu Val Lys Val Glu Val Glu Xaa Xaa Asn 60 55

Val Leu Val Ile Ser Gly Gln Arg Xaa Gly Arg Arg Arg Thr Arg Thr 75 70

Thr Ser Gly Thr Ala 85

- (2) INFORMATION FOR SEQ ID NO:1262:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..463
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597482
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

 accacagcat cogerttee ecgaceaeae egtteeteeg ageceaggag cacceeggg
 ccaggaggaa gtttgttett ttaacaatat gtegagggag gagaatgttt acatggeeaa 120
 gttggetgag caggetgaaa ggtatgagga gatggttgag tatatggaga aggtggetaa 180
 gactgtagat gtggaagage teaetgttga ggagegtaae ettetgtetg ttgeataeaa 240
 gaatgtgatt ggggetegee gegetteatg gegeattgtt tetteeattg aacaaaagga 300
 ggagteegt aagaacgaag ageatgtgaa eettateaag gaatategtg geaagatega 360
 ggetgaactg ageaatatet gtgatggaat ettgaagetg ettgaeteee acetagtgee 420
- ttcttctact gctgctgaat caaaggtctt ctacctcaag atg (2) INFORMATION FOR SEQ ID NO:1263:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597483
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:
- Pro Gln His Pro Xaa Phe Pro Asp His Thr Val Pro Pro Ser Pro Gly
- Ala Pro Pro Arg Gln Glu Glu Val Cys Ser Phe Asn Asn Met Ser Arg
 20 25 30
- Glu Glu Asn Val Tyr Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr 35 40 45
- Glu Glu Met Val Glu Tyr Met Glu Lys Val Ala Lys Thr Val Asp Val 50 55 60
- Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys
 65 70 75 80
- Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Val Ser Ser Ile 85 90 95
- Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu His Val Asn Leu Ile 100 105 110
- Lys Glu Tyr Arg Gly Lys Ile Glu Ala Glu Leu Ser Asn Ile Cys Asp 115 120 125
- Gly Ile Leu Lys Leu Leu Asp Ser His Leu Val Pro Ser Ser Thr Ala
 130 135 140
- Ala Glu Ser Lys Val Phe Tyr Leu Lys Met
- 145 150
- (2) INFORMATION FOR SEQ ID NO:1264:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597484

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    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:
Met Ser Arg Glu Glu Asn Val Tyr Met Ala Lys Leu Ala Glu Gln Ala
                                   10
               5
Glu Arg Tyr Glu Glu Met Val Glu Tyr Met Glu Lys Val Ala Lys Thr
                                                   30
                               25
Val Asp Val Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val
                           40
Ala Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Val
                       55
Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu His Val
                                       75
                  70
Asn Leu Ile Lys Glu Tyr Arg Gly Lys Ile Glu Ala Glu Leu Ser Asn
               85
Ile Cys Asp Gly Ile Leu Lys Leu Leu Asp Ser His Leu Val Pro Ser
           100 105
Ser Thr Ala Ala Glu Ser Lys Val Phe Tyr Leu Lys Met
       115 120
(2) INFORMATION FOR SEQ ID NO:1265:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 117 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..117
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597485
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:
Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Glu
                                   10
               5
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Tyr Met Glu Lys Val Ala Lys Thr Val Asp Val Glu Glu Leu Thr Val 30 25 20 Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala 40 Arg Arg Ala Ser Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu 55 Ser Arg Lys Asn Glu Glu His Val Asn Leu Ile Lys Glu Tyr Arg Gly 75 70 Lys Ile Glu Ala Glu Leu Ser Asn Ile Cys Asp Gly Ile Leu Lys Leu 90 85 Leu Asp Ser His Leu Val Pro Ser Ser Thr Ala Ala Glu Ser Lys Val 105 100 Phe Tyr Leu Lys Met

115 (2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..401
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266: 60 agaaacccta acactcatca cgccgccact gatctgctct gttgctggtg actaggagca gtagegrnga gggattetgg atggecaagt egaagaacca caeggegeat aaccagtegt 120 tcaaggcgca caagaacggc atcaagaagc ccaagcgcca ccgccagacc tccaccaagg 180 240 ggatggaccc gaagtttctg aggaacttga ggtactcaar gaagggcaac aagaagagtg

gcgaggctga gtccgaggag taagatgatg gtgattgagt ttgtggcgac aaatgcatct 300 cttgtatcgc taagagtctt agctgtgaac ttagttctca cttctgtgtg actgtgatca 360 aaggacttgt gtatgatcaa aggagatcca tcagttggta c

- (2) INFORMATION FOR SEQ ID NO:1267:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597500
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala 1 5 10 15

His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr 20 25 30

Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Xaa Lys 35 40 45

Gly Asn Lys Lys Ser Gly Glu Ala Glu Ser Glu Glu 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..456
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597502
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268: aaactacacc acaccgcacc ggcaccacca ccaaccgagc ggnnccaggc tcctgctcag 60 gaaggggaga agaggcgagc cttccttggg aagtcgcagg aggagagaag gggaacaaag 120 atggggegeg geaagatega gateaagegg ategagaaet eeaceaaceg eeagtgaeet 180 tctccaagcg ccgcaacggg atcctcaaga aggcgcggga gatcagcgtg ctctgcgacg 240 ccgaggtcgg cgtctcgtct tctccagcgc cggcaaagtg taccgggggt cattggtcga 300 gtgcgaggat aactggaatt gccagctcga gaacataacc ttcactgcca aggatgggaa 360 420 ggtttcgcag ctggagcacg tcttcatcag aggaagcaga gtbagattta tgattatacc tgatatgctc aagaacgctc ccatgttcaa gcgctt
- (2) INFORMATION FOR SEQ ID NO:1269:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..151
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597503
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

Asn Tyr Thr Thr Pro His Arg His His His Gln Pro Ser Xaa Xaa Arg 1 5 10 15

Leu Leu Leu Arg Lys Gly Arg Arg Gly Glu Pro Ser Leu Gly Ser Arg

Arg Arg Glu Gly Glu Gln Arg Trp Gly Ala Ala Arg Ser Arg Ser

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Ser Gly Ser Arg Thr Pro Pro Thr Ala Ser Asp Leu Leu Gln Ala Pro
                        55
Gln Arg Asp Pro Gln Glu Gly Ala Gly Asp Gln Arg Ala Leu Arg Arg
                                        75
                    70
Arg Gly Arg Arg Leu Val Phe Ser Ser Ala Gly Lys Val Tyr Arg Gly
                                    90
                85
Ser Leu Val Glu Cys Glu Asp Asn Trp Asn Cys Gln Leu Glu Asn Ile
                                                    110
                               105
            100
Thr Phe Thr Ala Lys Asp Gly Lys Val Ser Gln Leu Glu His Val Phe
                                                125
       115
                           120
Ile Arg Gly Ser Arg Xaa Arg Phe Met Ile Ile Pro Asp Met Leu Lys
                       135
Asn Ala Pro Met Phe Lys Arg
                   150
145
(2) INFORMATION FOR SEQ ID NO:1270:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 111 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..111
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597504
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:
Thr Thr Pro His Arg Thr Gly Thr Thr Thr Asn Arg Ala Xaa Pro Gly
                                     10
Ser Cys Ser Gly Arg Gly Glu Glu Ala Ser Leu Pro Trp Glu Val Ala
                                                     30
                                 25
            20
Gly Gly Glu Lys Gly Asn Lys Asp Gly Ala Arg Gln Asp Arg Asp Gln
                                                 45
                            4.0
Ala Asp Arg Glu Leu His Gln Pro Pro Val Thr Phe Ser Lys Arg Arg
                         55
Asn Gly Ile Leu Lys Lys Ala Arg Glu Ile Ser Val Leu Cys Asp Ala
                                         75
                     70
Glu Val Gly Val Ser Ser Pro Ala Pro Ala Lys Cys Thr Gly Gly
                                    90
                85
 His Trp Ser Ser Ala Arg Ile Thr Gly Ile Ala Ser Ser Arg Thr
                                 105
             100
 (2) INFORMATION FOR SEQ ID NO:1271:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 494 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..494
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597519
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:
 atcaactcgc aattccgcat tcgttccaac tcctgagcac tttctcctcg tcccagacaa
                                                                         60
 gccaatcgaa gccgagatac gaccatggac tccaccggca ccggagcagg gggtaagggg
                                                                        120
 aagaagggag cggccgggcg caaggtcggc gggccaagga agaagtcggt gtcgaggtcc
                                                                        180
 gtgaaggccg gtctccagtt ccccgtcggc cgcatcgggc gctacttgaa gaagggccgc
                                                                        240
 tacgcgcang ttcggcaccg gcgcccccgt ctacctcgcc gctgtcctcg aatacctcgc
                                                                        300
 cgctgaggtt ctggagctcg ccggtaatgc tgccagggac aaggcgatca agaggtttca
                                                                        360
                                                                        420
 ggtkaggaac atcgtggaac aggcggccat cagggacgtc caggaagcat gcgtctatga
 tggctacgtc ctcccgaagc tgtacgccaa ggtgcaccac tgcgtctcgt gcgcgatcca
                                                                        480
 mgstcacatc gtcc
```

(2) INFORMATION FOR SEQ ID NO:1272: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..60 (D) OTHER INFORMATION: / Ceres Seq. ID 1597520 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272: Ser Thr Arg Asn Ser Ala Phe Val Pro Thr Pro Glu His Phe Leu Leu 10 Val Pro Asp Lys Pro Ile Glu Ala Glu Ile Arg Pro Trp Thr Pro Pro 25 20 Ala Pro Glu Gln Gly Val Arg Gly Arg Arg Glu Arg Pro Gly Ala Arg 40 Ser Ala Gly Gln Gly Arg Ser Arg Cys Arg Gly Pro 55 (2) INFORMATION FOR SEQ ID NO:1273: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..73 (D) OTHER INFORMATION: / Ceres Seq. ID 1597521 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273: Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Lys Gly Ala 10 Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser 25 20 Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Leu 45 40 Lys Lys Gly Arg Tyr Ala Xaa Val Arg His Arg Arg Pro Arg Leu Pro - 55 Arg Arg Cys Pro Arg Ile Pro Arg Arg 70 (2) INFORMATION FOR SEQ ID NO:1274: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..56 (D) OTHER INFORMATION: / Ceres Seq. ID 1597522 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274: Met Leu Pro Gly Thr Arg Arg Ser Arg Gly Phe Arg Xaa Gly Thr Ser 1.0 Trp Asn Arg Arg Pro Ser Gly Thr Ser Arg Lys His Ala Ser Met Met 25 Ala Thr Ser Ser Arg Ser Cys Thr Pro Arg Cys Thr Thr Ala Ser Arg 35 40 Ala Arg Ser Xaa Xaa Thr Ser Ser

55 50 (2) INFORMATION FOR SEQ ID NO:1275: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 364 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..364 (D) OTHER INFORMATION: / Ceres Seq. ID 1597540 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275: aaactcgcaa ttccgcattc gttccaactc ctgagcactt tctcctcgtc cccgacaagc caatcgaagc cgagatacgg ccatggactc caccggcacc ggagcagggg gtaaggggaa 120 gangggagcg gccgggcgca aggtcggcgg gccaaggaag aagtcggtgt cgaggtccgt 180 gaaggccggg ctccagttcc ccgtcggccg catcgggcgc tacttgaaga agggccgcta 240 300 cgcgcastgt ncggcaccgg cgcccccgtc tacctcgcmg ctgtcctcga atacctckcc gkaatttotg mcaactmntd gtaatsctgc sasrgacamc agaagactcg cattattccr 360 cqcc (2) INFORMATION FOR SEQ ID NO:1276: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..59 (D) OTHER INFORMATION: / Ceres Seq. ID 1597541 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276: Thr Arg Asn Ser Ala Phe Val Pro Thr Pro Glu His Phe Leu Leu Val 10 Pro Asp Lys Pro Ile Glu Ala Glu Ile Arg Pro Trp Thr Pro Pro Ala 30 25 20 Pro Glu Gln Gly Val Arg Gly Arg Xaa Glu Arg Pro Gly Ala Arg Ser 40 35 Ala Gly Gln Gly Arg Ser Arg Cys Arg Gly Pro 55 50 (2) INFORMATION FOR SEQ ID NO:1277: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..94 (D) OTHER INFORMATION: / Ceres Seq. ID 1597542 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277: Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Xaa Gly Ala 10 Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser 25 Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Leu 45 40 Lys Lys Gly Arg Tyr Ala Xaa Cys Xaa Ala Pro Ala Pro Pro Ser Thr 60 50 55 Ser Xaa Leu Ser Ser Asn Thr Xaa Pro Xaa Phe Leu Xaa Thr Xaa Xaa

80 70 65 Asn Xaa Xaa Xaa Asp Xaa Arg Arg Leu Ala Leu Phe Xaa Ala 90 85 (2) INFORMATION FOR SEQ ID NO:1278: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 479 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..479 (D) OTHER INFORMATION: / Ceres Seq. ID 1597553 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278: attttcggca agattgcaac agggtcgtcc ggtcgcgttt ctcctacgcg gtccgtgggc 60 tgtgctgcct gctgttgcat cgtctcctcg tttaaacggg cgaactcaag attgcaacag 120 ggtcgtccgc cgccaccaat tgctagcgca atcctagccc tagcccagcg cccctccctg 180 240 cgtcgtgctc ggtagcgatg gcgtcgtttt ctgaagcgcc cccggggaac ccaactgctg qcqagaagat cttcaagacc aagtgcgcgc agtgccacac cgtcgacaag ggcgccggcc 300 360 acaagcaagg toctaatttg aatggtotgt ttgggaggca gtotggtaca acacotggot actcttactc ttcggctaac aagaacatgg ctgtgatttg ggaggagaac actttgtatg 420 actacttgct taatcccaag aagtacattc ctggaaccaa gatggtattc cctggactg (2) INFORMATION FOR SEQ ID NO:1279: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..64 (D) OTHER INFORMATION: / Ceres Seq. ID 1597554 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279: Ile Phe Gly Lys Ile Ala Thr Gly Ser Ser Gly Arg Val Ser Pro Thr 10 Arg Ser Val Gly Cys Ala Ala Cys Cys Cys Ile Val Ser Ser Phe Lys 25 Arg Ala Asn Ser Arg Leu Gln Gln Gly Arg Pro Pro Pro Pro Ile Ala 4.0 Ser Ala Ile Leu Ala Leu Ala Gln Arg Pro Ser Leu Arg Arg Ala Arg 55 (2) INFORMATION FOR SEQ ID NO:1280: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..51 (D) OTHER INFORMATION: / Ceres Seq. ID 1597555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

Phe Ser Ala Arg Leu Gln Gln Gly Arg Pro Val Ala Phe Leu Leu Arg

1 10 15

Gly Pro Trp Ala Val Leu Pro Ala Val Ala Ser Ser Pro Arg Leu Asn 20 25 30

Arg Val Trp Ala Lys Ala 35

(2) INFORMATION FOR SEQ ID NO:1284:

```
Gly Arg Thr Gln Asp Cys Asn Arg Val Val Arg Arg His Gln Leu Leu
                            40
Ala Gln Ser
    50
(2) INFORMATION FOR SEQ ID NO:1281:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 94 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..94
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597556
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:
Met Ala Ser Phe Ser Glu Ala Pro Pro Gly Asn Pro Thr Ala Gly Glu
                                     10
Lys Ile Phe Lys Thr Lys Cys Ala Gln Cys His Thr Val Asp Lys Gly
                                                     30
            20
                                 25
Ala Gly His Lys Gln Gly Pro Asn Leu Asn Gly Leu Phe Gly Arg Gln
                             40
Ser Gly Thr Thr Pro Gly Tyr Ser Tyr Ser Ser Ala Asn Lys Asn Met
                         55
Ala Val Ile Trp Glu Glu Asn Thr Leu Tyr Asp Tyr Leu Leu Asn Pro
                                         75
                    70
Lys Lys Tyr Ile Pro Gly Thr Lys Met Val Phe Pro Gly Leu
                85
(2) INFORMATION FOR SEQ ID NO:1282:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 116 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..116
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597579
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:
 cnaaaaaagg tacacatcat ctcttccaaa tcccaccagc aaatccccaa ttcctccgag
                                                                        60
 ttcgagcgac catgtcgggg cgtggcaagg gcgggaaggg tctgggcaaa ggcggc
 (2) INFORMATION FOR SEQ ID NO:1283:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 38 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..38
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597580
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:
 Xaa Lys Lys Val His Ile Ile Ser Ser Lys Ser His Gln Gln Ile Pro
                                      10
                 5
 Asn Ser Ser Glu Phe Glu Arg Pro Cys Arg Gly Val Ala Arg Ala Gly
                                  25
             20
```

(C) STRANDEDNESS:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..38 (D) OTHER INFORMATION: / Ceres Seq. ID 1597581 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284: Xaa Lys Arg Tyr Thr Ser Ser Leu Pro Asn Pro Thr Ser Lys Ser Pro 10 Ile Pro Pro Ser Ser Ser Asp His Val Gly Ala Trp Gln Gly Arg Glu 20 Gly Ser Gly Gln Arg Arg 35 (2) INFORMATION FOR SEQ ID NO:1285: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..38 (D) OTHER INFORMATION: / Ceres Seq. ID 1597582 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285: Lys Lys Gly Thr His His Leu Phe Gln Ile Pro Pro Ala Asn Pro Gln 10 5 Phe Leu Arg Val Arg Ala Thr Met Ser Gly Arg Gly Lys Gly Gly Lys 20 25 Gly Leu Gly Lys Gly Gly 35 (2) INFORMATION FOR SEQ ID NO:1286: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..486 (D) OTHER INFORMATION: / Ceres Seq. ID 1597589 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286: acegeageea caceceaaca teaaaaceet eccatetett eeceteegee geegtetetg 60 120 ctctcaagat cgccatggcg tcagaaaaga agcagtcgaa cccgatgcgg gagatcaagg tgcagaagct cgtgctcaat atctccgttg gagagagtgg agatcgactc acccgcgccg 180 ccaaggtgtt ggagcagttg agtgggcagt ctccggtttt ctccaaggca aggtatactg 240 tgaggtcttt cggtattcgt cgtaatgaga agattgcatg ctacgttacg gtcaggggtg 300 agaaggcaat gcagcttctt gagagtggcc tcaaggtgaa ggagtatgag cttctgagga 360 ggaacttcag tgatactggc tgctttggtt ttggtattca ggagcacatt gatcttggaa 420 tcaagtatga cccgtctact ggtatttatn gcatggactt ttacgtcgtt ctggaacgag 480 ctcgtt (2) INFORMATION FOR SEQ ID NO:1287: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 161 amino acids (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597590
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Arg Ser His Thr Pro Thr Ser Lys Pro Ser His Leu Phe Pro Ser Ala 1 5 10 15

Ala Val Ser Ala Leu Lys Ile Ala Met Ala Ser Glu Lys Lys Gln Ser 20 25 30

Asn Pro Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser

Val Gly Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu 50 55 60

Gln Leu Ser Gly Gln Ser Pro Val Phe Ser Lys Ala Arg Tyr Thr Val 65 70 75 80

Arg Ser Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Val Thr 85 90 95

Val Arg Gly Glu Lys Ala Met Gln Leu Leu Glu Ser Gly Leu Lys Val 100 105 110

Lys Glu Tyr Glu Leu Leu Arg Arg Asn Phe Ser Asp Thr Gly Cys Phe 115 120 125

Gly Phe Gly Ile Gln Glu His Ile Asp Leu Gly Ile Lys Tyr Asp Pro 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1288:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597591
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val 1 5 10 15 Cln Lys Leu Val Leu Asn Ile Ser Val Glv Glu Ser Gly Asp Arg Leu

Gln Lys Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu 20 25 30

Thr Arg Ala Ala Lys Val Leu Glu Gln Leu Ser Gly Gln Ser Pro Val
35 40 45

Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser Phe Gly Ile Arg Arg Asn 50 55 60 Glu Lys Ile Ala Cys Tyr Val Thr Val Arg Gly Glu Lys Ala Met Gln

65 70 75 80
Leu Leu Glu Ser Gly Leu Lys Val Lys Glu Tyr Glu Leu Leu Arg Arg

85 90 95
Asn Phe Ser Asp Thr Gly Cys Phe Gly Phe Gly Ile Gln Glu His Ile

Asp Leu Gly Ile Lys Tyr Asp Pro Ser Thr Gly Ile Tyr Xaa Met Asp 115 120 125

Phe Tyr Val Val Leu Glu Arg Ala Arg 130 135

- (2) INFORMATION FOR SEQ ID NO:1289:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..127 (D) OTHER INFORMATION: / Ceres Seq. ID 1597592 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289: Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly 15 5 1.0 Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu Gln Leu 25 20 Ser Gly Gln Ser Pro Val Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser 40 Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Val Thr Val Arg 55 Gly Glu Lys Ala Met Gln Leu Leu Glu Ser Gly Leu Lys Val Lys Glu 75 70 Tyr Glu Leu Leu Arg Arg Asn Phe Ser Asp Thr Gly Cys Phe Gly Phe 95 90 85 Gly Ile Gln Glu His Ile Asp Leu Gly Ile Lys Tyr Asp Pro Ser Thr 110 105 100 Gly Ile Tyr Xaa Met Asp Phe Tyr Val Val Leu Glu Arg Ala Arg 120 (2) INFORMATION FOR SEQ ID NO:1290: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 413 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..413 (D) OTHER INFORMATION: / Ceres Seq. ID 1597600 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290: accgacggca tttgcatctk agttcctgat tgttgtattc cagtttcttc tgtgagtttt 60 gtgggatcgc gaggwagaac tagaaggatg tcgtgctgcg gaggcaactg cgggtkcggc 120 geeggetgea agtgeggeae ggetgeggag ggtgeaagat gtaceeggae atggetgage 180 aggtgaccac cactacccag actotoatca tgggtgttgc accgtccaag ggcgggttcg 240 300 aggeggeege gangetgaga aeggegggtg caagtkegge gecaactgea eetgegaeee 360 ctgcacctgc aagtgagacg acggcgatga cgctkcaggg cgtcaattgg gatcggaagg actcttttat cttaagctct agtataatat tctagcagtg tcgtytgtgt ttt (2) INFORMATION FOR SEQ ID NO:1291: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..61 (D) OTHER INFORMATION: / Ceres Seq. ID 1597601 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291: Thr Asp Gly Ile Cys Ile Xaa Val Pro Asp Cys Cys Ile Pro Val Ser 10 Ser Val Ser Phe Val Gly Ser Arg Xaa Arg Thr Arg Arg Met Ser Cys

25

20

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
Cys Gly Gly Asn Cys Gly Xaa Gly Ala Gly Cys Lys Cys Gly Thr Ala
                            40
Ala Glu Gly Ala Arg Cys Thr Arg Thr Trp Leu Ser Arg
                        55
(2) INFORMATION FOR SEQ ID NO:1292:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 78 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..78
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597602
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:
Met Tyr Pro Asp Met Ala Glu Gln Val Thr Thr Thr Gln Thr Leu
                                    10
Ile Met Gly Val Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Xaa
                                25
            20
Leu Arg Thr Ala Gly Ala Ser Xaa Ala Pro Thr Ala Pro Ala Thr Pro
                                                45
                            40
Ala Pro Ala Ser Glu Thr Thr Ala Met Thr Xaa Gln Gly Val Asn Trp
                                             60
                        55
Asp Arg Lys Asp Ser Phe Ile Leu Ser Ser Ser Ile Ile Phe
                    70
 (2) INFORMATION FOR SEQ ID NO:1293:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 74 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..74
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597603
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:
 Met Ala Glu Gln Val Thr Thr Thr Gln Thr Leu Ile Met Gly Val
                                     10
                                                         15
 Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Xaa Leu Arg Thr Ala
                                 25
             20
 Gly Ala Ser Xaa Ala Pro Thr Ala Pro Ala Thr Pro Ala Pro Ala Ser
```

Gly Ala Ser Xaa Ala Pro Thr Ala Plo Ala III Tio Ala Tro Ala Ser 35 40 45

Glu Thr Thr Ala Met Thr Xaa Gln Gly Val Asn Trp Asp Arg Lys Asp 50 55 60

Ser Phe Ile Leu Ser Ser Ser Ile Ile Phe 65 70

- (2) INFORMATION FOR SEQ ID NO:1294:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..449
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597620
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294: gaagagggaa ggggggatat cggggaaaaa aacacaaggt accagcagcg caaagagccg

ggtgttggca cagatcagge ggccgcatgg cgatcmgttc gcggattcgg cgaacaacgt 120 gatcatcgag gaggtgaaca agggcctgaa cccaggaatg gtggttctgc tcgatggttg 180 ccagcttcct gctgctcttc ttcgccggga actacgcgct gtatgtgtac gcgcagaaga 240 cgctcccgcc gaagaagaag aagccggtct ccaagaggaa gctgaagagg gaaaagctga 300 agcagggggt ctcggcgca ggggagtgaa cagacaggga tgccgccgat cggcccgtcc 360 tgagcccgcc ccctatttac atgattgtcg aagaaaaaag atacacctgc tggagccgcg 420 gtgttcgtag taattttgtt ctgtagatg

- (2) INFORMATION FOR SEQ ID NO:1295:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597621
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

Glu Glu Gly Arg Gly Asp Ile Gly Glu Lys Asn Thr Arg Tyr Gln Gln
1 10 15

Arg Lys Glu Pro Gly Val Gly Thr Asp Gln Ala Ala Ala Trp Arg Xaa 20 25 30

Val Arg Gly Phe Gly Glu Gln Arg Asp His Arg Gly Gly Glu Gln Gly
35 40 45

Pro Glu Pro Arg Asn Gly Gly Ser Ala Arg Trp Leu Pro Ala Ser Cys 50 55 60

Cys Ser Ser Ser Pro Gly Thr Thr Arg Cys Met Cys Thr Arg Arg Arg 65 70 75 80

Arg Ser Arg Arg Arg Arg Ser Arg Ser Pro Arg Gly Ser 85 90

- (2) INFORMATION FOR SEQ ID NO:1296:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597622
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

Lys Arg Glu Gly Gly Ile Ser Gly Lys Lys Thr Gln Gly Thr Ser Ser 1 5 10 15

Ala Lys Ser Arg Val Leu Ala Gln Ile Arg Arg Pro His Gly Asp Xaa 20 25 30

Phe Ala Asp Ser Ala Asn Asn Val Ile Ile Glu Glu Val Asn Lys Gly 35 40 45

Leu Asn Pro Gly Met Val Val Leu Leu Asp Gly Cys Gln Leu Pro Ala 50 55 60

Ala Leu Leu Arg Arg Glu Leu Arg Ala Val Cys Val Arg Ala Glu Asp 65 70 75 80

Ala Pro Ala Glu Glu Glu Ala Gly Leu Gln Glu Glu Ala Glu Glu 85 90 95

Gly Lys Ala Glu Ala Gly Gly Leu Gly Ala Arg Gly Val Asn Arg Gl
n $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Gly Cys Arg Arg Ser Ala Arg Pro Glu Pro Ala Pro Tyr Leu His Asp 115 120 125

Cys Arg Arg Lys Lys Ile His Leu Leu Glu Pro Arg Cys Ser

(2) INFORMATION FOR SEQ ID NO:1297: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 90 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..90 (D) OTHER INFORMATION: / Ceres Seq. ID 1597623 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297: Met Val Val Leu Leu Asp Gly Cys Gln Leu Pro Ala Ala Leu Leu Arg 10 Arg Glu Leu Arg Ala Val Cys Val Arg Ala Glu Asp Ala Pro Ala Glu 2.0 2.5 Glu Glu Glu Ala Gly Leu Gln Glu Glu Ala Glu Glu Gly Lys Ala Glu 4.0 Ala Gly Gly Leu Gly Ala Arg Gly Val Asn Arg Gln Gly Cys Arg Arg Ser Ala Arg Pro Glu Pro Ala Pro Tyr Leu His Asp Cys Arg Arg Lys 70 Lys Ile His Leu Leu Glu Pro Arg Cys Ser 85 (2) INFORMATION FOR SEQ ID NO:1298: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..385 (D) OTHER INFORMATION: / Ceres Seq. ID 1597631 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298: aatcaactcg caattccgca ttcgttccaa ctcctgagca ctttctcctc gtcccagaca 60 agccaatcga agccgagata cgaccatgga ctccaccggc accggagcag ggggtaaggg 120 gaagaaggga gcggccgggc gcaaggtcgg cgggccaagg aagaagtcgg tgtcgaggtc 180 cgtgaaggcc ggtctccagt tccccgtcgg ccgcatcggg cgctacttka agaagggccg 240 ctacgcgcab gttcggcacc ggcgcccccg tctacctcgc cgctgtcctc gaatacctcg 300 ccqctqaqqt tctqqaqctc qccqgtaatq ctqccaqqqa caacaaqaaq actcqcatta 360 ttccgcgcca cgtgcttctk gcgat (2) INFORMATION FOR SEQ ID NO:1299: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..38 (D) OTHER INFORMATION: / Ceres Seq. ID 1597632 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299: Asn Gln Leu Ala Ile Pro His Ser Phe Gln Leu Leu Ser Thr Phe Ser 5 10 Ser Ser Gln Thr Ser Gln Ser Lys Pro Arg Tyr Asp His Gly Leu His 25 30

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(2) INFORMATION FOR SEQ ID NO:1300:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 60 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..60
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597633
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:
Ser Thr Arg Asn Ser Ala Phe Val Pro Thr Pro Glu His Phe Leu Leu
                                                         15
                                    10
Val Pro Asp Lys Pro Ile Glu Ala Glu Ile Arg Pro Trp Thr Pro Pro
                                25
            20
Ala Pro Glu Gln Gly Val Arg Gly Arg Glu Arg Pro Gly Ala Arg
                            40
        35
Ser Ala Gly Gln Gly Arg Ser Arg Cys Arg Gly Pro
                        55
(2) INFORMATION FOR SEQ ID NO:1301:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 73 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..73
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597634
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:
Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Gly Ala
                                     10
Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser
                                                      30
                                 25
             20
 Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Xaa
                                                  4.5
                             40
 Lys Lys Gly Arg Tyr Ala Xaa Val Arg His Arg Arg Pro Arg Leu Pro
                         55
                                              60
 Arg Arg Cys Pro Arg Ile Pro Arg Arg
                     70
 (2) INFORMATION FOR SEQ ID NO:1302:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 470 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
            (A) NAME/KEY: -
            (B) LOCATION: 1..470
            (D) OTHER INFORMATION: / Ceres Seq. ID 1597639
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:
 aacaatgcca attgccagca acccatccat actttcagct gttgatacaa aaagagaaga
                                                                          60
 gagaatggcg gavaacccag agttgagtgg tcttattact caaacaaaga agaaaatat
                                                                         120
 agtgccaaag ttcaccgaaa tcttccccgt ggaggacacg cctaccctta cagcgccttc
                                                                         180
 atcacctccg tccggaaaga agtgatcaaa tactgcacca accatacagg catcgtccag
                                                                         240
                                                                         300
 cccgtgctgc cgctggagaa gaatgtcccc gagctctggt tctacaccga gctcaaaacg
                                                                         360
 aagaccaggt ccatcacgct cgccatacgt atggacaacc tctacctggt cggcttcagg
 acccccggcg gtgtggtggg agttcggcaa ggacggcgac acccacctcc tcgacgacaa
                                                                         420
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cqccaaqtgq ctcqgctttg gcgggccggt accaggacct catcgggcag
(2) INFORMATION FOR SEQ ID NO:1303:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 67 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..67
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597640
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:
Thr Met Pro Ile Ala Ser Asn Pro Ser Ile Leu Ser Ala Val Asp Thr
               5
                                   10
Lys Arg Glu Glu Arg Met Ala Xaa Asn Pro Glu Leu Ser Gly Leu Ile
                                25
Thr Gln Thr Lys Lys Lys Asn Ile Val Pro Lys Phe Thr Glu Ile Phe
                           40
                                                45
Pro Val Glu Asp Thr Pro Thr Leu Thr Ala Pro Ser Ser Pro Pro Ser
    50
                        55
Gly Lys Lys
65
(2) INFORMATION FOR SEQ ID NO:1304:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 66 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..66
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597641
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:
Met Pro Ile Ala Ser Asn Pro Ser Ile Leu Ser Ala Val Asp Thr Lys
            5
                                    10
Arg Glu Glu Arg Met Ala Xaa Asn Pro Glu Leu Ser Gly Leu Ile Thr
                                25
           20
Gln Thr Lys Lys Lys Asn Ile Val Pro Lys Phe Thr Glu Ile Phe Pro
                            40
                                                 45
Val Glu Asp Thr Pro Thr Leu Thr Ala Pro Ser Ser Pro Pro Ser Gly
                        55
Lys Lys
65
(2) INFORMATION FOR SEQ ID NO:1305:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..69
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597642
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:
Met Ser Pro Ser Ser Gly Ser Thr Pro Ser Ser Lys Arg Arg Pro Gly
```

1.0

30

Pro Ser Arg Ser Pro Tyr Val Trp Thr Thr Ser Thr Trp Ser Ala Ser 25

Gly Pro Pro Ala Val Trp Trp Glu Phe Gly Lys Asp Gly Asp Thr His 35 40 45

Leu Leu Asp Asp Asn Ala Lys Trp Leu Gly Phe Gly Gly Pro Val Pro 50 55 60

Gly Pro His Arg Ala

65

- (2) INFORMATION FOR SEQ ID NO:1306:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..371
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597658
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

accaaggaaa ttcacaaagc gatactagct agtccctacc aaagcatact tcctgaaaca 60 ctcttgcaat ccactgagtt ctgtttgttg agacgcatag agctagagtc gacaatgtcg 120 ctcgtgaggc gcasaacgtg ttcgaccct tctccatgga cctctgggac cccttcgaca 180 ccatgttccg ctccatcgtc ccgtcggcga cctccaccaa ctccgagact gccgccttcg 240 ccagcgcccg catcgactgg aaggagacgc ccgaggcga cgtgttcaag gccgacctcc 300 ccggcgtcaa gaaggaagag gtcaaggtcg aggtcgagga cggcaacatg ctggtcatca 360 qcgqccagcg c

- (2) INFORMATION FOR SEQ ID NO:1307:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597659
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

Thr Lys Glu Ile His Lys Ala Ile Leu Ala Ser Pro Tyr Gln Ser Ile

1 5 10 15

Leu Pro Glu Thr Leu Leu Gln Ser Thr Glu Phe Cys Leu Leu Arg Arg

Leu Pro Glu Thr Leu Leu Gln Ser Thr Glu Phe Cys Leu Leu Arg Arg
20 25 30

Ile Glu Leu Glu Ser Thr Met Ser Leu Val Arg Arg Xaa Thr Cys Ser 35 40 45

Thr Pro Ser Pro Trp Thr Ser Gly Thr Pro Ser Thr Pro Cys Ser Ala 50 55 60

Pro Ser Ser Arg Arg Pro Pro Pro Thr Pro Arg Leu Pro Pro Ser 65 70 75 80

Pro Ala Pro Ala Ser Thr Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser 85 90 95

Arg Pro Thr Ser Pro Ala Ser Arg Arg Lys Arg Ser Arg Ser Arg Ser

100 105 110 Arg Thr Ala Thr Cys Trp Ser Ser Ala Ala Ser

- 115 120 (2) INFORMATION FOR SEQ ID NO:1308:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

120

180

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

Met Ser Leu Val Arg Arg Xaa Thr Cys Ser Thr Pro Ser Pro Trp Thr 10

Ser Gly Thr Pro Ser Thr Pro Cys Ser Ala Pro Ser Ser Arg Arg Arg 25 20

Pro Pro Pro Thr Pro Arg Leu Pro Pro Ser Pro Ala Pro Ala Ser Thr 40

Gly Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala 60

Ser Arg Arg Lys Arg Ser Arg Ser Arg Ser Arg Thr Ala Thr Cys Trp

Ser Ser Ala Ala Ser

- (2) INFORMATION FOR SEQ ID NO:1309:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..72
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597661
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro 5 10

Ser Ala Thr Ser Thr Asn Ser Glu Thr Ala Ala Phe Ala Ser Ala Arg 20 25 30

Ile Asp Trp Lys Glu Thr Pro Glu Ala His Val Phe Lys Ala Asp Leu 40 4.5

Pro Gly Val Lys Lys Glu Glu Val Lys Val Glu Val Glu Asp Gly Asn 55

Met Leu Val Ile Ser Gly Gln Arg 70

- (2) INFORMATION FOR SEQ ID NO:1310:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..236
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310: acqcqqaaac cctaqcagct caacaccctc gaggtacctc cattcgcagt cggccgtgtc ctoggagocg cgggagatgg cggatcagga gaccgtagct gtggttgagg caccaacccc ggttcttggg gaacgatgga cctgatgact gccctgcarc tcgtcatgaa gaagtcaggt

geteacgatk geettttgaa gggtettegt gaggetgeea aageategag aageat

- (2) INFORMATION FOR SEQ ID NO:1311:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

180

240

(ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..47 (D) OTHER INFORMATION: / Ceres Seq. ID 1597667 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311: Arg Gly Asn Pro Ser Ser Ser Thr Pro Ser Arg Tyr Leu His Ser Gln 10 Ser Ala Val Ser Ser Glu Pro Arg Glu Met Ala Asp Gln Glu Thr Val 25 Ala Val Val Glu Ala Pro Thr Pro Val Leu Gly Glu Arg Trp Thr 35 40 (2) INFORMATION FOR SEQ ID NO:1312: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..31 (D) OTHER INFORMATION: / Ceres Seq. ID 1597668 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312: Ala Glu Thr Leu Ala Ala Gln His Pro Arg Gly Thr Ser Ile Arg Ser 10 Arg Pro Cys Pro Arg Ser Arg Gly Arg Trp Arg Ile Arg Arg Pro 20 25 (2) INFORMATION FOR SEQ ID NO:1313: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..33 (D) OTHER INFORMATION: / Ceres Seq. ID 1597669 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313: Met Asp Leu Met Thr Ala Leu Xaa Leu Val Met Lys Lys Ser Gly Ala 10 5 His Asp Xaa Leu Leu Lys Gly Leu Arg Glu Ala Ala Lys Ala Ser Arg 25 Ser (2) INFORMATION FOR SEQ ID NO:1314: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..401 (D) OTHER INFORMATION: / Ceres Seq. ID 1597674 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

ttctgaagtt tcggcggcgg cgtaggtagc ggcggtgtgc ttgtgatctc aatctcaacc ccaggcgagc tcggctccgg tcacccgtcg atccacgcaa ccatgtcgag gaggaagacc

agggagecca aggaggagaa egttaceett ggaeccaetg teegtgaagg agagtttgtb

tttggtgttg ctcacatctt tgcatccttc aatgacacct tcattcatgt cactgatttg

tctgggaggg aaactttggt tcggatcact ggtggcatga aggttaaggc tgatcgtgat 300 gagtcgtctc cttatgctgc tatgcttgct gcccaagatg ttgcacagcg ttgcaaggag 360 ctcggtatca cagcgctgca cattaagctt cgtgccactg g

- (2) INFORMATION FOR SEQ ID NO:1315:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597675
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu 1 5 10 15

Gly Pro Thr Val Arg Glu Gly Glu Phe Xaa Phe Gly Val Ala His Ile $20 \hspace{1cm} 25 \hspace{1cm} 30$

Phe Ala Ser Phe Asn Asp Thr Phe Ile His Val Thr Asp Leu Ser Gly 35 40 45

Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp 50 60

Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val 65 70 75 80

Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu 85 90 95

Arg Ala Thr

- (2) INFORMATION FOR SEQ ID NO:1316:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..399
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597698
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

catcaatagc cagttctaat ctcaggttrg gggaaatagg cctcgcgggt cgcaaaccgc 60 tctctgctga tttrggatt cggaggcgct cgagttttca ggtaaactat agtttagtga 120 cccatggctc gtactaagca aactgctcgc aagtccactg gagggaaggc tccwaggaaa 180 caacttgcca ccaaggctgc ccgtaagtct gcacctacaa ctgggggagt aaagaagcct 240 caccgttacc gccctggaac tgttgctctt cgtgaaatcc gcaagtatca gaagagcact 300 gacctgctca taaggaagct tccgttccaa aggcttgtca gggagattkc ccaggatttc 360 aagactgatc ttcgtttcca gagccatgcg gtgcttgcg

- (2) INFORMATION FOR SEQ ID NO:1317:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597699
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala

- 85
 (2) INFORMATION FOR SEQ ID NO:1318:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..493
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597726
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

60 gaaggcatct ccaatctcct cgcccccac ggacctgaac cgagaaccgt taccgccgcc 120 geetetegee tageegeegg agaagegeeg etegeteagg aggacageea tggegeegga gccggagatg atattatgaa cgagaagaat ccccgcccgc tcgacgagga tracatcgcg 180 240 ctcctcaaaa cctatggact ggggccgtat tcgaccagca ttaagaaggt cgagaaggag atcaaggaaa tggccaagaa aatcaacgac ctctgtggga taaaggagtc tgatacaggg 300 360 ctgqctccac ctaqccagtg ggatttggtt tcagataagc agatgatgca agaagaacaa 420 ccgttacaag tagcaagatg tacaaagatt ataagcccta atacggatga tgccaaatat 480 gttataaatg traaacaaat tgcaaagttt gtggtcggat tgggagataa ggtctctcca actgatatcg agg

- (2) INFORMATION FOR SEQ ID NO:1319:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..164
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597727
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

Glu Gly Ile Ser Asn Leu Leu Ala Pro His Gly Pro Glu Pro Arg Thr 1 $$ 5 $$ 10 $$ 15

Val Thr Ala Ala Ser Arg Leu Ala Ala Gly Glu Ala Pro Leu Ala 20 25 30

Gln Glu Asp Ser His Gly Ala Gly Ala Gly Asp Asp Ile Met Asn Glu
35 40 45

Lys Asn Pro Arg Pro Leu Asp Glu Asp Xaa Ile Ala Leu Leu Lys Thr 50 55 60

Tyr Gly Leu Gly Pro Tyr Ser Thr Ser Ile Lys Lys Val Glu Lys Glu 65 70 75 80

Ile Lys Glu Met Ala Lys Lys Ile Asn Asp Leu Cys Gly Ile Lys Glu 85 90 95

Ser Asp Thr Gly Leu Ala Pro Pro Ser Gln Trp Asp Leu Val Ser Asp 100 105 110 Lys Gln Met Met Gln Glu Glu Gln Pro Leu Gln Val Ala Arg Cys Thr

115 120 125

Lys Ile Ile Ser Pro Asn Thr Asp Asp Ala Lys Tyr Val Ile Asn Xaa

135 130 Lys Gln Ile Ala Lys Phe Val Val Gly Leu Gly Asp Lys Val Ser Pro 155 150 Thr Asp Ile Glu

- (2) INFORMATION FOR SEQ ID NO:1320:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597728
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Asn Glu Lys Asn Pro Arg Pro Leu Asp Glu Asp Xaa Ile Ala Leu 10

Leu Lys Thr Tyr Gly Leu Gly Pro Tyr Ser Thr Ser Ile Lys Lys Val 25

Glu Lys Glu Ile Lys Glu Met Ala Lys Lys Ile Asn Asp Leu Cys Gly

Ile Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ser Gln Trp Asp Leu 55

Val Ser Asp Lys Gln Met Met Gln Glu Glu Gln Pro Leu Gln Val Ala 70 75

Arg Cys Thr Lys Ile Ile Ser Pro Asn Thr Asp Asp Ala Lys Tyr Val 90

Ile Asn Xaa Lys Gln Ile Ala Lys Phe Val Val Gly Leu Gly Asp Lys 100 105

Val Ser Pro Thr Asp Ile Glu

115

- (2) INFORMATION FOR SEQ ID NO:1321:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..425
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597732
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

caatgagttg aggagagtgg aacatgttga ccattctaga aagtytgcag agcargctgt 60 aaaggcgatc aagggcaaag agtccggtga accagttccg gagtatgact acctgccata 120 cttctactcc cgatcattcg acctggcgtg gcaattctac ggcgacaacg tgggcgaaac 180 tatcctgttt ggcgacagtg accccacctc cagcaagccc aagttcggct cgtactggat 240 caaggacggc aaggtcttgg gegeetteet ggagggeggg teaceggacg agaacaagge 300 cattqccaaq qtqqcqaaaa cccaqccqcc gqtcqctaac ctcqaqqaqc tcaaqaaqgm 360 tggcctccaq ttcgccagca agatctgaga cgstcccgtt ccatgtaaat ttccgtgtca 420 tcata

- (2) INFORMATION FOR SEQ ID NO:1322:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597733
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

Asn Glu Leu Arg Arg Val Glu His Val Asp His Ser Arg Lys Xaa Ala 10

Glu Xaa Ala Val Lys Ala Ile Lys Gly Lys Glu Ser Gly Glu Pro Val 20 25

Pro Glu Tyr Asp Tyr Leu Pro Tyr Phe Tyr Ser Arg Ser Phe Asp Leu 40

Ala Trp Gln Phe Tyr Gly Asp Asn Val Gly Glu Thr Ile Leu Phe Gly 55

Asp Ser Asp Pro Thr Ser Ser Lys Pro Lys Phe Gly Ser Tyr Trp Ile 70

Lys Asp Gly Lys Val Leu Gly Ala Phe Leu Glu Gly Gly Ser Pro Asp 85 90

Glu Asn Lys Ala Ile Ala Lys Val Ala Lys Thr Gln Pro Pro Val Ala 100 105 110

Asn Leu Glu Glu Leu Lys Lys Xaa Gly Leu Gln Phe Ala Ser Lys Ile 115 120

- (2) INFORMATION FOR SEQ ID NO:1323:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597734
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Met Thr Thr Cys His Thr Ser Thr Pro Asp His Ser Thr Trp Arg Gly 10

Asn Ser Thr Ala Thr Thr Trp Ala Lys Leu Ser Cys Leu Ala Thr Val 20 25 30

Thr Pro Pro Pro Ala Ser Pro Ser Ser Ala Arg Thr Gly Ser Arg Thr 40

Ala Arg Ser Trp Ala Pro Ser Trp Arg Ala Gly His Arg Thr Arg Thr 55 60

Arg Pro Leu Pro Arg Trp Arg Lys Pro Ser Arg Arg Ser Leu Thr Ser 70 75 80

Arg Ser Ser Arg Arg Xaa Ala Ser Ser Ser Pro Ala Arg Ser Glu Thr 85 90

Xaa Pro Phe His Val Asn Phe Arg Val Ile Val 100 105

- (2) INFORMATION FOR SEQ ID NO:1324:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..430
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597741
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

ataaaaccct actaaccgcg tetectetee agegeeegee gtegeegeeg ceetectett 60

ggtcccgccg tccgtcgagg tcatcatggt gagggtcagt gtgctcaacg atgcgctcaa 120 gtccatgtac aatgcagaga agaggggcaa gaggcaggtc atgatcaggc cgtcgtccaa 180 ggtgatcatc aagttcctga cggtcatgca gcgtcatgga tacattggcg agttcgagta 240 cgtggatgac cacagagctg ggaagattgt ggtggaactg aacggcagac taaacaaatg 300 cggtgtaatt agccccggt ttgatgttgg ggtaaaggaa atcgaaggct ggactgcgag 360 gctgcttccg tctcgccagt ttggctatat cgtgcttaca acctctgcgg gaattatgga 420 tcacgaggag

- (2) INFORMATION FOR SEQ ID NO:1325:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597742
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn 1 5 10 15

Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys 20 25 30

Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly Tyr Ile Gly $35 \hspace{1cm} 40 \hspace{1cm} 45$

Glu Phe Glu Tyr Val Asp Asp His Arg Ala Gly Lys Ile Val Val Glu 50 55 60

Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asp 65 70 75 80

Val Gly Val Lys Glu Ile Glu Gly Trp Thr Ala Arg Leu Leu Pro Ser 85 90 95

Arg Gln Phe Gly Tyr Ile Val Leu Thr Thr Ser Ala Gly Ile Met Asp 100 105 110

His Glu Glu

115

- (2) INFORMATION FOR SEQ ID NO:1326:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seg. ID 1597743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro 1 5 10 15

Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly 20 25 30

Tyr Ile Gly Glu Phe Glu Tyr Val Asp Asp His Arg Ala Gly Lys Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro 50 60

Arg Phe Asp Val Gly Val Lys Glu Ile Glu Gly Trp Thr Ala Arg Leu 65 70 75 80

Leu Pro Ser Arg Gln Phe Gly Tyr Ile Val Leu Thr Thr Ser Ala Gly
85 90 95

Ile Met Asp His Glu Glu

(2) INFORMATION FOR SEQ ID NO:1327: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 90 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..90 (D) OTHER INFORMATION: / Ceres Seq. ID 1597744 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327: Met Ile Arg Pro Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Met 10 Gln Arg His Gly Tyr Ile Gly Glu Phe Glu Tyr Val Asp Asp His Arg 25 20 Ala Gly Lys Ile Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly 45 40 35 Val Ile Ser Pro Arg Phe Asp Val Gly Val Lys Glu Ile Glu Gly Trp 60 55 Thr Ala Arg Leu Leu Pro Ser Arg Gln Phe Gly Tyr Ile Val Leu Thr 75 70 Thr Ser Ala Gly Ile Met Asp His Glu Glu 85 (2) INFORMATION FOR SEQ ID NO:1328: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..378 (D) OTHER INFORMATION: / Ceres Seq. ID 1597745 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328: atcccacttc cacccaaatc caccaccgcc ataccagcgt gtccgcgatt ccgtcgagtt 60 agaccagtcg agagagcagt cccagacgag aagaggtgaa tatgagttcc ggcggcggca 120 ggggcaagcc caaggggtcc aaggctgtgt cgcggtcgac caaggctggg ctgcagttcc 180 ccgtcggccg catcgcgcgc tacctcaagg cgggcaagta cgccgagcgc gtcggcggtg 240 gtgcgcccgt ctacctctcc gccgtcctcg agtatctcgc ggcagaggtg ttggaactgg 300 cgggcaacgc ggcgcgcgac aacaagaaga accgcatcgt gccgcgccac atccagctcg 360 ccqtqcgcaa cgacgagg (2) INFORMATION FOR SEQ ID NO:1329: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..125 (D) OTHER INFORMATION: / Ceres Seq. ID 1597746 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329: Ser His Phe His Pro Asn Pro Pro Pro Pro Tyr Gln Arg Val Arg Asp 10 Ser Val Glu Leu Asp Gln Ser Arg Glu Gln Ser Gln Thr Arg Arg Gly 25 20 Glu Tyr Glu Phe Arg Arg Gln Gly Gln Ala Gln Gly Val Gln Gly 40

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Cys Val Ala Val Asp Gln Gly Trp Ala Ala Val Pro Arg Arg Pro His
                        55
Arg Ala Leu Pro Gln Gly Gly Gln Val Arg Arg Ala Arg Arg Arg Trp
                    70
                                        75
Cys Ala Arg Leu Pro Leu Arg Arg Pro Arg Val Ser Arg Gly Arg Gly
                                    90
               85
Val Gly Thr Gly Gly Gln Arg Gly Ala Arg Gln Gln Glu Glu Pro His
                                105
            100
Arg Ala Ala Pro His Pro Ala Arg Arg Ala Gln Arg Arg
                            120
        115
(2) INFORMATION FOR SEQ ID NO:1330:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 92 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..92
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597747
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:
Met Ser Ser Gly Gly Gly Arg Gly Lys Pro Lys Gly Ser Lys Ala Val
                                     10
Ser Arg Ser Thr Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Ala
                                                     30
                                25
            20
Arg Tyr Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly Gly Gly Ala
                            40
                                                 45
        35
Pro Val Tyr Leu Ser Ala Val Leu Glu Tyr Leu Ala Ala Glu Val Leu
                                            60
                        55
Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Asn Arg Ile Val
                                        75
                    70
Pro Arg His Ile Gln Leu Ala Val Arg Asn Asp Glu
                85
(2) INFORMATION FOR SEQ ID NO:1331:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 456 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..456
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597748
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:
 ctctagaacc ctagcgcbnc gcccgtcctg ccgccgccgc agccgccatc gcacggccat
                                                                         60
 gggtatcgat ctcgtagccg gcggccgcaa caagaakacc aagcgcacgg cgcccaagtc
                                                                        120
                                                                        180
 cgacgatgtc tacctcaagc toctcgtcaa gctctaccgc ttccttgtgc gcaggacaaa
 gagcaacttc aacgeegtga teetcaageg eetetteatg ageaagaeea aeegeeegee
                                                                        240
 gctctcggat gcgccgcctc gtcaggttca tggaggggaa gggtgatcag atcgccgtga
                                                                        300
 ttgtgggcac cgtgaccgac gacaagagga tcagcgaggt gccggcgatg aaggtctgcg
                                                                        360
 cgctcaggtt cactgagaca gcgagggcca ggatcatcaa tgctggcgga gagtgcctca
                                                                        420
 ccttcgacca gctcgcgctc cgtgccccac ttgggc
 (2) INFORMATION FOR SEQ ID NO:1332:
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597749
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:
- Ser Arg Thr Leu Ala Xaa Arg Pro Ser Cys Arg Arg Arg Ser Arg His
 1 5 10 15
- Arg Thr Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Xaa 20 25 30
- Thr Lys Arg Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu Lys Leu Leu 35 40 45
- Val Lys Leu Tyr Arg Phe Leu Val Arg Arg Thr Lys Ser Asn Phe Asn 50 55 60
- Ala Val Ile Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro 65 70 75 80
- Leu Ser Asp Ala Pro Pro Arg Gln Val His Gly Gly Glu Gly 85 90
- (2) INFORMATION FOR SEQ ID NO:1333:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..75
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333: Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Xaa Thr Lys Arg
- 1 5 10 15

 Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu Lys Leu Leu Val Lys Leu 20 25 30
- Tyr Arg Phe Leu Val Arg Arg Thr Lys Ser Asn Phe Asn Ala Val Ile
- Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Leu Ser Asp 50 55 60
- Ala Pro Pro Arg Gln Val His Gly Gly Glu Gly 65 70 75
- (2) INFORMATION FOR SEQ ID NO:1334:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597751
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:
- Met Arg Arg Leu Val Arg Phe Met Glu Gly Lys Gly Asp Gln Ile Ala 1 10 15
- Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Ser Glu Val Pro
- Ala Met Lys Val Cys Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg 35 40 45
- Ile Ile Asn Ala Gly Gly Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu
 50 55 60
- Arg Ala Pro Leu Gly

(2) INFORMATION FOR SEQ ID NO:1335: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..294 (D) OTHER INFORMATION: / Ceres Seq. ID 1597752 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335: gttgttttgt tcttgcggaa acgagacgag actaggcgac gcgasgtyag ggagtcgagg 60 aggatcgggg ctcaggcaag atgaacagga agccaggaga ctgggactgc agggcgtgcc 120 ancacctcaa cttcagccgc cgagacatat gccagckctg tagcgagcca cgtggagttg 180 ctgatcgtgg cagtggcggc ggcggaggag gaggaggagg cgactacgca agctttcggt 240 ggccgcggtg gctcctcctt cggcggcggc tttgggcgct gctggctctg acgt (2) INFORMATION FOR SEQ ID NO:1336: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..53 (D) OTHER INFORMATION: / Ceres Seq. ID 1597753 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336: Leu Phe Cys Ser Cys Gly Asn Glu Thr Arg Leu Gly Asp Ala Xaa Xaa 10 Gly Ser Arg Gly Gly Ser Gly Leu Arg Gln Asp Glu Gln Glu Ala Arg Arg Leu Gly Leu Gln Gly Val Pro Xaa Pro Gln Leu Gln Pro Pro Arg 40 35 His Met Pro Xaa Leu 50 (2) INFORMATION FOR SEQ ID NO:1337: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1597754 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337: Met Asn Arg Lys Pro Gly Asp Trp Asp Cys Arg Ala Cys Xaa His Leu 10 Asn Phe Ser Arg Arg Asp Ile Cys Gln Xaa Cys Ser Glu Pro Arg Gly 30 25 20 Val Ala Asp Arg Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Asp 4.0 Tyr Ala Ser Phe Arg Trp Pro Arg Trp Leu Leu Leu Arg Arg Leu 55 Trp Ala Leu Leu Ala Leu Thr 70 (2) INFORMATION FOR SEQ ID NO:1338: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..442
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597755
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

 cttttaacct cgcgccgcca tccgacgcc atctgctcca ccctccacc agccgccgcc 60
 gccgccgcct aaggagaaga gggtccggcc gtctccttgc cccgatggcg tccgagaaga 120
 agcagtccaa cccgatgcgg gagatcaagg tgcagaagct ggtcctcaac atatccgtag 180
 ggagagcggc gaccgcctca cccgcgccgc caaggtgctg gagcagctca gcgccagacc 240
 cccgtcttct ccaaggcgag gtacacggtg cgctcgttcg gcatccggcg taacgagaag 300
 atcgcctgct acgtcacggt cagggggac aaggccatgc agctgcttga gagcggcctc 360
 aaggtcaagg agtacgagct gctcaggag aacttcagcg acaccggctg cttcgggttc 420
- (2) INFORMATION FOR SEQ ID NO:1339:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

ggcatccagg agcacatcga cc

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339: Phe Asn Leu Ala Pro Pro Ser Asp Ala His Leu Leu His Pro Pro

1 5 10 15 Ser Arg Arg Arg Arg Leu Arg Arg Gly Ser Gly Arg Leu Leu 20 25 30

Ala Pro Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile

35 40 45
Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly Arg Ala Ala Thr
50 55 60

Ala Ser Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser Ala Pro Asp Pro
65 70 75 80

Arg Leu Leu Gln Gly Glu Val His Gly Ala Leu Val Arg His Pro Ala 85 90 95

- (2) INFORMATION FOR SEQ ID NO:1340:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597757
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val 1 10 15

Gln Lys Leu Val Leu Asn Ile Ser Val Gly Arg Ala Ala Thr Ala Ser

20 25 30
Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser Ala Pro Asp Pro Arg Leu

40 35 Leu Gln Gly Glu Val His Gly Ala Leu Val Arg His Pro Ala 55 (2) INFORMATION FOR SEQ ID NO:1341: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1597758 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341: Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly 10 Arg Ala Ala Thr Ala Ser Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser 30 25 Ala Pro Asp Pro Arg Leu Leu Gln Gly Glu Val His Gly Ala Leu Val 40 35 Arg His Pro Ala 50 (2) INFORMATION FOR SEQ ID NO:1342: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 422 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..422 (D) OTHER INFORMATION: / Ceres Seq. ID 1597797 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342: ategeceege gaaccetage tecegeaact geogeogeca etcecaeget egeagecatg 60 ccgcccaage tcgacccgtc gcaggtggtg gaggtgttcg tccgtgtgac cggcggcgag 120 gteggegeae gtettegetg geeeceaaga teggeeeget eggtetttee eecaagaaga 180 teggagagga categecaag gagaeggeca aggaetggaa gggeeteege gteacegtea 240 ageteacegt ecagaacegg cagecaaggt eteegtegte eceteegeeg eggegetegt 300 catcaaggcg ctcaaggagc cagagaggga ccgcaagaag gtcaagaaca tcaagcacag 360 cgncaacatc agcctcgacg acgtcatcga gatcgccagg accatgaggc acaggtccat 420 (2) INFORMATION FOR SEQ ID NO:1343: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..140 (D) OTHER INFORMATION: / Ceres Seq. ID 1597798 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343: Ile Ala Pro Arg Thr Leu Ala Pro Ala Thr Ala Ala Ala Thr Pro Thr 10 Leu Ala Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val 25 Phe Val Arg Val Thr Gly Gly Glu Val Gly Ala Arg Leu Arg Trp Pro

40

Pro Arg Ser Ala Arg Ser Val Phe Pro Pro Arg Arg Ser Glu Arg Thr 50 55 60

Ser Pro Arg Arg Pro Arg Thr Gly Arg Ala Ser Ala Ser Pro Ser 65 70 75 80

Ser Ser Pro Ser Arg Thr Gly Ser Gln Gly Leu Arg Arg Pro Leu Arg 85 90 95

Arg Gly Ala Arg His Gln Gly Ala Gln Gly Ala Arg Glu Gly Pro Gln
100 105 110

Glu Gly Gln Glu His Gln Ala Gln Xaa Gln His Gln Pro Arg Arg 115 120 125

His Arg Asp Arg Gln Asp His Glu Ala Gln Val His 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1344:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597799
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Arg Pro Ala Asn Pro Ser Ser Arg Asn Cys Arg Arg His Ser His Ala 1 5 10 15

Arg Ser His Ala Ala Gln Ala Arg Pro Val Ala Gly Gly Gly Val 20 25 30

Arg Pro Cys Asp Arg Arg Arg Gly Arg Arg Thr Ser Ser Leu Ala Pro 35 40 45

Lys Ile Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile 50 55 60

Ala Lys Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys 65 70 75 80

Leu Thr Val Gln Asn Arg Gln Pro Arg Ser Pro Ser Ser Pro Pro Pro 85 90 95

Arg Arg Ser Ser Ser Arg Arg Ser Arg Ser Gln Arg Gly Thr Ala Arg

Arg Ser Arg Thr Ser Ser Thr Ala Xaa Thr Ser Ala Ser Thr Thr Ser 115

Ser Arg Ser Pro Gly Pro 130

- (2) INFORMATION FOR SEQ ID NO:1345:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..121
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597800
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val Arg

Val Thr Gly Gly Glu Val Gly Ala Arg Leu Arg Trp Pro Pro Arg Ser 20 25 30

Ala Arg Ser Val Phe Pro Pro Arg Arg Ser Glu Arg Thr Ser Pro Arg 35 40 45

Arg Arg Pro Arg Thr Gly Arg Ala Ser Ala Ser Pro Ser Ser Pro

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55
    50
Ser Arg Thr Gly Ser Gln Gly Leu Arg Arg Pro Leu Arg Arg Gly Ala
                                        75
                    70
Arg His Gln Gly Ala Gln Gly Ala Arg Glu Gly Pro Gln Glu Gly Gln
                                    90
Glu His Gln Ala Gln Xaa Gln His Gln Pro Arg Arg Arg His Arg Asp
                                105
            100
Arg Gln Asp His Glu Ala Gln Val His
        115
(2) INFORMATION FOR SEQ ID NO:1346:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 483 base pairs
```

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..483
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597805
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346: aaaaccctag ccgcctgcyt ctcctcctcc agagctcgtc gccaccggcc accgccaccc 60 tcgatcacgc cgtccgtcga ggtaaggtca gcatggtgag ggtcagtgtg ctcaacgatg 120 cgctcaagtc catgtacaac gctgagaaga tcggcaagag gcaggtcatg atcaggccgt 180 cgtccaaggt catcatcaag ttcctgacgg tcatgcagcg ccacggctac attggagagt 240 tcgagtacgt tgatgaccac cgatcgggca agatcgtggt cgaactcaac gggaggctga 300 acaagtgcgg cgtcatcagc cctcgctttg atatcggcgt gaaagacatt gagggatgga 360 ctgcaagetg ctcccgtcca ggcagttcgg atacategtc ctcacaactt cggcaggcat 420 catggaccac gaggaggccc gccggaagag cgtaggaggc aaggttctag gtttcttcta 480 ttg
- (2) INFORMATION FOR SEQ ID NO:1347:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..150
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Asn Pro Ser Arg Leu Xaa Leu Leu Leu Gln Ser Ser Ser Pro Pro Ala 10

Thr Ala Thr Leu Asp His Ala Val Arg Arg Gly Lys Val Ser Met Val 30 2.5

Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn Ala Glu 40

Lys Ile Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys Val Ile 60 55

Ile Lys Phe Leu Thr Val Met Gln Arg His Gly Tyr Ile Gly Glu Phe 75 70

Glu Tyr Val Asp Asp His Arg Ser Gly Lys Ile Val Val Glu Leu Asn 90

Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asp Ile Gly 105 100

Val Lys Asp Ile Glu Gly Trp Thr Ala Ser Cys Ser Arg Pro Gly Ser 125 120 115

Ser Asp Thr Ser Ser Ser Gln Leu Arg Gln Ala Ser Trp Thr Thr Arg 130 135

Arg Pro Ala Gly Arg Ala

150 145 (2) INFORMATION FOR SEQ ID NO:1348: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..120 (D) OTHER INFORMATION: / Ceres Seq. ID 1597807 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348: Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn 15 10 Ala Glu Lys Ile Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys 25 Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly Tyr Ile Gly 4.5 40 Glu Phe Glu Tyr Val Asp Asp His Arg Ser Gly Lys Ile Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asp 75 Ile Gly Val Lys Asp Ile Glu Gly Trp Thr Ala Ser Cys Ser Arg Pro 90 85 Gly Ser Ser Asp Thr Ser Ser Ser Gln Leu Arg Gln Ala Ser Trp Thr 100 105 Thr Arg Arg Pro Ala Gly Arg Ala 115 120 (2) INFORMATION FOR SEQ ID NO:1349: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1597808 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349: Met Tyr Asn Ala Glu Lys Ile Gly Lys Arg Gln Val Met Ile Arg Pro 1.0 Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly 25 20 Tyr Ile Gly Glu Phe Glu Tyr Val Asp Asp His Arg Ser Gly Lys Ile 40 Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro 55 Arg Phe Asp Ile Gly Val Lys Asp Ile Glu Gly Trp Thr Ala Ser Cys 75 70 Ser Arg Pro Gly Ser Ser Asp Thr Ser Ser Ser Gln Leu Arg Gln Ala 90 85 Ser Trp Thr Thr Arg Arg Pro Ala Gly Arg Ala 105 100 (2) INFORMATION FOR SEQ ID NO:1350: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA '(genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..133 (D) OTHER INFORMATION: / Ceres Seq. ID 1597809 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350: 60 qtttccttct cccccacta cccaaaccca acaggcggcg cmagcattcg ccaccaccgt 120 ccaaagagca aagatggtga agttcctcaa gcccggcaag gccgttatcc tcctccaggg ccggttcgcc ggc (2) INFORMATION FOR SEQ ID NO:1351: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..44 (D) OTHER INFORMATION: / Ceres Seq. ID 1597810 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351: Val Ser Phe Ser Pro His Tyr Pro Asn Pro Thr Gly Gly Xaa Ser Ile 5 10 Arg His His Arg Pro Lys Ser Lys Asp Gly Glu Val Pro Gln Ala Arg 20 25 Gln Gly Arg Tyr Pro Pro Pro Gly Pro Val Arg Arg 40 35 (2) INFORMATION FOR SEQ ID NO:1352: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..44 (D) OTHER INFORMATION: / Ceres Seq. ID 1597811 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352: Phe Pro Ser Pro Pro Thr Thr Gln Thr Gln Gln Ala Ala Xaa Ala Phe 10 Ala Thr Thr Val Gln Arg Ala Lys Met Val Lys Phe Leu Lys Pro Gly 20 25 Lys Ala Val Ile Leu Leu Gln Gly Arg Phe Ala Gly 35 40 (2) INFORMATION FOR SEQ ID NO:1353: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..469 (D) OTHER INFORMATION: / Ceres Seq. ID 1597813 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:
 - aataaaagga tegeeeteeg egegeegeeg eteettegea aaceeteeta eeceatteeg 60 eegeeegeee egegaeeeeg aggaggagge aagatgaaga egateetgge gteggagvat 120 ggacateeeg agggegteae agtgaeggtg geggeeaage tggtgaeggt ggagggeeee 180 egeggaaget caceeggaae tteaageace teaacetega ettecagetg eaggagggeg 240

geogeaaget caaggtggae geatggtteg geaecegeeg eaceatggee geeateegea 300 cegecatete eeacgteeag aaceteatea agggggteae eagggetae egetaeaaga 360 tgaggtttgt etaegeeeat tteeceatea aegegteeat eaceaactee aacacegeea tegagataag gaaetteete ggegagaaga aggteagaaa ggtggaeat

- (2) INFORMATION FOR SEQ ID NO:1354:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597814
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

Asn Lys Arg Ile Ala Leu Arg Ala Pro Pro Leu Leu Arg Lys Pro Ser 1 10 15

Tyr Pro Ile Pro Pro Pro Ala Pro Arg Pro Arg Gly Gly Lys Met 20 25 30

Lys Thr Ile Leu Ala Ser Glu Xaa Gly His Pro Glu Gly Val Thr Val
35 40 45

Thr Val Ala Ala Lys Leu Val Thr Val Glu Gly Pro Arg Gly Ser Ser 50 55 60

Pro Gly Thr Ser Ser Thr Ser Thr Ser Thr Ser Ser Cys Arg Arg Ala 70 75 80

Ala Ala Ser Ser Arg Trp Thr His Gly Ser Ala Pro Ala Ala Pro Trp 85 90 95

Pro Pro Ser Ala Pro Pro Ser Pro Thr Ser Arg Thr Ser Ser Arg Gly
100 105 110

Ser Pro Arg Ala Thr Ala Thr Arg

- (2) INFORMATION FOR SEQ ID NO:1355:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597815
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

Met Lys Thr Ile Leu Ala Ser Glu Xaa Gly His Pro Glu Gly Val Thr

Val Thr Val Ala Ala Lys Leu Val Thr Val Glu Gly Pro Arg Gly Ser 20 25 30

Ser Pro Gly Thr Ser Ser Thr Ser Thr Ser Thr Ser Ser Cys Arg Arg
35
40
45

Ala Ala Ser Ser Arg Trp Thr His Gly Ser Ala Pro Ala Ala Pro
50 55 60

Trp Pro Pro Ser Ala Pro Pro Ser Pro Thr Ser Arg Thr Ser Ser Arg 65 70 75 80

- Gly Ser Pro Arg Ala Thr Ala Thr Arg 85
- (2) INFORMATION FOR SEQ ID NO:1356: (i) SEQUENCE CHARACTERISTICS:
 - SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

120

180

240

300

360

420

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597816
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

Met Val Arg His Pro Pro His His Gly Arg His Pro His Arg His Leu 5 10

Pro Arg Pro Glu Pro His Gln Gly Gly His Gln Gly Leu Pro Leu Gln 25 20

Asp Glu Val Cys Leu Arg Pro Phe Pro His Gln Arg Val His His Gln 40

Leu Gln His Arg His Arg Asp Lys Glu Leu Pro Arg Arg Glu Glu Gly 55

Gln Lys Gly Gly His

65

- (2) INFORMATION FOR SEQ ID NO:1357:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..472
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597821
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357: actogagect gaccottacg cottogcteg egeogeegee geogeegeeg etacgeeeeg cacctcgctt catttcgtgt cgccaagatg acgaagcgca ctaagaaggc aggaattgtt ggcaaatatg gaaccaggta tggtgctagc ttgcgtaasa aattcaagaa gatggaggta tctcagcatt ccaagtactt ttgcgagttc tgtgggaagt ttgctgtgaa gaggaaagca gttggaattt gggggtgcaa ggactgtggg aaggtgaagg ctggtggtgc ttacaccatg aacactqcta gtgcggtcac cgtcagagca cgatccgccg cctgagggag ctgagcggag agttatggta cggtgtgtat ccgaccagtc tcctgttgtt tngggggtca acatcgtgtc tcttttgttt ttggttcatc atatcagtta gttatctatc agtgtttgtt cg
- (2) INFORMATION FOR SEQ ID NO:1358:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 1.0

Arg Tyr Gly Ala Ser Leu Arg Xaa Lys Phe Lys Lys Met Glu Val Ser 25 20

Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys 40

Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys 55 60

Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Val Arg 70

Ala Arg Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:1359: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..57 (D) OTHER INFORMATION: / Ceres Seq. ID 1597823 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359: Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys 10 5 Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys 30 25 20 Gly Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala 40 35 Val Thr Val Arg Ala Arg Ser Ala Ala 55 50 (2) INFORMATION FOR SEQ ID NO:1360: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 423 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..423 (D) OTHER INFORMATION: / Ceres Seq. ID 1597825 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360: gaaacccgtc tcgcaccaca agckagckag ggacccgggg cggaagaaga gagagaagac 60 120 gtctctctcc tctcggcgtc ccacgttccc maacctctcg tctgctgcct gcctgcctgc 180 ctgcctgcaa aaaggagttt gtcatggcgt ctaagcgcat cctcaaggag ctgaaggacc 240 tgcagaaaga ccccccaca tcatgcagtg caggtcctgc tggtgaggac atgtttcatt ggcaagcaac aattatggga ccacctgaca gtccctatgc tggcggtgtt ttcttagtga 300 acattcattt cccgccagat taccccttca aacctccaaa ggtttctttc aagacaaagg 360 tettecatee taatateaae ageaatggaa gtatatgeet tgaeattete aagageagtg 420 gag (2) INFORMATION FOR SEQ ID NO:1361: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..140 (D) OTHER INFORMATION: / Ceres Seq. ID 1597826 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361: Asn Pro Ser Arg Thr Thr Ser Xaa Xaa Gly Thr Arg Gly Gly Arg Arg 10 Glu Arg Arg Arg Leu Ser Pro Leu Gly Val Pro Arg Ser Xaa Thr Ser 25 Arg Leu Leu Pro Ala Cys Leu Pro Ala Cys Lys Lys Glu Phe Val Met 40 Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp Pro

55

Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Met Phe His Trp

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

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75
                    70
Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly Val
                                   90
Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro
                                                    110
                               105
Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser Asn
                            120
Gly Ser Ile Cys Leu Asp Ile Leu Lys Ser Ser Gly
                       135
    130
(2) INFORMATION FOR SEQ ID NO:1362:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 93 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..93
          (D) OTHER INFORMATION: / Ceres Seq. ID 1597827
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
                                                        15
                                    10
Pro Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Met Phe His
                                25
            20
Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly
                                                 45
                            40
Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
                        55
Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser
                   70
                                        75
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Ser Ser Gly
                85
(2) INFORMATION FOR SEQ ID NO:1363:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 482 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..482
           (D) OTHER INFORMATION: / Ceres Seq. ID 1597830
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:
ctctagccaa aaccctagca gccgcccggt gctccctctc tgcaggtggc ggcgcgctcc
                                                                         60
cctcgcctcc cgccgaggaa ccccttcaca gcgcggaaga tggctgaaca ggaggcccca
                                                                        120
gtcgcggttg aaggcaccaa ccccagttct tggggagcct atggacttga tgactgctct
                                                                        180
 gcrctcgtga tgaagaagtc aagtgctcat gacggtcttg tgaagggtct ccgtgagctg
                                                                        240
                                                                        300
 ccaaggccat cgagaagcac geegeteage tttgegtget tgetgaggae tgtgaecage
 cagattacgt caagttggtg aaggcactct gcgctgagca caatgttcac ctggtgcact
                                                                        360
 gttcctgccg ctaagactct tggcgagtgg gccgggcttt scaagattga ctctgagggc
                                                                        420
 aaggcaagga aggttgtagg ckmgctcctg cgtcgtcgtc aaggactacg gtgaagaatc
                                                                        480
 tg
 (2) INFORMATION FOR SEQ ID NO:1364:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 62 amino acids
           (B) TYPE: amino acid
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- (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..62 (D) OTHER INFORMATION: / Ceres Seq. ID 1597831 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364: Ser Ser Gln Asn Pro Ser Ser Arg Pro Val Leu Pro Leu Cys Arg Trp 10 15 5 Arg Arg Ala Pro Leu Ala Ser Arg Arg Gly Thr Pro Ser Gln Arg Gly 25 Arg Trp Leu Asn Arg Arg Pro Gln Ser Arg Leu Lys Ala Pro Thr Pro 40 Val Leu Gly Glu Pro Met Asp Leu Met Thr Ala Leu Xaa Ser 55 (2) INFORMATION FOR SEQ ID NO:1365: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..73 (D) OTHER INFORMATION: / Ceres Seq. ID 1597832 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365: Met Ala Glu Gln Glu Ala Pro Val Ala Val Glu Gly Thr Asn Pro Ser 10 15 Ser Trp Gly Ala Tyr Gly Leu Asp Asp Cys Ser Xaa Leu Val Met Lys 25 2.0 Lys Ser Ser Ala His Asp Gly Leu Val Lys Gly Leu Arg Glu Leu Pro 4.5 40 Arg Pro Ser Arg Ser Thr Pro Leu Ser Phe Ala Cys Leu Leu Arg Thr 60 55 Val Thr Ser Gln Ile Thr Ser Ser Trp 70 (2) INFORMATION FOR SEQ ID NO:1366: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1597833 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366: Met Phe Thr Trp Cys Thr Val Pro Ala Ala Lys Thr Leu Gly Glu Trp 10 Ala Gly Leu Xaa Lys Ile Asp Ser Glu Gly Lys Ala Arg Lys Val Val 30 25 20 Gly Xaa Leu Leu Arg Arg Arg Gln Gly Leu Arg 40 35 (2) INFORMATION FOR SEQ ID NO:1367: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597848
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367: awaggaccc ggcccacctg gaagccggag agaatcgagc agagccaccg atcgctcctg agcactttcc acattccagt tccactccgc ctccgctgcc ggtcgccgtc tccgagactc

ageactttce acattccagt tccactccgc ctccgctgcc ggtcgccgtc tccgagactc 120 cgacagtccg accgcaagaa ggatgagtga agaggataag actgctgctt ctrctgagca 180 gccgaagagg gcccctaagc tcaatgaaag gatcctctct tctctgtcca ggaggtccgt 240 agctgctcat ccatggcatg atcttgagat cggtcctgat gctcctgctg ttttcaatgt 300 tgttgttgag atcacaaagg gaagcaaagt taaatatgag cttgacaaga aaactggact gattaaggtt gatcgagtcc tgtactcatc agttgtatac cctcacaatt atggtttcgt tccaaggact ctttgtgaag acaatgaccc aatggatgt ttagtcctga tgcaggagcc 480

- (2) INFORMATION FOR SEQ ID NO:1368:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597849
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

Met Ser Glu Glu Asp Lys Thr Ala Ala Ser Xaa Glu Gln Pro Lys Arg
1 5 10 15

Ala Pro Lys Leu Asn Glu Arg Ile Leu Ser Ser Leu Ser Arg Arg Ser 20 25 30

Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Asp Ala Pro
35 40 45

Ala Val Phe Asn Val Val Glu Ile Thr Lys Gly Ser Lys Val Lys
50 55 60

Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys Val Asp Arg Val Leu 65 70 75 80

Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly Phe Val Pro Arg Thr 85 90 95

Leu Cys Glu Asp Asn Asp Pro Met Asp Val Leu Val Leu Met Gln Glu
100 105 110

Pro

- (2) INFORMATION FOR SEQ ID NO:1369:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..362
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597850
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

aaccatcatt gcaaaagcga mawagcaatn nggaattete tgcgattet etagateteg 60 actacecee actagtttg gtteeneett tegttykaga gagegattet ggtggcaatg 120 gegaaswneg agggteegge gategggate gaceteggea ecacetaete gtgegtegge 180 rtgtggeage acgaeegggt ggagateate gecaaegaee aggggaaege aceaeggegt eteatemrge gaegetgeea anraceaggt 240 egecatgaae eceaecaaea eegtettega tteeaagegg ttgateggea ggagggttet 260 et

(2) INFORMATION FOR SEQ ID NO:1370:

- Client Docket No. 80146.003 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..120 (D) OTHER INFORMATION: / Ceres Seq. ID 1597851 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370: Thr Ile Ile Ala Lys Ala Xaa Xaa Gln Xaa Gly Ile Leu Cys Asp Phe 10 5 Ser Arg Ser Arg Leu Pro Pro Thr Ser Phe Gly Ser Xaa Phe Arg Xaa 25 Arg Glu Arg Phe Trp Trp Gln Trp Arg Xaa Xaa Arg Val Arg Arg Ser 40 Gly Ser Thr Ser Ala Pro Pro Thr Arg Ala Ser Xaa Cys Gly Ser Thr 55 Thr Gly Trp Arg Ser Ser Pro Thr Thr Arg Gly Thr His His Ala Val 75 70 Leu Cys Arg Leu His Arg His Pro Ser Gly Ser Xaa Xaa Asp Ala Ala 90 Xaa Xaa Gln Val Ala Met Asn Pro Thr Asn Thr Val Phe Asp Ser Lys 100 105 110 Arg Leu Ile Gly Arg Arg Val Leu 115 120 (2) INFORMATION FOR SEQ ID NO:1371: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..101 (D) OTHER INFORMATION: / Ceres Seq. ID 1597852 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371: Pro Ser Leu Gln Lys Arg Xaa Ser Asn Xaa Glu Phe Ser Ala Ile Ser 10 Leu Asp Leu Asp Tyr Pro Pro Leu Val Leu Val Xaa Pro Phe Val Xaa 25 20 Glu Ser Asp Ser Gly Gly Asn Gly Glu Xaa Arg Gly Ser Gly Asp Arg 4.0 Asp Arg Pro Arg His His Leu Leu Val Arg Arg Xaa Val Ala Ala Arg 55 Pro Gly Gly Asp His Arg Gln Arg Pro Gly Glu Arg Thr Thr Pro Ser 75 70 Tyr Val Gly Phe Thr Asp Thr Arg Ala Ala His Xaa Ala Thr Leu Pro 85 Xaa Thr Arg Ser Pro 100 (2) INFORMATION FOR SEQ ID NO:1372: (i) SEQUENCE CHARACTERISTICS:
 - - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

180 240

300

360

420

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597853

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372: Met Ala Xaa Xaa Glu Gly Pro Ala Ile Gly Ile Asp Leu Gly Thr Thr

Tyr Ser Cys Val Gly Xaa Trp Gln His Asp Arg Val Glu Ile Ile Ala
20 25 30

Asn Asp Gln Gly Asn Ala Pro Arg Arg Pro Met Ser Ala Ser Pro Thr

Pro Glu Arg Leu Ile Xaa Arg Arg Cys Gln Xaa Pro Gly Arg His Glu 50 55 60

Pro His Gln His Arg Leu Arg Phe Gln Ala Val Asp Arg Gln Glu Gly 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:1373:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..465
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597854
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

 acacacacac acacatccat caaagaaaca ggcacacaag aacaaatacc tcgccaccaa caatggcete caggteetee atcetacttg caacggcgat getggttgek ctgtttgegg ttggtttgtg caccacccg etcaccttee aggttggcaa gggatecaag ectggecace tgatecteae ecceaatgtt gcaaccatat etgacgtgga gateaaagag cacgggggg atgacttete etttacgete aaggagggee egaceggeae etggacgete gacaccaagg eccegeteaa gtaccecett tgcateeget ttgetgteaa gteeggtgge tacegeateg ecgacgacgt eateeegge gattteaagg eeggeaee etacaagaee acactacage atetaateag ectetgatga tgaattatat ttcaaaagag etcae
- (2) INFORMATION FOR SEQ ID NO:1374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

85

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Thr His Thr His Ile His Gln Arg Asn Arg His Thr Arg Thr Asn Thr

Ser Pro Pro Thr Met Ala Ser Arg Ser Ser Ile Leu Leu Ala Thr Ala 20 25 30

Met Leu Val Xaa Leu Phe Ala Val Gly Leu Cys Thr Thr Pro Leu Thr

Phe Gln Val Gly Lys Gly Ser Lys Pro Gly His Leu Ile Leu Thr Pro 50 55 60

Asn Val Ala Thr Ile Ser Asp Val Glu Ile Lys Glu His Gly Gly Asp 65 70 75 80
Asp Phe Ser Phe Thr Leu Lys Glu Gly Pro Thr Gly Thr Trp Thr Leu

Asp Thr Lys Ala Pro Leu Lys Tyr Pro Leu Cys Ile Arg Phe Ala Val

90

Lys Ser Gly Gly Tyr Arg Ile Ala Asp Asp Val Ile Pro Ala Asp Phe
115

Lys Ala Gly Thr Thr Tyr Lys Thr Thr Leu Gln His Leu Ile Ser Leu
130

- (2) INFORMATION FOR SEQ ID NO:1375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597856
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

Met Ala Ser Arg Ser Ser Ile Leu Leu Ala Thr Ala Met Leu Val Xaa 1 5 10 15

Leu Phe Ala Val Gly Leu Cys Thr Thr Pro Leu Thr Phe Gln Val Gly 20 25 30

Lys Gly Ser Lys Pro Gly His Leu Ile Leu Thr Pro Asn Val Ala Thr 35 40 45

Ile Ser Asp Val Glu Ile Lys Glu His Gly Gly Asp Asp Phe Ser Phe 50 55 60

Thr Leu Lys Glu Gly Pro Thr Gly Thr Trp Thr Leu Asp Thr Lys Ala 65 70 75 80

Pro Leu Lys Tyr Pro Leu Cys Ile Arg Phe Ala Val Lys Ser Gly Gly 85 90 95

Tyr Arg Ile Ala Asp Asp Val Ile Pro Ala Asp Phe Lys Ala Gly Thr 100 105 110

Thr Tyr Lys Thr Thr Leu Gln His Leu Ile Ser Leu 115 120

- (2) INFORMATION FOR SEQ ID NO:1376:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

Met Leu Val Xaa Leu Phe Ala Val Gly Leu Cys Thr Thr Pro Leu Thr 1 5 10 15

Phe Gln Val Gly Lys Gly Ser Lys Pro Gly His Leu Ile Leu Thr Pro 20 25 30

Asn Val Ala Thr Ile Ser Asp Val Glu Ile Lys Glu His Gly Gly Asp 35 40 45

Asp Phe Ser Phe Thr Leu Lys Glu Gly Pro Thr Gly Thr Trp Thr Leu 50 55 60

Asp Thr Lys Ala Pro Leu Lys Tyr Pro Leu Cys Ile Arg Phe Ala Val 65 70 75 80

Lys Ser Gly Gly Tyr Arg Ile Ala Asp Asp Val Ile Pro Ala Asp Phe 85 90 95

Lys Ala Gly Thr Thr Tyr Lys Thr Thr Leu Gln His Leu Ile Ser Leu 100 105 110

(2) INFORMATION FOR SEQ ID NO:1377:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 335 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(ix) FEATURE:	
(A) NAME/KEY: -	
(B) LOCATION: 1335	
(D) OTHER INFORMATION: / Ceres Seq. ID 1597871	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:	
cactegtete atetetteca tacgaccata ecetacetee aaatteecaa ttgtcaacet	60
ctcctcagag ttcgagtgac catgtcgggg cgcggaaagg gcgggaaggg gctgggcaag	120
ggcggcgcga mstcaccgca agtcctccgc gacaacatcc agggcattac gaagccggcg	180 240
atccggagct ggcganaagg ggcggcgtga agcsattctc ggggctcatc tacgaggaga	300
cccgcggcgt gctcaagatc ttcctcgaga atgtcattcg cgacgctgtc acctacacgg	300
agcacgcccg ccgtaagacc gtcaccgcca tggac	
(2) INFORMATION FOR SEQ ID NO:1378:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 69 amino acids	
(B) TYPE: amino acid (C) STRANDEDNESS:	
(C) STRANDEDNESS. (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(ix) FEATURE:	
(A) NAME/KEY: peptide	
(B) LOCATION: 169	
(D) OTHER INFORMATION: / Ceres Seq. ID 1597872	
(vi) SEQUENCE DESCRIPTION: SEO ID NO:1378:	
His Ser Ser His Leu Phe His Thr Thr Ile Pro Tyr Leu Gln Ile Pro	
1 10 15	
Asn Cys Gln Pro Leu Leu Arg Val Arg Val Thr Met Ser Gly Arg Gly	
20 25 30	
Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala Xaa Ser Pro Gln Val	
35 40 45	
Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Ser Trp	
50 55	
Arg Xaa Gly Ala Ala	
65	
(2) INFORMATION FOR SEQ ID NO:1379:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 111 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS: (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(ix) FEATURE:	
(A) NAME/KEY: peptide	
(B) LOCATION: 1111	
(D) OTHER INFORMATION: / Ceres Seq. ID 1597873	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:	
Leu Val Ser Ser Leu Pro Tyr Asp His Thr Leu Pro Pro Asn Ser Gln	
1 10 15	
Leu Ser Thr Ser Pro Gln Ser Ser Ser Asp His Val Gly Ala Arg Lys	
20 25 30	
Gly Arg Glu Gly Ala Gly Gln Gly Arg Arg Xaa Xaa Thr Ala Ser Pro	
35 40 45 Ann Dao Clu Iou Ala	
Pro Arg Gln His Pro Gly His Tyr Glu Ala Gly Asp Pro Glu Leu Ala	

- (2) INFORMATION FOR SEQ ID NO:1380:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597878
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380: awatagcaca cagccaaagc caccagcgct cgttcacctc caatcaacaa attcccaatc 60 cgccgcttcc catcccgcgt tcgccgctcc atttgatcga attcccgatg gcgcccaagg 120 180 ccgagaagaa gcccgcggag aagaagccga cggaggagaa ggccgagaag aagcccaggg cgagaagcgc gtgccgggca aggagggcgg cgagaagaag gggaagaaga aggccaagaa 240 gagcgtcgag acgtacaaga tctacatctt caaggtgctc aagcaggtgc acccggacat 300 tggtatctcg tccaaggcca tgtccatcat gaactccttc atcaacgaca tcttcgagaa 360 gctggctgcc gaggccgcca agctcgcccg ctacaacaag aagcccacca taacctcccg 420 ggagatccag acttcggtgc gcctcgtcct tcctggcgag ctcgcaagca cgccgtctcc 480 gaggg
- (2) INFORMATION FOR SEQ ID NO:1381:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

Arq

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381: Xaa Ser Thr Gln Pro Lys Pro Pro Ala Leu Val His Leu Gln Ser Thr 10 Asn Ser Gln Ser Ala Ala Ser His Pro Ala Phe Ala Ala Pro Phe Asp 25 20 Arg Ile Pro Asp Gly Ala Gln Gly Arg Glu Glu Ala Arg Gly Glu Glu 40 Ala Asp Gly Gly Glu Gly Arg Glu Glu Ala Gln Gly Glu Lys Arg Val 55 Pro Gly Lys Glu Gly Gly Glu Lys Lys Gly Lys Lys Lys Ala Lys Lys 75 70 Ser Val Glu Thr Tyr Lys Ile Tyr Ile Phe Lys Val Leu Lys Gln Val 90 85 His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Ser Ile Met Asn Ser 105 100 Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Ala Glu Ala Ala Lys Leu 125 120 Ala Arg Tyr Asn Lys Lys Pro Thr Ile Thr Ser Arg Glu Ile Gln Thr 140 135 Ser Val Arg Leu Val Leu Pro Gly Glu Leu Ala Ser Thr Pro Ser Pro 155 145 150

(2) INFORMATION FOR SEQ ID NO:1382: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..109 (D) OTHER INFORMATION: / Ceres Seq. ID 1597880 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382: Ile Ala His Ser Gln Ser His Gln Arg Ser Phe Thr Ser Asn Gln Gln 10 5 Ile Pro Asn Pro Pro Leu Pro Ile Pro Arg Ser Pro Leu His Leu Ile 25 Glu Phe Pro Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Glu Lys Lys 45 40 Pro Thr Glu Glu Lys Ala Glu Lys Lys Pro Arg Ala Arg Ser Ala Cys 60 55 Arg Ala Arg Arg Ala Ala Arg Arg Arg Gly Arg Arg Pro Arg Arg 75 Ala Ser Arg Arg Thr Arg Ser Thr Ser Ser Arg Cys Ser Ser Arg Cys 90 85 Thr Arg Thr Leu Val Ser Arg Pro Arg Pro Cys Pro Ser 105 100 (2) INFORMATION FOR SEQ ID NO:1383: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..149 (D) OTHER INFORMATION: / Ceres Seq. ID 1597881 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383: caaaccctag tctcagagca gccgcatcca caacctgcct ctctcgtccc ctggcggcgt 60 ccgggcagga tggcggaatc tacggcgagg acggtgaagg atgtcaaccc gcacgagttc 120 gtcaaggcct actccgccca cctcaagcg (2) INFORMATION FOR SEQ ID NO:1384: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..49 (D) OTHER INFORMATION: / Ceres Seq. ID 1597882 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384: Gln Thr Leu Val Ser Glu Gln Pro His Pro Gln Pro Ala Ser Leu Val 10 Pro Trp Arg Arg Pro Gly Arg Met Ala Glu Ser Thr Ala Arg Thr Val 25 20 Lys Asp Val Asn Pro His Glu Phe Val Lys Ala Tyr Ser Ala His Leu

40

- (2) INFORMATION FOR SEQ ID NO:1385: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..49 (D) OTHER INFORMATION: / Ceres Seq. ID 1597883 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385: Asn Pro Ser Leu Arg Ala Ala Ala Ser Thr Thr Cys Leu Ser Arg Pro 10 Leu Ala Ala Ser Gly Gln Asp Gly Gly Ile Tyr Gly Glu Asp Gly Glu 25 Gly Cys Gln Pro Ala Arg Val Arg Gln Gly Leu Leu Arg Pro Pro Gln Ala (2) INFORMATION FOR SEQ ID NO:1386: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..242 (D) OTHER INFORMATION: / Ceres Seq. ID 1597890 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386: gegeanteat ceatteeate atecettgea agtatagtet eggeggetet agaataegat 60 120 gggcaaggac gacgtgatcg agagcggcgc tggcggcggc gagttcgctg ccaaggacta cacggaccet ceceeggege egetgatega egeggetgag etgggggatee tggtegetgt 180 amcgcgccgt gatcgccgag ttcatcgcca cgctgctgtt cctgtacatc acggtgdcca 240 (2) INFORMATION FOR SEQ ID NO:1387: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1597891 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387: Ala Xaa Ser Ser Ile Pro Ser Ser Leu Ala Ser Ile Val Ser Ala Ala 10 Leu Glu Tyr Asp Gly Gln Gly Arg Arg Asp Arg Glu Arg Arg Trp Arg 25 Arg Arg Val Arg Cys Gln Gly Leu His Gly Pro Ser Pro Gly Ala Ala 40 35 Asp Arg Arg Gly 50
 - (2) INFORMATION FOR SEQ ID NO:1388:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids

(B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..61 (D) OTHER INFORMATION: / Ceres Seq. ID 1597892 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388: Met Gly Lys Asp Asp Val Ile Glu Ser Gly Ala Gly Gly Glu Phe 1.0 Ala Ala Lys Asp Tyr Thr Asp Pro Pro Pro Ala Pro Leu Ile Asp Ala 25 Ala Glu Leu Gly Ile Leu Val Ala Val Xaa Arg Arg Asp Arg Arg Val 40 His Arg His Ala Ala Val Pro Val His His Gly Xaa His 55 (2) INFORMATION FOR SEQ ID NO:1389: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..460 (D) OTHER INFORMATION: / Ceres Seq. ID 1597900 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389: aagcaaattt cccaaacgca aaaccgcatc ctctcatcag cttccttcca cattcgtctc 60 gagatetege ecceptegeea tggaegegat egaeagegtg gtggateece teegegaett 120 cgccaaggac agcgtcgccc tcgtcaagcg ctgccacaag cccgaccgca agagttcacc 180 aaggtggegg egeggaegge gategggtte gtegteatgg gettegtegg ettettegtt 240 300 aagctcatct tcatccccat caacaacatc atcgtcggtt ccggctaggc ttacaggagt acagggcgac tagcatggga gtagtgcaat acttttggga gcaatagata acgaggatcc 360 tggtctttcg aatagtattg tttaatgaat ttttcgttcg gttgtgtttc tgatgtaatc 420 gttsgtactg agtagacctt ctggataccg gattctgagt (2) INFORMATION FOR SEQ ID NO:1390: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..95 (D) OTHER INFORMATION: / Ceres Seq. ID 1597901 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390: Lys Gln Ile Ser Gln Thr Gln Asn Arg Ile Leu Ser Ser Ala Ser Phe 10 His Ile Arg Leu Glu Ile Ser Pro Arg Arg His Gly Arg Asp Arg Gln 25 Arg Gly Gly Ser Pro Pro Arg Leu Arg Gln Gly Gln Arg Arg Pro Arg 40 Gln Ala Leu Pro Gln Ala Arg Pro Gln Glu Phe Thr Lys Val Ala Ala 60 55 Arg Thr Ala Ile Gly Phe Val Val Met Gly Phe Val Gly Phe Phe Val

75

90

70

Lys Leu Ile Phe Ile Pro Ile Asn Asn Ile Ile Val Gly Ser Gly

- Attorney Docket No. 2750-1237P Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:1391: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..103 (D) OTHER INFORMATION: / Ceres Seq. ID 1597902 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391: Ser Lys Phe Pro Lys Arg Lys Thr Ala Ser Ser His Gln Leu Pro Ser 10 Thr Phe Val Ser Arg Ser Arg Pro Val Ala Met Asp Ala Ile Asp Ser 30 25 20 Val Val Asp Pro Leu Arg Asp Phe Ala Lys Asp Ser Val Ala Leu Val 45 40 Lys Arg Cys His Lys Pro Asp Arg Lys Ser Ser Pro Arg Trp Arg Arg 60 55 Gly Arg Arg Ser Gly Ser Ser Ser Trp Ala Ser Ser Ala Ser Ser Leu 75 70 Ser Ser Ser Ser Pro Ser Thr Thr Ser Ser Ser Val Pro Ala Arg 90 85 Leu Thr Gly Val Gln Gly Asp 100 (2) INFORMATION FOR SEQ ID NO:1392: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..79 (D) OTHER INFORMATION: / Ceres Seq. ID 1597903 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392: Ala Asn Phe Pro Asn Ala Lys Pro His Pro Leu Ile Ser Phe Leu Pro 10 5 His Ser Ser Arg Asp Leu Ala Pro Ser Pro Trp Thr Arg Ser Thr Ala 25 Trp Trp Ile Pro Ser Ala Thr Ser Pro Arg Thr Ala Ser Pro Ser Ser 40 Ser Ala Ala Thr Ser Pro Thr Ala Arg Val His Gln Gly Gly Ala 55 Asp Gly Asp Arg Val Arg Arg His Gly Leu Arg Arg Leu Leu Arg
 - (2) INFORMATION FOR SEQ ID NO:1393:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..478
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393: gcattagcac tagggtttcc catctcttaa ggctgccacc gccagckccg cccctcggt

gcatcctcag tgcgtactgt ctgtgcgaag gcgaccattc cttcttcgct ccttcgccgc 120 cgctatggtt aagtactcgc aggagccggg caaccctacc aaatcggcca aggccatggg 180 aagggacctg agggtcactt caagaacaca agggagacag cttttgcgct tcgcaagctg 240 cctttgacca aggctaagcg ataccttgag gatgttattg ctcacaagca ggcaattccc tccggagat actgtggagg tgttggtcgc accgcacaag caaagtctcg ccactccaat gggcagggtc gctggcctgt taagtcagcc aggttcatat tggatttgct gaagaatgct 420 gagagtaacg ctgatgtgaa aggcttggac gtggacaacc tctatgtttc acacatcc

- (2) INFORMATION FOR SEQ ID NO:1394:
 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597906
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Ile Ser Thr Arg Val Ser His Leu Leu Arg Leu Pro Pro Pro Xaa Pro 1 5 10

Pro Pro Arg Cys Ile Leu Ser Ala Tyr Cys Leu Cys Glu Gly Asp His 20 25 30

Ser Phe Phe Ala Pro Ser Pro Pro Leu Trp Leu Ser Thr Arg Arg Ser 35 40 45

Arg Ala Thr Leu Pro Asn Arg Pro Arg Pro Trp Glu Gly Thr 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1395:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..40
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597907
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

Met Val Lys Tyr Ser Gln Glu Pro Gly Asn Pro Thr Lys Ser Ala Lys
1 5 10 15

Ala Met Gly Arg Asp Leu Arg Val Thr Ser Arg Thr Gln Gly Arg Gln 20 25 30

Leu Leu Arg Phe Ala Ser Cys Leu 35

- (2) INFORMATION FOR SEQ ID NO:1396:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

20

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

Met Leu Leu Leu Thr Ser Arg Gln Phe Pro Ser Gly Asp Thr Val Glu 1 5 10 15 Val Leu Val Ala Pro His Lys Gln Ser Leu Ala Thr Pro Met Gly Arg

25

Page 818 Client Docket No. 80146.003 Val Ala Gly Leu Leu Ser Gln Pro Gly Ser Tyr Trp Ile Cys 40 (2) INFORMATION FOR SEQ ID NO:1397: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 457 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..457 (D) OTHER INFORMATION: / Ceres Seq. ID 1597913 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397: 60 gtocgtotot cgttototoc ttootatogg otocacacot ccacgoaact ggaagottog 120 ctgcaatctg ccctactcct cttccgccgc ctccaacacc gcagacgcag ctgccgcggg 180 cgggagcttg gacgtgctac gctgctctca tctcgtttcc gcgcaggaat tgttctcaat 240 ggcccgcgtg tatgttggca acttggattc acgggtgact tctgggggaac tcgaagatga gttccgcgtg tttggagttc tgcgaagtgt ttggattgca cgtaaaccac ctggctttgc 300 atttrttgat tttkacgaca ggagggatgc ggaggatgct attcgtgatc tagatggtaa 360 gaatggatgg agagttgaac tatctcgtaa ttccagtggt cgtggtggtc gtgatcggta 420 tggtggatct gagtcgamgt kctatgaatg tggtgag (2) INFORMATION FOR SEQ ID NO:1398: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..79 (D) OTHER INFORMATION: / Ceres Seq. ID 1597914 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398: Val Arg Leu Ser Phe Ser Pro Ser Tyr Arg Leu His Thr Ser Thr Gln 10 Leu Glu Ala Ser Leu Gln Ser Ala Leu Leu Leu Phe Arg Arg Leu Gln 30 25 20 His Arg Arg Arg Ser Cys Arg Gly Arg Glu Leu Gly Arg Ala Thr Leu 40 45 Leu Ser Ser Arg Phe Arg Ala Gly Ile Val Leu Asn Gly Pro Arg Val 55 60 Cys Trp Gln Leu Gly Phe Thr Gly Asp Phe Trp Gly Thr Arg Arg 70 (2) INFORMATION FOR SEQ ID NO:1399: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 152 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597915
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

Ser Val Ser Arg Ser Leu Leu Pro Ile Gly Ser Thr Pro Pro Arg Asn 10 5 Trp Lys Leu Arg Cys Asn Leu Pro Tyr Ser Ser Ser Ala Ala Ser Asn 25

Thr Ala Asp Ala Ala Ala Gly Gly Ser Leu Asp Val Leu Arg Cys

45 35 40 Ser His Leu Val Ser Ala Gln Glu Leu Phe Ser Met Ala Arg Val Tyr 55 60 Val Gly Asn Leu Asp Ser Arg Val Thr Ser Gly Glu Leu Glu Asp Glu 75 70 Phe Arg Val Phe Gly Val Leu Arg Ser Val Trp Ile Ala Arg Lys Pro 95 90 Pro Gly Phe Ala Phe Xaa Asp Phe Xaa Asp Arg Arg Asp Ala Glu Asp 110 105 Ala Ile Arg Asp Leu Asp Gly Lys Asn Gly Trp Arg Val Glu Leu Ser 125 120 115 Arg Asn Ser Ser Gly Arg Gly Gly Arg Asp Arg Tyr Gly Gly Ser Glu 135 140 Ser Xaa Xaa Tyr Glu Cys Gly Glu 150 (2) INFORMATION FOR SEQ ID NO:1400: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1597916 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400: Met Ala Arg Val Tyr Val Gly Asn Leu Asp Ser Arg Val Thr Ser Gly 15 10 Glu Leu Glu Asp Glu Phe Arg Val Phe Gly Val Leu Arg Ser Val Trp 25 20 Ile Ala Arg Lys Pro Pro Gly Phe Ala Phe Xaa Asp Phe Xaa Asp Arg 40 Arg Asp Ala Glu Asp Ala Ile Arg Asp Leu Asp Gly Lys Asn Gly Trp 60 55 Arg Val Glu Leu Ser Arg Asn Ser Ser Gly Arg Gly Gly Arg Asp Arg 75 70 Tyr Gly Gly Ser Glu Ser Xaa Xaa Tyr Glu Cys Gly Glu 85 (2) INFORMATION FOR SEQ ID NO:1401: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..280 (D) OTHER INFORMATION: / Ceres Seq. ID 1597917 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401: 60 aaaaacccta gcgtccaact catatacctg ctgctcgccc cgacgcgcat caactcccgc 120 egeogecect tecteteegt egetegeete gsgeetaege eaceaectet gecatggeee 180 cgaagaagga taaggccccg cgccgtcgtc caagccggcc aagtccggag cgggaagcag 240 aagaagaaga agtggagcaa gggtaagcaa aaggagaagg tcaacaacgc tgtgctcttc gtgcgcgcgt ggcgtgccag tcgcgtcgcg cgcgctggcg

(2) INFORMATION FOR SEQ ID NO:1402: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1597918 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402: Lys Asn Pro Ser Val Gln Leu Ile Tyr Leu Leu Leu Ala Pro Thr Arg 10 5 Ile Asn Ser Arg Arg Pro Phe Leu Ser Val Ala Arg Leu Xaa Pro 25 Thr Pro Pro Pro Leu Pro Trp Pro Arg Arg Ile Arg Pro Arg Ala 45 40 Val Val Gln Ala Gly Gln Val Arg Ser Gly Lys Gln Lys Lys Lys 55 Trp Ser Lys Gly Lys Gln Lys Glu Lys Val Asn Asn Ala Val Leu Phe 75 70 Val Arg Ala Trp Arg Ala Ser Arg Val Ala Arg Ala Gly 85 (2) INFORMATION FOR SEQ ID NO:1403: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 490 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..490 (D) OTHER INFORMATION: / Ceres Seq. ID 1597937 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403: acctegitee ceateegete aggecaatea acagaagtga egegageaeg ageacaeate 60 coctcocttc ttcggttatt cctcgccgcg tgccctcgcc gcagacctct gccatggcgg 120 accageteae egacgageag ategeggagt teaaggagge etteageete ttegataagg 180 240 atggcgacgg ctgcatcact accaaggagc ttggaacggt gatgcgctcc cttggccaga accctaccga ggcagagctg caggacatga tcaacgaggt cgatgcggat ggcaatggga 300 ccatcgactt cccgragttc ctgaacctga tggcgaggaa gatgaaggac acggactcag 360 aggaggaget caaggaggee tteegegtet tegacaagga ceagaaeggt tteatetegg 420 ctgccgagct ccgccatgtc atgaccaacc ttggcgagaa gctgactgac gaggaggtcg 480 acqagatgat (2) INFORMATION FOR SEQ ID NO:1404: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..162 (D) OTHER INFORMATION: / Ceres Seq. ID 1597938 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404: Leu Val Pro His Pro Leu Arg Pro Ile Asn Arg Ser Asp Ala Ser Thr 10 Ser Thr His Pro Leu Pro Ser Ser Val Ile Pro Arg Arg Val Pro Ser 25 20 Pro Gln Thr Ser Ala Met Ala Asp Gln Leu Thr Asp Glu Gln Ile Ala 40 Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys

5.5

Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn

- (2) INFORMATION FOR SEQ ID NO:1405:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597939
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

Met Ala Asp Gln Leu Thr Asp Glu Gln Ile Ala Glu Phe Lys Glu Ala 1 5 10 15

Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu

Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu

Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile

Asp Phe Pro Xaa Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr 65 70 75 80

Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp 85 90 95

Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn 100 105 110

Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met 115 120 125

- (2) INFORMATION FOR SEQ ID NO:1406:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597940
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met
1 5 10 15

Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Xaa 20 25 30

Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu
35 40 45

Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe

Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys 65 70 75 80

Leu Thr Asp Glu Glu Val Asp Glu Met

85
(2) INFORMATION FOR SEQ ID NO:1407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..483
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597941
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407: 60 caagaagaat gtgattgtgg ccattacctc tgataaggga ctctgtggtg gtattaattc 120 aacatcagtg aaagttagca gggcccttca caaattgaca tctggtccag aaaaagaaac 180 caagtatgtt atattaggag aaaagggcaa agttcagctg ttgcgtgact caaaggacag 240 cattgaaatg actgcaactg aactgcagaa gaaccctatc aactacacac aggttgccgt gctcgcggat gacatattga aaaatgtgga atatgatgct ctgagggtta ttttcaacaa 300 360 gttccaatct gtcatatcgt ttaagcccac aatggtaaca atactttccc ccgaggttgc 420 agaaaaagaa tcagaagctg gtgggaagat gggtgaccta gattcttatg agattgaagg 480 cggcgagaca aaatcagaga ttttgcagaa tctagctgag ttccagtttt cttgtgtctg tac
- (2) INFORMATION FOR SEQ ID NO:1408:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597942
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408: Lys Lys Asn Val Ile Val Ala Ile Thr Ser Asp Lys Gly Leu Cys Gly

1 5 10 15

Gly Ile Asn Ser Thr Ser Val Lys Val Ser Arg Ala Leu His Lys Leu
20 25 30

Thr Ser Gly Pro Glu Lys Glu Thr Lys Tyr Val Ile Leu Gly Glu Lys 35 40 45

Gly Lys Val Gln Leu Leu Arg Asp Ser Lys Asp Ser Ile Glu Met Thr 50 55 60

Ala Thr Glu Leu Gln Lys Asn Pro Ile Asn Tyr Thr Gln Val Ala Val 65 70 75 80

Leu Ala Asp Asp Ile Leu Lys Asn Val Glu Tyr Asp Ala Leu Arg Val
85 90 95

Ile Phe Asn Lys Phe Gln Ser Val Ile Ser Phe Lys Pro Thr Met Val

Thr Ile Leu Ser Pro Glu Val Ala Glu Lys Glu Ser Glu Ala Gly Gly 115 120 125

Lys Met Gly Asp Leu Asp Ser Tyr Glu Ile Glu Gly Glu Thr Lys 130 135 140

Ser Glu Ile Leu Gln Asn Leu Ala Glu Phe Gln Phe Ser Cys Val Cys 145 150 155 160

- (2) INFORMATION FOR SEQ ID NO:1409:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

Met Thr Ala Thr Glu Leu Gln Lys Asn Pro Ile Asn Tyr Thr Gln Val 5 Ala Val Leu Ala Asp Asp Ile Leu Lys Asn Val Glu Tyr Asp Ala Leu

30 25 20 Arg Val Ile Phe Asn Lys Phe Gln Ser Val Ile Ser Phe Lys Pro Thr

40 Met Val Thr Ile Leu Ser Pro Glu Val Ala Glu Lys Glu Ser Glu Ala

55 Gly Gly Lys Met Gly Asp Leu Asp Ser Tyr Glu Ile Glu Gly Gly Glu 75 70

Thr Lys Ser Glu Ile Leu Gln Asn Leu Ala Glu Phe Gln Phe Ser Cys 85

Val Cys

- (2) INFORMATION FOR SEQ ID NO:1410:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..444
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597958
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410: ctcgagcctg accettacge ettcgctcge geegeegeeg eegeegeege taegeeeege acctcgcttc atttcgtgtc gccaagatga cgaagcgcac taagaaggca ggaattgttg 120 gcaaatatgg aaccaggtat ggtgctagct tgcgtaasaa attcaagaag atggaggtat 180 ctcagcattc caagtacttt tgcgagttct gtgggaagtt tgctgtgaag aggaaagcag 240 ttggaatgct ttatcccttg ttttctggaa acttcgtaac catattttct ccaatgaaac 300 cgactacaac aatteecata ttteetette agaaattget gaateaaatg caaccageca 360 ggcgaatatt tattcaacaa tccaatattc agtggacaat gagccataag gttgatcata 420
- gatcccctct cagttatgga gtgg (2) INFORMATION FOR SEQ ID NO:1411:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597959
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 15 10 Arg Tyr Gly Ala Ser Leu Arg Xaa Lys Phe Lys Lys Met Glu Val Ser

25 20 Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Client Docket No. 80146.003 35 40 Arg Lys Ala Val Gly Met Leu Tyr Pro Leu Phe Ser Gly Asn Phe Val 55 Thr Ile Phe Ser Pro Met Lys Pro Thr Thr Thr Ile Pro Ile Phe Pro 75 Leu Gln Lys Leu Leu Asn Gln Met Gln Pro Ala Arg Arg Ile Phe Ile 90 Gln Gln Ser Asn Ile Gln Trp Thr Met Ser His Lys Val Asp His Arg 105 100 Ser Pro Leu Ser Tyr Gly Val 115 (2) INFORMATION FOR SEQ ID NO:1412: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..91 (D) OTHER INFORMATION: / Ceres Seq. ID 1597960 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412: Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys 10 Phe Ala Val Lys Arg Lys Ala Val Gly Met Leu Tyr Pro Leu Phe Ser 25 20 Gly Asn Phe Val Thr Ile Phe Ser Pro Met Lys Pro Thr Thr Ile 40 Pro Ile Phe Pro Leu Gln Lys Leu Leu Asn Gln Met Gln Pro Ala Arg 55 Arg Ile Phe Ile Gln Gln Ser Asn Ile Gln Trp Thr Met Ser His Lys 75 70 Val Asp His Arg Ser Pro Leu Ser Tyr Gly Val 85 (2) INFORMATION FOR SEQ ID NO:1413: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..66 (D) OTHER INFORMATION: / Ceres Seq. ID 1597961 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413: Met Leu Tyr Pro Leu Phe Ser Gly Asn Phe Val Thr Ile Phe Ser Pro 10 Met Lys Pro Thr Thr Ile Pro Ile Phe Pro Leu Gln Lys Leu Leu 25 20 Asn Gln Met Gln Pro Ala Arg Arg Ile Phe Ile Gln Gln Ser Asn Ile 40 Gln Trp Thr Met Ser His Lys Val Asp His Arg Ser Pro Leu Ser Tyr 50 Gly Val (2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..193 (D) OTHER INFORMATION: / Ceres Seq. ID 1597962 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414: accagacgcc ctctactaat ccagcccatt tcgaactctc tctagacgct tcctcggtct 60 120 ctctgttcac cgctgccccg taccgtactc ctcttcgcgc cgtagaaatg gcgctgccga 180 atcagcaggg cgtggattac cccagcttca agctcgtcat cgttggcgac ggtggaactg gtaaaaccac att (2) INFORMATION FOR SEQ ID NO:1415: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..63 (D) OTHER INFORMATION: / Ceres Seq. ID 1597963 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415: Gln Thr Pro Ser Thr Asn Pro Ala His Phe Glu Leu Ser Leu Asp Ala 10 Ser Ser Val Ser Leu Phe Thr Ala Ala Pro Tyr Arg Thr Pro Leu Arg 30 25 2.0 Ala Val Glu Met Ala Leu Pro Asn Gln Gln Gly Val Asp Tyr Pro Ser 40 Phe Lys Leu Val Ile Val Gly Asp Gly Gly Thr Gly Lys Thr Thr 55 (2) INFORMATION FOR SEQ ID NO:1416: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 285 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..285 (D) OTHER INFORMATION: / Ceres Seq. ID 1597964 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416: akatcagatc acaccacagc cgcggatana gaaggaaaaa tttccccaaa ccctagcttc 60 ggatetegat ggegaaceee egegtettet tegacatgae egteggeggt geeceageeg 120 geeggategt gatggagetg taegeeaaeg aggtgeeeaa kaeegeggag aactteegeg 180 cgctgtgcac gggcgagaag ggcgtgggca agtccgggaa gccgctccac tacaagggct 240 ctamcttcca ccgcgtcatc ccccagttca tgtgccaggg cggcg (2) INFORMATION FOR SEQ ID NO:1417: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids (B) TYPE: amino acid

 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597965
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

Client Docket No. 80146.003 Xaa Gln Ile Thr Pro Gln Pro Arg Ile Xaa Lys Glu Lys Phe Pro Gln 10 Thr Leu Ala Ser Asp Leu Asp Gly Glu Pro Pro Arg Leu Leu Arg His 25 Asp Arg Arg Cys Pro Ser Arg Pro Asp Arg Asp Gly Ala Val Arg 40 Gln Arg Gly Ala Gln Xaa Arg Gly Glu Leu Pro Arg Ala Val His Gly 60 55 Arg Glu Gly Arg Gly Gln Val Arg Glu Ala Ala Pro Leu Gln Gly Leu 75 70 Xaa Leu Pro Pro Arg His Pro Pro Val His Val Pro Gly Arg 85 (2) INFORMATION FOR SEQ ID NO:1418: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..72 (D) OTHER INFORMATION: / Ceres Seq. ID 1597966 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418: Met Ala Asn Pro Arg Val Phe Phe Asp Met Thr Val Gly Gly Ala Pro 10 Ala Gly Arg Ile Val Met Glu Leu Tyr Ala Asn Glu Val Pro Xaa Thr 25 20 Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys 40 Ser Gly Lys Pro Leu His Tyr Lys Gly Ser Xaa Phe His Arg Val Ile 55 Pro Gln Phe Met Cys Gln Gly Gly 70 (2) INFORMATION FOR SEQ ID NO:1419: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..63 (D) OTHER INFORMATION: / Ceres Seq. ID 1597967 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419: Met Thr Val Gly Gly Ala Pro Ala Gly Arg Ile Val Met Glu Leu Tyr 10 Ala Asn Glu Val Pro Xaa Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr 25 Gly Glu Lys Gly Val Gly Lys Ser Gly Lys Pro Leu His Tyr Lys Gly 40 Ser Xaa Phe His Arg Val Ile Pro Gln Phe Met Cys Gln Gly Gly 55 50 (2) INFORMATION FOR SEQ ID NO:1420: (i) SEQUENCE CHARACTERISTICS:

- - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..391
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597985
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

aactacggta actegtetge tegeatttee teccaateea tecegeetee aaaceegaac 60 tecaagtege eeegatega tggegeeaa ggeegagaag aageeegetg gegaagaage 120 eggeggagag ggageeeget geegagaagg egeeggeegg aagaageeaa aggegagaag 180 egtgteeaag eaggeaagg egeeggeegg aggkawatka kgggeeggaa gaagggeaag aagaggeegg aggkawatka kgggeeggaa gaaceeeggae ateggeatet eetetaagge eatgteeate atgaacteet teateaaega 300 eatettegag aagetegeeg eegaggeege e

- (2) INFORMATION FOR SEQ ID NO:1421:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597986
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

Asn Tyr Gly Asn Ser Ser Ala Arg Ile Ser Ser Gln Ser Ile Pro Pro 1 5 10 15

Pro Asn Pro Asn Ser Lys Ser Pro Arg Ile Asp Gly Ala Gln Gly Arg 20 25 30

Glu Glu Ala Arg Trp Arg Arg Ser Arg Arg Arg Arg Ser Pro Leu Pro
35 40 45

Arg Arg Arg Pro Glu Glu Ala Gln Gly Glu Lys Arg Val Pro Ala 50 55 60

Gly Lys Ser Ala Gly Lys Glu Gly Gly Glu Xaa Xaa Xaa Gly Pro Glu 65 70 75 80

Glu Gly Gln Glu Glu Arg Gly Asp Leu Gln Asp Leu His Leu Gln Gly 85 90 95
Ala Glu Ala Gly Ala Pro Gly His Arg His Leu Leu

- 100 105 (2) INFORMATION FOR SEQ ID NO:1422:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597987
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

Thr Thr Val Thr Arg Leu Leu Ala Phe Pro Pro Asn Pro Ser Arg Leu
1 5 10 15

Gln Thr Arg Thr Pro Ser Arg Pro Ala Ser Met Ala Pro Lys Ala Glu 20 25 30

Lys Lys Pro Ala Gly Glu Glu Ala Gly Gly Gly Gly Ala Arg Cys Arg

Glu Gly Ala Gly Arg Lys Lys Pro Lys Ala Arg Ser Val Ser Gln Gln 50 55 60

Ala Ser Pro Pro Ala Arg Arg Ala Ala Arg Xaa Xaa Xaa Gly Arg Lys
65 70 75 80

Lys Gly Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr Ile Phe Lys Val

90 85 Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Ser 110 105 100 Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Ala Glu 120 115 Ala Ala 130 (2) INFORMATION FOR SEQ ID NO:1423: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..104 (D) OTHER INFORMATION: / Ceres Seq. ID 1597988 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423: Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Gly Glu Glu Ala Gly Gly 10 5 Gly Gly Ala Arg Cys Arg Glu Gly Ala Gly Arg Lys Lys Pro Lys Ala 25 Arg Ser Val Ser Gln Gln Ala Ser Pro Pro Ala Arg Arg Ala Ala Arg 40 Xaa Xaa Xaa Gly Arg Lys Lys Gly Lys Lys Ser Val Glu Thr Tyr Lys 55 Ile Tyr Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile 75 Ser Ser Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe 90 85 Glu Lys Leu Ala Ala Glu Ala Ala 100 (2) INFORMATION FOR SEQ ID NO:1424: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 440 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..440 (D) OTHER INFORMATION: / Ceres Seq. ID 1598004 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424: actegageet gaccettacg cettegeteg ekcegeegee geegaegeeg etaegeeeeg 60 cacctcgctt catttcgtgt cgccaagatg acgaagcgca ctaagaaggc aggaattgtt 120 ggcaaatatg gaaccaggta tggtgctagc ttgcgtaasa aatccaagaa gatggaggta 180 tctcagcatt ccaagtactt ttgckagttc tgtgggaagt ttgctgtgaa gaggaaagca 240 gttggaattt gggggtgcaa ggactgtggg aaggtgaagg ctggtggtgc ttacaccatg 300 aacactgcta gtgcggtcac cgtcagagca cgatccgcca tggcccagcc cgctttcctc 360 tectetete agetecegee tetgeteege geegeegeee eegeegaace ategeeteea 420 qcctaqqcqg cggctaccac (2) INFORMATION FOR SEQ ID NO:1425: (i) SEQUENCE CHARACTERISTICS:

- - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598005
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:
- Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 1 5 10 15
- Arg Tyr Gly Ala Ser Leu Arg Xaa Lys Ser Lys Lys Met Glu Val Ser 20 25 30
- Gln His Ser Lys Tyr Phe Cys Xaa Phe Cys Gly Lys Phe Ala Val Lys 35 40 45
- Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys 50 55 60
- Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Val Arg 65 70 75 80
- Ala Arg Ser Ala Met Ala Gln Pro Ala Phe Leu Ser Ser Leu Gln Leu 85 90 95
- Pro Pro Leu Leu Arg Ala Ala Ala Pro Ala Glu Pro Ser Pro Pro Ala 100 105 110
- (2) INFORMATION FOR SEQ ID NO:1426:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598006
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:
- Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys 25 30
- Gly Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala
- Val Thr Val Arg Ala Arg Ser Ala Met Ala Gln Pro Ala Phe Leu Ser 50 60
- Ser Leu Gln Leu Pro Pro Leu Leu Arg Ala Ala Ala Pro Ala Glu Pro 65 70 75 80
- Ser Pro Pro Ala
- (2) INFORMATION FOR SEQ ID NO:1427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..476
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598007
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:
- atctcgcct cgctcaccta catctccgtc cgcaagcntc acgcaggctg ccccgggagg 60 ccgggaggaa gcagatcgga gaagccaagc cacggatttc cttctcgcct tctggacccc 120 atgtgatctg ttgtaatggc tcgattgtac atcggcaacc tggatcccg ggtgaccgct 180 cgggagctgg aggacgagtt ccgcacgttc ggggttcttc gcagtgtctg ggttgctcgg 240 aaaccacctg gctttgcgtt tattgatttt gatgataaga gggacgcaga ggatgcaatc 300

gkggacctag atggcaagaa tggatggaga gttgagttat ctcgtaatgc cagcggtggt 360 cgtggaggtc gtgaccggca tggtgggtct gagtccaagt gttacgagtg tggtgagact 420 ggccactttg ctcgtgagtg ccgtttgagg attggttctg gaggtctagg cagcgg

(2) INFORMATION FOR SEQ ID NO:1428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598008
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

Leu Ala Leu Ala His Leu His Leu Arg Pro Gln Xaa Ser Arg Arg Leu 1 5 10 15

Pro Arg Glu Ala Gly Arg Lys Gln Ile Gly Glu Ala Lys Pro Arg Ile 20 25 30

Ser Phe Ser Pro Ser Gly Pro His Val Ile Cys Cys Asn Gly Ser Ile 35 40 45

Val His Arg Gln Pro Gly Ser Pro Gly Asp Arg Ser Gly Ala Gly Gly

Arg Val Pro His Val Arg Gly Ser Ser Gln Cys Leu Gly Cys Ser Glu 65 70 75 80

Thr Thr Trp Leu Cys Val Tyr 85

- (2) INFORMATION FOR SEQ ID NO:1429:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

Met Ala Arg Leu Tyr Ile Gly Asn Leu Asp Pro Arg Val Thr Ala Arg 1 5 10 10 15 15 Glu Leu Glu Asp Glu Phe Arg Thr Phe Gly Val Leu Arg Ser Val Trp

20 25 30
Val Ala Arg Lys Pro Pro Gly Phe Ala Phe Ile Asp Phe Asp Lys

35 40 45 Arg Asp Ala Glu Asp Ala Ile Xaa Asp Leu Asp Gly Lys Asn Gly Trp

50 55 60

Arg Val Glu Leu Ser Arg Asn Ala Ser Gly Gly Arg Gly Gly Arg Asp
70 75 80

Arg His Gly Gly Ser Glu Ser Lys Cys Tyr Glu Cys Gly Glu Thr Gly 85 90 95

His Phe Ala Arg Glu Cys Arg Leu Arg Ile Gly Ser Gly Gly Leu Gly
100 105 110

Ser

- (2) INFORMATION FOR SEQ ID NO:1430:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- Page 831 (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..230 (D) OTHER INFORMATION: / Ceres Seq. ID 1598010 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430: 60 aacaaggage acteattgee tecceatete gtgtaggete tecceeteet eegegeteeg teegtetete ateaeegtte egeegeegee ceaeetetee eteetetege egeegeetee 120 gaaccegeca eggegeggeg gagatecaae eggaeggate tkgategaee taeteegaea 180 ccgctttccg aagatagata gatagataac aaggttgtgc tgtgcttgct (2) INFORMATION FOR SEQ ID NO:1431: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..67 (D) OTHER INFORMATION: / Ceres Seq. ID 1598011 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431: Thr Arg Ser Thr His Cys Leu Pro Ile Ser Cys Arg Leu Ser Pro Ser 10 5 Ser Ala Leu Arg Pro Ser Leu Ile Thr Val Pro Pro Pro Pro His Leu 30 25 Ser Leu Leu Ser Pro Pro Pro Pro Asn Pro Pro Arg Arg Gly Gly Asp 40 45 Pro Thr Gly Arg Ile Xaa Ile Asp Leu Leu Arg His Arg Phe Pro Lys 50 Ile Asp Arg (2) INFORMATION FOR SEQ ID NO:1432: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:
- - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598012
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

Gln Gly Ala Leu Ile Ala Ser Pro Ser Arg Val Gly Ser Pro Pro Pro 10 5

Pro Arg Ser Val Arg Leu Ser Ser Pro Phe Arg Arg Pro Thr Ser 30 25 2.0

Pro Ser Ser Arg Arg Arg Leu Arg Thr Arg His Gly Ala Ala Glu Ile 45 40

Gln Pro Asp Gly Ser Xaa Ser Thr Tyr Ser Asp Thr Ala Phe Arg Arg 55 50

- (2) INFORMATION FOR SEQ ID NO:1433:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..348
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598024
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

acacacaca cnvagcagag agattactac gatccaacag ttctagagca agagagagga 60 agacacaccg cagagttage aggctaataa cttgcaggag cagcaggaat ggyggcgacs 120 gtcstctctt gctttctcct cgccgtgctt ctggcaggag tggccgctgc mcgccttcga cgaagcggct gctgccggct tcgggcttgg ccacggcgg cgtttcnngn catggacgtg ctgccgctga gatgcccag ccggagcac aacctaaaac taagccgag ccccatatgc 300 agccactgcc ccagccagaa cctaaaccga aacctatgcc acatccag

- (2) INFORMATION FOR SEQ ID NO:1434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598025
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

Thr His Asn Xaa Ala Glu Arg Leu Leu Arg Ser Asn Ser Ser Arg Ala
1 10 15

Arg Glu Arg Lys Thr His Arg Arg Val Ser Arg Leu Ile Thr Cys Arg 20 25 30

Ser Ser Arg Asn Xaa Gly Asp Xaa Xaa Leu Leu Leu Ser Pro Arg Arg 35 40 45

Ala Ser Gly Arg Ser Gly Arg Cys Xaa Pro Ser Thr Lys Arg Leu Leu 50 55 60

Pro Ala Ser Gly Leu Ala Thr Ala Arg Val Xaa Xaa His Gly Arg Ala 65 70 75 80

Ala Ala Glu Met Pro Gln Pro Glu Pro Gln Pro Lys Thr Lys Pro Glu 85 90 95

Pro His Met Gln Pro Leu Pro Gln Pro Glu Pro Lys Pro Lys Pro Met

Pro His Pro 115

- (2) INFORMATION FOR SEQ ID NO:1435:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

Met Xaa Ala Xaa Val Xaa Ser Cys Phe Leu Leu Ala Val Leu Leu Ala 1 5 10 15

Gly Val Ala Ala Xaa Arg Leu Arg Arg Ser Gly Cys Cys Arg Leu Arg 20 25 30

Ala Trp Pro Arg Arg Ala Phe Xaa Xaa Met Asp Val Leu Pro Leu Arg 35 40 45

Cys Pro Ser Arg Ser His Asn Leu Lys Leu Ser Arg Ser Pro Ile Cys 50 55 60

Ser His Cys Pro Ser Gln Asn Leu Asn Arg Asn Leu Cys His Ile Gln 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:1436:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..486
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598040
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436: acctctcgct ccgttgctcg cctcgggtca aaccctaagc agggagttga tttatccgct 60 gcagccatga gtaagttgca gtctgagtct gtcaaggatg ccatctccca gattgttggg 120 gatgccaagg agaagaatag gaagttcact gagactgtgg aacttcagat tggtctgaag 180 aattatgatc cacagaagga caagcgtttc agtggctctg ttaagttgcc ccatatccct 240 cgtcccaaga tgaaggtgtg catgcttggt gatgcccagc atgttgagga ggccgagaag 300 atgggacttg actacatgga tgttgaggct ctcaagaaaa tgaacaagaa caagaagctt 360 420 gttaagaggc ttgccaagaa gtaccatgct ttcttggcat cagaggccat catcaagcag 480 attccccgtc tccttggtcc tggtctcaac aaggcaggca agttcccgac cctggttact caccaq
- (2) INFORMATION FOR SEQ ID NO:1437:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598041
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:
- Thr Ser Arg Ser Val Ala Arg Leu Gly Ser Asn Pro Lys Gln Gly Val 10
- Asp Leu Ser Ala Ala Ala Met Ser Lys Leu Gln Ser Glu Ser Val Lys 25 20
- Asp Ala Ile Ser Gln Ile Val Gly Asp Ala Lys Glu Lys Asn Arg Lys 40
- Phe Thr Glu Thr Val Glu Leu Gln Ile Gly Leu Lys Asn Tyr Asp Pro 55
- Gln Lys Asp Lys Arg Phe Ser Gly Ser Val Lys Leu Pro His Ile Pro 75 70
- Arg Pro Lys Met Lys Val Cys Met Leu Gly Asp Ala Gln His Val Glu 90
- Glu Ala Glu Lys Met Gly Leu Asp Tyr Met Asp Val Glu Ala Leu Lys 105
- Lys Met Asn Lys Asn Lys Lys Leu Val Lys Arg Leu Ala Lys Lys Tyr 120 His Ala Phe Leu Ala Ser Glu Ala Ile Ile Lys Gln Ile Pro Arg Leu
- 140 135 Leu Gly Pro Gly Leu Asn Lys Ala Gly Lys Phe Pro Thr Leu Val Thr 155
- His Gln
- (2) INFORMATION FOR SEQ ID NO:1438:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598042
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:
- Met Ser Lys Leu Gln Ser Glu Ser Val Lys Asp Ala Ile Ser Gln Ile 1 5 10 15
- Val Gly Asp Ala Lys Glu Lys Asn Arg Lys Phe Thr Glu Thr Val Glu 20 25 30
- Leu Gln Ile Gly Leu Lys Asn Tyr Asp Pro Gln Lys Asp Lys Arg Phe 35 40 45
- Ser Gly Ser Val Lys Leu Pro His Ile Pro Arg Pro Lys Met Lys Val 50 55 60
- Cys Met Leu Gly Asp Ala Gln His Val Glu Glu Ala Glu Lys Met Gly 65 70 75 80
- Leu Asp Tyr Met Asp Val Glu Ala Leu Lys Lys Met Asn Lys Asn Lys 85 90 95
- Lys Leu Val Lys Arg Leu Ala Lys Lys Tyr His Ala Phe Leu Ala Ser 100 105 110
- Glu Ala Ile Ile Lys Gln Ile Pro Arg Leu Leu Gly Pro Gly Leu Asn 115 120 125
- Lys Ala Gly Lys Phe Pro Thr Leu Val Thr His Gln 130 135 140
- (2) INFORMATION FOR SEQ ID NO:1439:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..439
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598043
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

acttccctc cgatcctcgt cgccgacgca tccacccgaa ccctcctccg cgacctcgcc 60 gtcgccgcag ccttggccat gtcgatcttc gagtataatg ggtccgccgt ggtggcgatg 120 gtggggaaga actgttcgc gatcgccagc gaccggcggc tgggcgtgca gcttcagacc 180 atcgcgacag acttccageg ggtgttcaag gtccaccgaca agctttacat cggcctctct gggctcgcca ctgacgcca gacgctgtac cagcggttgg tgttcaggca caagctgtat cagctgcggg aggagangga catnaagccc gagacctttg ccagccttgt ctctgcgctc 360 ctctacgaga agagattcgg gccatatttc tgccagccag tcattgctgg acttggagat 420 gacaacgtac catttattt

- (2) INFORMATION FOR SEQ ID NO:1440:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598044
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

Thr Ser Pro Pro Ile Leu Val Ala Asp Ala Ser Thr Arg Thr Leu Leu 1 5 5 5 8 10 10 5 15 4 15 Arg Asp Leu Ala Val Ala Ala Ala Leu Ala Met Ser Ile Phe Glu Tyr

25 2.0 Asn Gly Ser Ala Val Val Ala Met Val Gly Lys Asn Cys Phe Ala Ile 40 Ala Ser Asp Arg Arg Leu Gly Val Gln Leu Gln Thr Ile Ala Thr Asp 55 Phe Gln Arg Val Phe Lys Val His Asp Lys Leu Tyr Ile Gly Leu Ser 75 70 Gly Leu Ala Thr Asp Ala Gln Thr Leu Tyr Gln Arg Leu Val Phe Arg 90 His Lys Leu Tyr Gln Leu Arg Glu Glu Xaa Asp Xaa Lys Pro Glu Thr 100 105 110 Phe Ala Ser Leu Val Ser Ala Leu Leu Tyr Glu Lys Arg Phe Gly Pro 115 120 Tyr Phe Cys Gln Pro Val Ile Ala Gly Leu Gly Asp Asp Asn Val Pro 135 Phe Ile 145 (2) INFORMATION FOR SEQ ID NO:1441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..146 (D) OTHER INFORMATION: / Ceres Seq. ID 1598045 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441: Leu Pro Leu Arg Ser Ser Ser Pro Thr His Pro Pro Glu Pro Ser Ser 10 Ala Thr Ser Pro Ser Pro Gln Pro Trp Pro Cys Arg Ser Ser Ser Ile 25 2.0 Met Gly Pro Pro Trp Trp Arg Trp Trp Gly Arg Thr Val Ser Arg Ser 40 Pro Ala Thr Gly Gly Trp Ala Cys Ser Phe Arg Pro Ser Arg Gln Thr 55 Ser Ser Gly Cys Ser Arg Ser Thr Thr Ser Phe Thr Ser Ala Ser Leu 75 70 Gly Ser Pro Leu Thr Pro Arg Arg Cys Thr Ser Gly Trp Cys Ser Gly 90 85 Thr Ser Cys Ile Ser Cys Gly Arg Arg Xaa Thr Xaa Ser Pro Arg Pro 105 100 Leu Pro Ala Leu Ser Leu Arg Ser Ser Thr Arg Arg Asp Ser Gly His 115 120 125 Ile Ser Ala Ser Gln Ser Leu Leu Asp Leu Glu Met Thr Thr Tyr His 135 Leu Phe 145 (2) INFORMATION FOR SEQ ID NO:1442: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598046
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

```
Met Ser Ile Phe Glu Tyr Asn Gly Ser Ala Val Val Ala Met Val Gly
                                   10
Lys Asn Cys Phe Ala Ile Ala Ser Asp Arg Arg Leu Gly Val Gln Leu
                               25
           20
Gln Thr Ile Ala Thr Asp Phe Gln Arg Val Phe Lys Val His Asp Lys
                           40
Leu Tyr Ile Gly Leu Ser Gly Leu Ala Thr Asp Ala Gln Thr Leu Tyr
                       55
Gln Arg Leu Val Phe Arg His Lys Leu Tyr Gln Leu Arg Glu Glu Xaa
                                       75
                   70
Asp Xaa Lys Pro Glu Thr Phe Ala Ser Leu Val Ser Ala Leu Leu Tyr
                                   90
               8.5
Glu Lys Arg Phe Gly Pro Tyr Phe Cys Gln Pro Val Ile Ala Gly Leu
                    105
           100
Gly Asp Asp Asn Val Pro Phe Ile
                          120
        115
(2) INFORMATION FOR SEQ ID NO:1443:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..437
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598047
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443: aaaatcctca gatccgccc ctcctccacc cttgckccgc gctttcacag ctctcccgcc 60 teeggateca gateegeege caccaaegee tgeteeteee ceteetgetg caccaccaee 120 atcaagaggt ccagcagggc ggcacggcas sncggcggcg gcgacatggg gcgtgacggc 180 ggtggcggtg tcgcggcggc atgtctgact cggtgctccg gaaggtgctc ctctcctact 240 tetacgtggc ggtgtggatc ttectetet tetecgteat egtetacaac aagtacatee 300 tegacecaaa gatgtacaae tggceettee ceateteget caccatggta cacatgggtt 360 tetgeteate cetegeegte gegetegtee gegteeteeg ggtegtegae teeccacate 420 gccctccatg acgccgc
- (2) INFORMATION FOR SEQ ID NO:1444:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..145
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598048
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444: Lys Ile Leu Arg Ser Ala Pro Ser Ser Thr Leu Xaa Pro Arg Phe His 10 Ser Ser Pro Ala Ser Gly Ser Arg Ser Ala Ala Thr Asn Ala Cys Ser 25 20 Ser Pro Ser Cys Cys Thr Thr Thr Ile Lys Arg Ser Ser Arg Ala Ala 40 Arg Xaa Xaa Gly Gly Gly Asp Met Gly Arg Asp Gly Gly Gly Val 55 Ala Ala Ala Cys Leu Thr Arg Cys Ser Gly Arg Cys Ser Ser Pro Thr 75 70 Ser Thr Trp Arg Cys Gly Ser Ser Ser Pro Ser Pro Ser Ser Ser Thr 90 85

Thr Ser Thr Ser Ser Thr Gln Arg Cys Thr Thr Gly Pro Ser Pro Ser

105 100 Arg Ser Pro Trp Tyr Thr Trp Val Ser Ala His Pro Ser Pro Ser Arg 115 120 125 Ser Ser Ala Ser Ser Gly Ser Ser Thr Pro His Ile Ala Leu His Asp 135 Ala 145 (2) INFORMATION FOR SEQ ID NO:1445: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 90 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..90 (D) OTHER INFORMATION: / Ceres Seq. ID 1598049 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445: Met Gly Arg Asp Gly Gly Gly Val Ala Ala Ala Cys Leu Thr Arg 10 Cys Ser Gly Arg Cys Ser Ser Pro Thr Ser Thr Trp Arg Cys Gly Ser 25 Ser Ser Pro Ser Pro Ser Ser Ser Thr Thr Ser Thr Ser Ser Thr Gln 40 Arg Cys Thr Thr Gly Pro Ser Pro Ser Arg Ser Pro Trp Tyr Thr Trp 55 60 Val Ser Ala His Pro Ser Pro Ser Arg Ser Ser Ala Ser Ser Gly Ser 70 75 Ser Thr Pro His Ile Ala Leu His Asp Ala 85 (2) INFORMATION FOR SEQ ID NO:1446: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..76 (D) OTHER INFORMATION: / Ceres Seq. ID 1598050 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446: Met Ser Asp Ser Val Leu Arg Lys Val Leu Leu Ser Tyr Phe Tyr Val 10 Ala Val Trp Ile Phe Leu Ser Phe Ser Val Ile Val Tyr Asn Lys Tyr 25 Ile Leu Asp Pro Lys Met Tyr Asn Trp Pro Phe Pro Ile Ser Leu Thr 4.5 40 35 Met Val His Met Gly Phe Cys Ser Ser Leu Ala Val Ala Leu Val Arg 60 55 Val Leu Arg Val Val Asp Ser Pro His Arg Pro Pro 70 (2) INFORMATION FOR SEQ ID NO:1447: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 468 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598051
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447: cacaccgcaa tetteaatet eeccagcaat eectagcaga ageetteeat eetcaetege 60 tcgatggccc gcacgaagca gacggcgagg aagtccaccg gcggcaaggc gccgaggaag 120 cagetggega ctaaggegge eegeaagtet geeeetgega eeggetgagt gaagaageee 180 caccgcttcc gccccggcac cgtcgcgctc cgggagatcc gcaagtacca gaagagcacg 240 gagetgetga teegeaaget geegtteeag egeetggtge gggagatege geaggaette 300 aagaccgacc tacgetteca gagetetget gteteegege tgeaggagge ggetgaggee 360 taccttgtcg ggctcttcta ggacaccaac ctctgcgcca tccacgccaa gcgcgtcacc 420 atcatgecca aggacateca gettgecege egeateegeg ggagaggg
- (2) INFORMATION FOR SEQ ID NO:1448:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598052
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

Thr Pro Gln Ser Ser Ile Ser Pro Ala Ile Pro Ser Arg Ser Leu Pro 1 5 10 15

Ser Ser Leu Ala Arg Trp Pro Ala Arg Ser Arg Arg Arg Gly Ser Pro 20 25 30

Pro Ala Ala Arg Arg Gly Ser Ser Trp Arg Leu Arg Arg Pro Ala 35 40 45

Ser Leu Pro Leu Arg Pro Ala Glu 50 55

- (2) INFORMATION FOR SEQ ID NO:1449:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..43
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598053
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

His Arg Asn Leu Gln Ser Pro Gln Gln Ser Leu Ala Glu Ala Phe His

Pro His Ser Leu Asp Gly Pro His Glu Ala Asp Gly Glu Glu Val His 20 25 30

Arg Arg Gln Gly Ala Glu Glu Ala Ala Gly Asp 35 40

- (2) INFORMATION FOR SEQ ID NO:1450:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..34
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450: Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala 15 10 5 Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Ala 25 Thr Gly (2) INFORMATION FOR SEQ ID NO:1451: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..325 (D) OTHER INFORMATION: / Ceres Seq. ID 1598059 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451: tytegateeg gaaacetete aaaceetage egyhteetge aagttteaga geteaggaat 60 ctgcgccatg gcgagtgaga cggagacctt cgcatttcag gctgagatca accagctgct 120 180 ctcactcatc atcaacacct tctactccaa caaggagatc ttcctccgcg agcttatctc caactettee gatgegetgg acaagateea ggttegagag teteaetgae aagageaage 240 tcgatgcgcm sctgagcttt tcatccacct tgtcccagac aaggccaccg aacacgctct 300 ccatcatcga cagcggmwtc ggcat (2) INFORMATION FOR SEQ ID NO:1452: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..75 (D) OTHER INFORMATION: / Ceres Seq. ID 1598060 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452: Xaa Asp Pro Glu Thr Ser Gln Thr Leu Ala Xaa Ser Cys Lys Phe Gln 10 5 Ser Ser Gly Ile Cys Ala Met Ala Ser Glu Thr Glu Thr Phe Ala Phe 2.5 20 Gln Ala Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr 40 Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp 55 Ala Leu Asp Lys Ile Gln Val Arg Glu Ser His 70 (2) INFORMATION FOR SEQ ID NO:1453: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453: Met Ala Ser Glu Thr Glu Thr Phe Ala Phe Gln Ala Glu Ile Asn Gln 1 10 15

(D) OTHER INFORMATION: / Ceres Seq. ID 1598061

(B) LOCATION: 1..53

Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe 25 Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Gln 35 40 Val Arg Glu Ser His 50 (2) INFORMATION FOR SEQ ID NO:1454: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..44 (D) OTHER INFORMATION: / Ceres Seq. ID 1598062 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454: Met Arg Trp Thr Arg Ser Arg Phe Glu Ser Leu Thr Asp Lys Ser Lys 10 Leu Asp Ala Xaa Leu Ser Phe Ser Ser Thr Leu Ser Gln Thr Arg Pro 25 20 Pro Asn Thr Leu Ser Ile Ile Asp Ser Xaa Xaa Gly 40 35 (2) INFORMATION FOR SEQ ID NO:1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..225 (D) OTHER INFORMATION: / Ceres Seq. ID 1598063 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455: 60 gtcgagtcta accctagege gegeegecae acctgeegtt getaeegeee egtaeetege ttgctttccc gtcgccgaaa tgacgaagcg caccaagaag gctggaattg ttggcaaata 120 tggaaccagg tatggcgcta cttgcgtaas aaattcaaga agatggaggt atctcagcac 180 tccaagtact tctgcgagtt ttgtgggaag tttgctgtga agagg (2) INFORMATION FOR SEQ ID NO:1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..75 (D) OTHER INFORMATION: / Ceres Seq. ID 1598064 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456: Val Glu Ser Asn Pro Ser Ala Arg Arg His Thr Cys Arg Cys Tyr Arg 10 Pro Val Pro Arg Leu Leu Ser Arg Arg Arg Asn Asp Glu Ala His Gln 25 Glu Gly Trp Asn Cys Trp Gln Ile Trp Asn Gln Val Trp Arg Tyr Leu 45 40 Arg Xaa Lys Phe Lys Lys Met Glu Val Ser Gln His Ser Lys Tyr Phe 50 55

Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Arg

70 75 65 (2) INFORMATION FOR SEQ ID NO:1457: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..72 (D) OTHER INFORMATION: / Ceres Seq. ID 1598065 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457: Ser Ser Leu Thr Leu Ala Arg Ala Ala Thr Pro Ala Val Ala Thr Ala 10 Pro Tyr Leu Ala Cys Phe Pro Val Ala Glu Met Thr Lys Arg Thr Lys 25 Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr Gly Ala Thr Cys 45 40 Val Xaa Asn Ser Arg Arg Trp Arg Tyr Leu Ser Thr Pro Ser Thr Ser 55 Ala Ser Phe Val Gly Ser Leu Leu 70 (2) INFORMATION FOR SEQ ID NO:1458: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..46 (D) OTHER INFORMATION: / Ceres Seq. ID 1598066 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458: Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 10 Arg Tyr Gly Ala Thr Cys Val Xaa Asn Ser Arg Arg Trp Arg Tyr Leu 25 20 Ser Thr Pro Ser Thr Ser Ala Ser Phe Val Gly Ser Leu Leu 40 35 (2) INFORMATION FOR SEQ ID NO:1459: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..305 (D) OTHER INFORMATION: / Ceres Seq. ID 1598071 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459: ctacgcggtr cgacacagcc aaaccatect ceteteegee geeegeegea geageaceea ccggcaagat gaagacgatc ctggcgtcgg agaattggac atcccggagc gtcacggtca 120 cggtggccgc caagctggtc acggtggagg gcccccgcgg caakctcacc cgcaacttca 180 agcacctcaa cctcgacttc canctgcagg aggccggccg caagctcaag gtggacgcct 240 ggttcggcac ccgccgcacc atggccgcca tccgcaccgc catctcccac gtccagaacc (2) INFORMATION FOR SEQ ID NO:1460: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598072
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

Tyr Ala Xaa Arg His Ser Gln Thr Ile Leu Leu Ser Ala Ala Arg Arg 1 5 10 15

Ser Ser Thr His Arg Gln Asp Glu Asp Asp Pro Gly Val Gly Glu Leu 20 25 30

Asp Ile Pro Glu Arg His Gly His Gly Gly Arg Gln Ala Gly His Gly 35 40 45

Gly Gly Pro Pro Arg Gln Xaa His Pro Gln Leu Gln Ala Pro Gln Pro 50 55 60

Arg Leu Pro Xaa Ala Gly Gly Arg Pro Gln Ala Gln Gly Gly Arg Leu 65 70 75 80

Val Arg His Pro Pro His His Gly Arg His Pro His Arg His Leu Pro

Arg Pro Glu Pro His

- (2) INFORMATION FOR SEQ ID NO:1461:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598073
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

Thr Arg Xaa Asp Thr Ala Lys Pro Ser Ser Ser Pro Pro Pro Ala Ala 1 5 10 15

Ala Ala Pro Thr Gly Lys Met Lys Thr Ile Leu Ala Ser Glu Asn Trp

Thr Ser Arg Ser Val Thr Val Thr Val Ala Ala Lys Leu Val Thr Val
35 40 45

Glu Gly Pro Arg Gly Xaa Leu Thr Arg Asn Phe Lys His Leu Asn Leu 50 55 60

Asp Phe Xaa Leu Gln Glu Ala Gly Arg Lys Leu Lys Val Asp Ala Trp 65 70 75 80

Phe Gly Thr Arg Arg Thr Met Ala Ala Ile Arg Thr Ala Ile Ser His 85 90 95

Val Gln Asn Leu Ile

100

- (2) INFORMATION FOR SEQ ID NO:1462:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598074

Client Docket No. 00140.003	
TO TO NO. 1460	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462: Met Lys Thr Ile Leu Ala Ser Glu Asn Trp Thr Ser Arg Ser Val Thr 5 10 15	
Val Thr Val Ala Ala Lys Leu Val Thr Val Glu Gly Pro Arg Gly Xaa 20 25 30	
Leu Thr Arg Asn Phe Lys His Leu Asn Leu Asp Phe Xaa Leu Gln Glu 35 40 45	
Ala Gly Arg Lys Leu Lys Val Asp Ala Trp Phe Gly Thr Arg Arg Thr 50 55 60	
Met Ala Ala Ile Arg Thr Ala Ile Ser His Val Gln Asn Leu Ile 70 75	
(2) INFORMATION FOR SEQ ID NO:1463:(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 331 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE:</pre>	
(A) NAME/KEY: -	
(B) LOCATION: 1331	
(D) OTHER INFORMATION: / Ceres Seq. ID 1598092	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463: attatcacgg cggcggtggc ggasggaagg cgaaggagta gcagcagcag gcgrcgcgat	60
gtagoggoto cocacetega gettrecace atggetagag gattgaagaa geatttgaag	120
aggeteaatg egeceaagea ttggatgetg gaeaagettg geggastttt geteecaage	180 240
Carer elle accedada cecaqqqaic accegoodoc gacoocodos accesos	300
tgttgatggc aaggtcagga cagacaagac c	
(2) INFORMATION FOR SEQ ID NO:1464:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 73 amino acids	
(B) TYPE: amino acid (C) STRANDEDNESS:	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(ix) FEATURE:	
(A) NAME/KEY: peptide (B) LOCATION: 173	
(D) OTHER INFORMATION: / Ceres Seq. ID 1598093	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:	
Ile Ile Thr Ala Ala Val Ala Xaa Gly Arg Arg Arg Ser Ser Ser 1 5 10 15	
Arg Xaa Arg Asp Val Ala Ala Pro His Leu Glu Leu Xaa Thr Met Ala	
20 25 30	
Arg Gly Leu Lys Lys His Leu Lys Arg Leu Asn Ala Pro Lys His Trp 35 40 45	
Met Leu Asp Lys Leu Gly Gly Xaa Leu Leu Pro Ser His Leu Leu Asp 50 55 60	
Leu Thr Ser Leu Gly Xaa Xaa Cys His 65 70	
(2) INFORMATION FOR SEQ ID NO:1465:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 43 amino acids	
(B) TYPE: amino acid (C) STRANDEDNESS:	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(ix) FEATURE: (A) NAME/KEY: peptide	
(A) NAME,/NETT DEDLICE	

(A) NAME/KEY: peptide (B) LOCATION: 1..43

120 180

240

300

360

420

(D) OTHER INFORMATION: / Ceres Seq. ID 1598094 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465: Met Ala Arg Gly Leu Lys Lys His Leu Lys Arg Leu Asn Ala Pro Lys 10 5 His Trp Met Leu Asp Lys Leu Gly Gly Xaa Leu Leu Pro Ser His Leu 25 20 Leu Asp Leu Thr Ser Leu Gly Xaa Xaa Cys His 40 (2) INFORMATION FOR SEQ ID NO:1466: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 423 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..423 (D) OTHER INFORMATION: / Ceres Seq. ID 1598108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466: gtetecgece tagegecact gagecactea acgtegagat egagaegace egagteegee gegecegtge accaeegace gtegaactee egaaagtaac tetattett gateaacate aacatgtcgc gggaggataa tgtttacatg gccaagctgg ctgagcaagc agaacgatac gaggaaatgg ttgagtacat ggagaaggtg gctaagactg tagatgtgga agagctcacc gttgaggagc ggaacctctt atctgttgcc tacaagaacg taattggggc ccgccgtgcc tcatggcgca ttatctcctc catcgagcat aaggaggagt cccgtaagaa tgaggaacat gttattcaga tcaaggagta ccgtggcaag attgaggctg aattgagcaa catttgtgat ggt (2) INFORMATION FOR SEQ ID NO:1467: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..100 (D) OTHER INFORMATION: / Ceres Seq. ID 1598109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467: Met Ser Arg Glu Asp Asn Val Tyr Met Ala Lys Leu Ala Glu Gln Ala 10 Glu Arg Tyr Glu Glu Met Val Glu Tyr Met Glu Lys Val Ala Lys Thr 25 20 Val Asp Val Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val 40 Ala Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile 60 55 Ser Ser Ile Glu His Lys Glu Glu Ser Arg Lys Asn Glu Glu His Val 75 70 Ile Gln Ile Lys Glu Tyr Arg Gly Lys Ile Glu Ala Glu Leu Ser Asn 90 Ile Cys Asp Gly 100 (2) INFORMATION FOR SEQ ID NO:1468: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..92 (D) OTHER INFORMATION: / Ceres Seq. ID 1598110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Glu 10 5 Tyr Met Glu Lys Val Ala Lys Thr Val Asp Val Glu Glu Leu Thr Val 25 Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala 45 40 Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu His Lys Glu Glu 55 Ser Arg Lys Asn Glu Glu His Val Ile Gln Ile Lys Glu Tyr Arg Gly 75 70 Lys Ile Glu Ala Glu Leu Ser Asn Ile Cys Asp Gly 85 (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..79 (D) OTHER INFORMATION: / Ceres Seq. ID 1598111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469: Met Val Glu Tyr Met Glu Lys Val Ala Lys Thr Val Asp Val Glu Glu 5 10 Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val 25 20 Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu His 40 Lys Glu Glu Ser Arg Lys Asn Glu Glu His Val Ile Gln Ile Lys Glu 55 Tyr Arg Gly Lys Ile Glu Ala Glu Leu Ser Asn Ile Cys Asp Gly 70 (2) INFORMATION FOR SEQ ID NO:1470: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 414 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..414 (D) OTHER INFORMATION: / Ceres Seq. ID 1598115
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

 attettecce cteeggegee geteceecag acacttegee geeggeaaga tgggeegegt
 gattegeget cagsaagggt geggggteeg tgtteaagte ccataccat cacegeaagg
 cectgeegtt ceggteecte gactteggeg agegeaacgg gtacetgaag ggegtggtea
 cegaegteat ceaegaeceg ggeegeggeg egeegettgg ceaaggteae etteegeeat
 ceatteeggt acaageacea gaaggagetg ttegtggetg etgagggeat gtacaetgge
 cagttegttt actgeggaeg eegttgetae acteteeatt ggeaaegtee tgeegeteag
 ggggateetg tagggtgeeg ttgtetgeaa egtttgagea ecaegteggg rate
 - (2) INFORMATION FOR SEQ ID NO:1471:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598116
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:
- Phe Phe Pro Leu Arg Arg Arg Ser Pro Arg His Phe Ala Ala Gly Lys
 1 5 10 15
- Met Gly Arg Val Ile Arg Ala Gl
n Xaa Gly Cys Gly Val Arg Val Gl
n 20 25 30
- Val Pro Tyr Pro Ser Pro Gln Gly Pro Ala Val Pro Val Pro Arg Leu 35 40 45
- Arg Arg Ala Gln Arg Val Pro Glu Gly Arg Gly His Arg Arg His Pro 50 55 60
- Arg Pro Gly Pro Arg Arg Ala Ala Trp Pro Arg Ser Pro Ser Ala Ile 65 70 75 80
- His Ser Gly Thr Ser Thr Arg Arg Ser Cys Ser Trp Leu Leu Arg Ala 85 90 95
- Cys Thr Leu Ala Ser Ser Phe Thr Ala Asp Ala Val Ala Thr Leu Ser 100 105 110
- Ile Gly Asn Val Leu Pro Leu Arg Gly Ile Leu 115 120
- (2) INFORMATION FOR SEQ ID NO:1472:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598117
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:
- Met Gly Arg Val Ile Arg Ala Gln Xaa Gly Cys Gly Val Arg Val Gln 1 5 10 $\frac{15}{1}$
- Val Pro Tyr Pro Ser Pro Gln Gly Pro Ala Val Pro Val Pro Arg Leu 20 25 30
- Arg Arg Ala Gln Arg Val Pro Glu Gly Arg Gly His Arg Arg His Pro
 35 40 45
- Arg Pro Gly Pro Arg Arg Ala Ala Trp Pro Arg Ser Pro Ser Ala Ile 50 55 60
- His Ser Gly Thr Ser Thr Arg Arg Ser Cys Ser Trp Leu Leu Arg Ala 65 70 75 80
- Cys Thr Leu Ala Ser Ser Phe Thr Ala Asp Ala Val Ala Thr Leu Ser 85 90 95
- Ile Gly Asn Val Leu Pro Leu Arg Gly Ile Leu 100 105
- (2) INFORMATION FOR SEQ ID NO:1473:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..465

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acco gtac agaa tccc gctg ctcc camo	(D) OTHER INFORMATION: / Ceres Seq. ID 1598124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473: attegteece ggeegeeges cteccagtet ceaegegaa sagegeeteg caaegeteyd acceaatgge gnngacgteg aagetgtega tgggcateaa gekegegtns gategeaege gtaceaeege egtggetetg ggeeateaaag geaagaaegg mggegtette eccaaggeeg agaagaeege egeegeegeg gaaeceaagt tetaeeeege egaegaegte aageetegek 240 teccageaee egeagegta wteccaceaa geteaggteg ageateaege etgggaeggt 300 getgateete eteggeggg getteatggg gaagakagtg gtgtteetea ageageteaa eteeggeetg eteetegtet etggteeatt eaagateaat ggagtaeega teegtegtg cameagaeet atgteattge tacateaaee aaggttgaea teete (2) INFORMATION FOR SEQ ID NO:1474: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1155																
											7. II	159	9812	5			
Ile 1	(xi) Arg	SE(Pro	OUENC Arg	E DE Pro 5	Pro	Xaa	Ser	Gln	Ser 10	Pro	Arg	Gly	Xaa	Ala 15	Pro		
Arg	Asn	Ala	Xaa 20		Gln	Trp	Xaa	Xaa 25		Arg	Ser	Cys	Arg 30	Trp	Ala		
Ser	Ser	Xaa 35		Xaa	Ile	Ala	Arg 40	Val	Pro	Pro	Pro	Trp 45	Leu	Trp	Ala		
Ile	Lys 50	Ala	Arg	Thr	Xaa	Ala 55	Ser	Ser	Pro	Arg	Pro 60	Arg	Ser	Pro	Pro		
Pro 65	Pro	Arg	Asn	Pro	Ser 70	Ser	Thr	Pro	Pro	Thr 75	Thr	Ser	Ser	Leu	Xaa 80		
Ser	Gln	His	Pro	Gln 85	Xaa	Xaa	Ser	His	Gln 90	Ala	Gln	Val	Glu	His 95	His		
Ala	Trp	Asp	Gly 100		Asp	Pro	Pro	Arg 105	Gly	Ala	Leu	His	Gly 110	Glu	Xaa		
Ser	Gly	Val 115	Pro	Gln	Ala	Ala	Gln 120	Leu	Arg	Pro	Ala	Pro 125	Arg	Leu	Trp		
Ser	Ile 130		Asp	Gln	Trp	Ser 135		Asp	Pro	Ser	Cys 140	Xaa	Gln	Thr	Tyr		
Val 145	Ile	Ala	Thr	Ser	Thr 150	Lys	Val		Ile	Ser 155							

- (2) INFORMATION FOR SEQ ID NO:1475:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598126
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475: Phe Val Pro Gly Arg Arg Xaa Pro Ser Leu His Ala Glu Xaa Arg Leu 10 Ala Thr Leu Xaa Pro Asn Gly Xaa Asp Val Glu Ala Val Asp Gly His 25 Gln Xaa Arg Xaa Xaa Ser His Ala Tyr His Arg Arg Gly Ser Gly Pro 40 Ser Arg Gln Glu Arg Xaa Arg Leu Pro Gln Gly Arg Glu Ala Arg Arg

(2) INFORMATION FOR SEQ ID NO:1478:

60 50 Arg Arg Gly Thr Gln Val Leu Pro Arg Arg Arg Gln Ala Ser Xaa 75 70 Pro Ser Thr Arg Lys Xaa Xaa Pro Thr Lys Leu Arg Ser Ser Ile Thr 90 8.5 Pro Gly Thr Val Leu Ile Leu Leu Ala Gly Arg Phe Met Gly Lys Xaa 110 105 100 Val Val Phe Leu Lys Gln Leu Asn Ser Gly Leu Leu Val Ser Gly 120 115 Pro Phe Lys Ile Asn Gly Val Pro Ile Arg Arg Val Xaa Arg Pro Met 135 Ser Leu Leu His Gln Pro Arg Leu Thr Ser 150 (2) INFORMATION FOR SEQ ID NO:1476: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..100 (D) OTHER INFORMATION: / Ceres Seq. ID 1598127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476: Ser Ser Pro Ala Ala Xaa Leu Pro Val Ser Thr Arg Xaa Ser Ala Ser 10 Gln Arg Xaa Xaa Pro Met Ala Xaa Thr Ser Lys Leu Ser Met Gly Ile 25 2.0 Lys Xaa Ala Xaa Asp Arg Thr Arg Thr Thr Ala Val Ala Leu Gly His 4.0 Gln Gly Lys Asn Xaa Gly Val Phe Pro Lys Ala Glu Lys Pro Ala Ala 55 Ala Ala Glu Pro Lys Phe Tyr Pro Ala Asp Asp Val Lys Pro Arg Xaa 70 75 Pro Ala Pro Ala Ser Xaa Xaa Pro Pro Ser Ser Gly Arg Ala Ser Arg 85 Leu Gly Arg Cys 100 (2) INFORMATION FOR SEQ ID NO:1477: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..484 (D) OTHER INFORMATION: / Ceres Seq. ID 1598131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477: acacccatct cctgagtcct gcctgcnctc gcctcagctc ctttcttccc cgccccttgg 60 cttttgcttg gttgcatcgg gccggtcgag ccggagagga aaagctagct actagctacc 120 agctctcggc cggcggtggt agtctgcctg cagctggggt tagctgcaag ggttgggagc 180 tagccatggg gaggggtcgg gtggagctga agcgatcgag aacaagatca accgccagtc 240 accttcgcca agcgccgcaa cggcctgctc aagaaggcgt acgagctctc cgtgctctgc 300 gacgccgaag tcgcgctcat catcttctcc aaccgcggca agctctacga gttctgcagc 360 420 ggacagagca tcaccaaaac acttgagagg tatgaaaaaa acagttatgg aggaccagat 480 actgctgtac agaacaagga gaaacgagtt agtccagagc agtcgtaatg agtacctcaa acta

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..127 (D) OTHER INFORMATION: / Ceres Seq. ID 1598132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478: Thr His Leu Leu Ser Pro Ala Cys Xaa Arg Leu Ser Ser Phe Leu Pro 10 Arg Pro Leu Ala Phe Ala Trp Leu His Arg Ala Gly Arg Ala Gly Glu 25 20 Glu Lys Leu Ala Thr Ser Tyr Gln Leu Ser Ala Gly Gly Ser Leu 40 Pro Ala Ala Gly Val Ser Cys Lys Gly Trp Glu Leu Ala Met Gly Arg 55 Gly Arg Val Glu Leu Lys Arg Ser Arg Thr Arg Ser Thr Ala Ser His 7.0 Leu Arg Gln Ala Pro Gln Arg Pro Ala Gln Glu Gly Val Arg Ala Leu 85 Arg Ala Leu Arg Arg Arg Ser Arg Ala His His Leu Leu Gln Pro Arg 105 100 Gln Ala Leu Arg Val Leu Gln Arg Thr Glu His His Gln Asn Thr 120 115 (2) INFORMATION FOR SEQ ID NO:1479: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..66 (D) OTHER INFORMATION: / Ceres Seq. ID 1598133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479: Met Gly Arg Gly Arg Val Glu Leu Lys Arg Ser Arg Thr Arg Ser Thr 10 Ala Ser His Leu Arg Gln Ala Pro Gln Arg Pro Ala Gln Glu Gly Val 25 Arg Ala Leu Arg Ala Leu Arg Arg Arg Ser Arg Ala His His Leu Leu 4.5 40 Gln Pro Arg Gln Ala Leu Arg Val Leu Gln Arg Thr Glu His His Gln Asn Thr (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (2) INFORMATION FOR SEQ ID NO:1480:

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

akagtgtcta gctgagaaca tggtgacctc aagcaagggc aaggtatgtg taaccggggc 60 ctcaggettt gttgeetett ggettateaa aeggeteete gagtetggat ateatgtsgt agggactgtc agggacccag gtatttgcga aatatcatta cwttcgtatc gtcagt (2) INFORMATION FOR SEQ ID NO:1481: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..58 (D) OTHER INFORMATION: / Ceres Seq. ID 1598139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481: Xaa Cys Leu Ala Glu Asn Met Val Thr Ser Ser Lys Gly Lys Val Cys 15 10 Val Thr Gly Ala Ser Gly Phe Val Ala Ser Trp Leu Ile Lys Arg Leu 30 Leu Glu Ser Gly Tyr His Xaa Val Gly Thr Val Arg Asp Pro Gly Ile 40 Cys Glu Ile Ser Leu Xaa Ser Tyr Arg Gln 55 50 (2) INFORMATION FOR SEQ ID NO:1482: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1598140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482: Met Val Thr Ser Ser Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly 10 Phe Val Ala Ser Trp Leu Ile Lys Arg Leu Leu Glu Ser Gly Tyr His 25 20 Xaa Val Gly Thr Val Arg Asp Pro Gly Ile Cys Glu Ile Ser Leu Xaa 40 Ser Tyr Arg Gln (2) INFORMATION FOR SEQ ID NO:1483: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1598141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483: Met Cys Asn Arg Gly Leu Arg Leu Cys Cys Leu Leu Ala Tyr Gln Thr 10 Ala Pro Arg Val Trp Ile Ser Cys Xaa Arg Asp Cys Gln Gly Pro Arg

25

40

2.0

Tyr Leu Arg Asn Ile Ile Xaa Phe Val Ser Ser

- (2) INFORMATION FOR SEQ ID NO:1484:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598152
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

akatccaggt actottcctt togccgcggc tgagaagcaa ctctccctct ctgtcctctt 60 cctgtcgccg cactcatttt ctcttgccgg gtggaatagg gaacggccat acaccatggc 120 ggatttctcc aaggaatctt gcccttctgt gaagaacatt ttacttctgg attctgaagg 180 aaagcgtgtt gctgtaaagt atttctcaga tgattggccg actaatgcat caaagttagc 240 ctacgaaaag tctgttttta ctaaaactct aaagacaaat gcacggacag aagctgagat 300 360 aacattgttt gatggttata ttgtcgttta caagtttgta catgaccttc acttttttgt 420 caccgctgga gatgatgaga atgagctcat cttagcaagt gtactacatg gtttttctga 480 ttctgttggt cttctactca ggggtgatgt tgagaagcgg actgcgcttg agaacttgga tttgatactt ctctgcattg

- (2) INFORMATION FOR SEQ ID NO:1485:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598153
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

Xaa Pro Gly Thr Leu Pro Phe Ala Ala Ala Glu Lys Gln Leu Ser Leu 1 5 10 15 Ser Val Leu Phe Leu Ser Pro His Ser Phe Ser Leu Ala Gly Trp Asn

20 25 30

Arg Glu Arg Pro Tyr Thr Met Ala Asp Phe Ser Lys Glu Ser Cys Pro
35 40 45

Ser Val Lys Asn Ile Leu Leu Leu Asp Ser Glu Gly Lys Arg Val Ala

Val Lys Tyr Phe Ser Asp Asp Trp Pro Thr Asn Ala Ser Lys Leu Ala 65 70 75 80

Tyr Glu Lys Ser Val Phe Thr Lys Thr Leu Lys Thr Asn Ala Arg Thr 85 90 95

Glu Ala Glu Ile Thr Leu Phe Asp Gly Tyr Ile Val Val Tyr Lys Phe $100 \,$ $\,$ $105 \,$ $\,$ $110 \,$

Val His Asp Leu His Phe Phe Val Thr Ala Gly Asp Asp Glu Asn Glu 115 120 125

Leu Ile Leu Ala Ser Val Leu His Gly Phe Ser Asp Ser Val Gly Leu 130 135 140

Leu Leu Arg Gly Asp Val Glu Lys Arg Thr Ala Leu Glu Asn Leu Asp 145 150 155 160

Leu Ile Leu Leu Cys Ile

165

- (2) INFORMATION FOR SEQ ID NO:1486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598154
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:
- Met Ala Asp Phe Ser Lys Glu Ser Cys Pro Ser Val Lys Asn Ile Leu 1 5 10 15
- Leu Leu Asp Ser Glu Gly Lys Arg Val Ala Val Lys Tyr Phe Ser Asp 20 25 30
- Asp Trp Pro Thr Asn Ala Ser Lys Leu Ala Tyr Glu Lys Ser Val Phe 35 40 45
- Thr Lys Thr Leu Lys Thr Asn Ala Arg Thr Glu Ala Glu Ile Thr Leu 50 55 60
- Phe Asp Gly Tyr Ile Val Val Tyr Lys Phe Val His Asp Leu His Phe 65 70 75 80
- Phe Val Thr Ala Gly Asp Asp Glu Asn Glu Leu Ile Leu Ala Ser Val $85 \hspace{0.5cm} 90 \hspace{0.5cm} 95$
- Leu His Gly Phe Ser Asp Ser Val Gly Leu Leu Leu Arg Gly Asp Val 100 $$ 105 $$ 110
- Glu Lys Arg Thr Ala Leu Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile 115 120 125
- (2) INFORMATION FOR SEQ ID NO:1487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..496
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598163
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

ctcqqtaqca	gctggctcac	ttctccagga	aagtgttcgt	cctcatggcg	ccgcgcagcc	60
gaagtcgggc	ctcttcgtgg	gcatcaacaa	gggccatgtc	gtcaccaagc	gcgastgcct	120
		gggaaagcaa				180
		gctccttatg				240
		aagcttgcca				300
		atgggcgtcc				360
		atttcaagtt				420
gtgtttttc	cctacctcta	gaaactagac	atggcaaagt	atttttgacc	gaaacattgt	480
ttattagtaa	tatatt					

- (2) INFORMATION FOR SEQ ID NO:1488:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..110
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598164
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

Met Ala Pro Arg Ser Arg Ser Arg Ala Ser Ser Trp Ala Ser Thr Arg 1 5 10 15

Ala Met Ser Ser Pro Ser Ala Xaa Ala Ser Ala Pro Val Pro Pro Gln
20 25 30

Gly Lys Ala Thr Lys Arg Val Ser Met Val Arg Gly Leu Ile Arg Glu
35 40 45

Val Ala Gly Phe Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys 50 55 60

Val Gly Lys Asp Lys Arg Ala Leu Lys Leu Ala Lys Arg Lys Leu Gly 65 70 75 80

Thr His Lys Arg Ala Lys Lys Lys Arg Glu Glu Met Met Gly Val Leu 85 90 95

Arg Lys Met Arg Ser Ala Gly Thr His Thr Asp Lys Lys 100 105 110

- (2) INFORMATION FOR SEQ ID NO:1489:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

Met Ser Ser Pro Ser Ala Xaa Ala Ser Ala Pro Val Pro Pro Gln Gly
1 5 10 15

Lys Ala Thr Lys Arg Val Ser Met Val Arg Gly Leu Ile Arg Glu Val $20 \\ 25 \\ 30 \\$

Ala Gly Phe Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys Val 35 40 45

Gly Lys Asp Lys Arg Ala Leu Lys Leu Ala Lys Arg Lys Leu Gly Thr 50 55 60

His Lys Arg Ala Lys Lys Lys Arg Glu Glu Met Met Gly Val Leu Arg 65 70 75 80

Lys Met Arg Ser Ala Gly Thr His Thr Asp Lys Lys 85 90

- (2) INFORMATION FOR SEQ ID NO:1490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

Met Val Arg Gly Leu Ile Arg Glu Val Ala Gly Phe Ala Pro Tyr Glu 1 5 10 15

Lys Arg Ile Thr Glu Leu Leu Lys Val Gly Lys Asp Lys Arg Ala Leu 20 25 30

Lys Leu Ala Lys Arg Lys Leu Gly Thr His Lys Arg Ala Lys Lys Lys 35 40 45

Arg Glu Glu Met Met Gly Val Leu Arg Lys Met Arg Ser Ala Gly Thr 50 60

His Thr Asp Lys Lys Lys 65 70

- (2) INFORMATION FOR SEQ ID NO:1491:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..494
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598171
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

aatttttggg cacgtageeg eetegettte teetetteeg eeceaeeeeg gtgaggeget 60 gatccatcgc ctcggacagc ggctccagaa cctccgcgtt gcagaaacac agtagcgaga 120 actattcggt ggggccgaag atggtgtcgc tgaaggtgcc aaagcgcctc gccgcaagcg 180 ttctcaagtg tgggaaaggc aaagtgtggc ttgaccccaa tgaagttagt gagatctcca 240 tggcgaactc ccgccataac atccggaagt tggttaagga tgggtttatc atcaagaagc 300 360 ctcagaaaat ccactctaga tctcgtgcaa gawgggcgca cgaggctaag cagaagggac ggcactcagg atatgggaag cgtagaggtt accagggagg ctaggctccc caccaaggta 420 ctgtggatga ggaggatgcg cgtgctgagg cgcctgctcc gcaagtaccg cgagccaaga 480 agatcgacaa gcac

- (2) INFORMATION FOR SEQ ID NO:1492:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598172
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

Met Val Ser Leu Lys Val Pro Lys Arg Leu Ala Ala Ser Val Leu Lys 1 $$ 5 $$ 10 $$ 15

Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Val Ser Glu Ile $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$

Ser Met Ala Asn Ser Arg His Asn Ile Arg Lys Leu Val Lys Asp Gly 35 40 45

Phe Ile Ile Lys Lys Pro Gln Lys Ile His Ser Arg Ser Arg Ala Arg 50 55 60

Xaa Ala His Glu Ala Lys Gln Lys Gly Arg His Ser Gly Tyr Gly Lys 65 70 75 80

Arg Arg Gly Tyr Gln Gly Gly 85

- (2) INFORMATION FOR SEQ ID NO:1493:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598173
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

Met Lys Leu Val Arg Ser Pro Trp Arg Thr Pro Ala Ile Thr Ser Gly
1 10 15

Ser Trp Leu Arg Met Gly Leu Ser Ser Arg Ser Leu Arg Lys Ser Thr 20 25 30

Leu Asp Leu Val Gln Xaa Gly Arg Thr Arg Leu Ser Arg Arg Asp Gly
35 40 45

Thr Gln Asp Met Gly Ser Val Glu Val Thr Arg Glu Ala Arg Leu Pro 50 55 60 Thr Lys Val Leu Trp Met Arg Arg Met Arg Val Leu Arg Arg Leu Leu

80 65 70 75 Arg Lys Tyr Arg Glu Pro Arg Arg Ser Thr Ser 85 (2) INFORMATION FOR SEQ ID NO:1494: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1598174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494: Met Gly Leu Ser Ser Arg Ser Leu Arg Lys Ser Thr Leu Asp Leu Val 10 Gln Xaa Gly Arg Thr Arg Leu Ser Arg Arg Asp Gly Thr Gln Asp Met 25 Gly Ser Val Glu Val Thr Arg Glu Ala Arg Leu Pro Thr Lys Val Leu 40 Trp Met Arg Arg Met Arg Val Leu Arg Arg Leu Leu Arg Lys Tyr Arg 55 Glu Pro Arg Arg Ser Thr Ser 70 (2) INFORMATION FOR SEQ ID NO:1495: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 459 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..459 (D) OTHER INFORMATION: / Ceres Seq. ID 1598193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495: 60 atatctccct qtttaatcaa tccttcaagc qcaangcetc ctcctcgtcg tccggtcgtg 120 agaagggatg gcgggccgtg gcaaggctat cggcgctggc gccgaagaag gcaacgtcga ggagctccaa ggccggactc cagttccccg tcggcaggat tgctaggttc ctcaaggcgg 180 240 gcaagtacgc tgagcgcgtc ggcscggcgc ccccgtgtac ctcgccgccg tcctcgagta 300 cctcgcggct gaggttctcg aacttgccgg gaacgccgcg aggacaacaa gaagacccgc 360 attgtgccgc gccacatcca gcttgctgtg cgcaacgacg agganctgac caaactgttg 420 qqtqqtqcca ccatcqcqac cggaggtgtt atgcctaaca tccatcagca tctqctcccc aaqaaqqctq cctcctccaa qqccaqtqtc gacqacqac (2) INFORMATION FOR SEQ ID NO:1496: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..83 (D) OTHER INFORMATION: / Ceres Seq. ID 1598194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496: Ile Ser Pro Cys Leu Ile Asn Pro Ser Ser Ala Xaa Pro Pro Pro Arg 10 Arg Pro Val Val Arg Arg Asp Gly Gly Pro Trp Gln Gly Tyr Arg Arg 25

Trp Arg Arg Arg Gln Arg Arg Gly Ala Pro Arg Pro Asp Ser Ser 40 Ser Pro Ser Ala Gly Leu Leu Gly Ser Ser Arg Arg Ala Ser Thr Leu 60 55 Ser Ala Ser Xaa Arg Arg Pro Arg Val Pro Arg Arg Pro Arg Val 70 Pro Arg Gly

- (2) INFORMATION FOR SEQ ID NO:1497:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598195
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

Ile Ser Leu Phe Asn Gln Ser Phe Lys Arg Xaa Ala Ser Ser Ser Ser 10

Ser Gly Arg Glu Lys Gly Trp Arg Ala Val Ala Arg Leu Ser Ala Leu 25 30

Ala Pro Lys Lys Ala Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe 40

Pro Val Gly Arg Ile Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu 55

Arg Val Gly Xaa Ala Pro Pro Cys Thr Ser Pro Pro Ser Ser Ser Thr 70 75

Ser Arg Leu Arg Phe Ser Asn Leu Pro Gly Thr Pro Arg Gly Gln Gln 90 8.5

Glu Asp Pro His Cys Ala Ala Pro His Pro Ala Cys Cys Ala Gln Arg 105 100

Arg Gly Xaa Asp Gln Thr Val Gly Trp Cys His His Arg Asp Arg Arg 120 115

Cys Tyr Ala

130

- (2) INFORMATION FOR SEQ ID NO:1498:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498: tgtgtgggaa gtggtggaga gaagctattg cctgagtggt actcagagaa aggcattgag

120 ctgatcctta gtacagaaat tgtcaaagct gatctttcca ccaagactct gactagtgca 180 gctggagcaa actttacata tgagatcttg ctcattgcta ctggctcctc ggtcataaag ctcaccgatt ttggcacaca aggagctgat tctaacaaca ttctatatct aagggaaatt 240 300 gatgatgctg acaagctggt tgcagctatc caggcaaaga agggtggcaa ggcagtggtt gttggaggag gttatatcgg cctcgaactg agtgcagccc tgaagatcaa tgactttgat 360 gtcactatgg tgtttcctga accttggtgc atgcctcgcc tcttcactgc cgatattgct 420 gctttctatg aggcttacta tactaacaaa ggtgtaaaga tcttgaaggg cacgctagct 480

- gttgg (2) INFORMATION FOR SEQ ID NO:1499:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (iì) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598208
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

Cys Val Gly Ser Gly Gly Glu Lys Leu Leu Pro Glu Trp Tyr Ser Glu 1 $$ 5 $$ 10 $$ 15

Lys Gly Ile Glu Leu Ile Leu Ser Thr Glu Ile Val Lys Ala Asp Leu 20 25 30

Ser Thr Lys Thr Leu Thr Ser Ala Ala Gly Ala Asn Phe Thr Tyr Glu 35 40 45

Ile Leu Leu Ile Ala Thr Gly Ser Ser Val Ile Lys Leu Thr Asp Phe 50 55 60

Gly Thr Gln Gly Ala Asp Ser Asn Asn Ile Leu Tyr Leu Arg Glu Ile 65 70 75 80

Asp Asp Ala Asp Lys Leu Val Ala Ala Ile Gln Ala Lys Lys Gly Gly 85 90 95

Lys Ala Val Val Gly Gly Gly Tyr Ile Gly Leu Glu Leu Ser Ala 100 \$105\$

Ala Leu Lys Ile Asn Asp Phe Asp Val Thr Met Val Phe Pro Glu Pro 115 120 125

Trp Cys Met Pro Arg Leu Phe Thr Ala Asp Ile Ala Ala Phe Tyr Glu 130 135 140

Ala Tyr Tyr Thr Asn Lys Gly Val Lys Ile Leu Lys Gly Thr Leu Ala 145 150 150 160

- (2) INFORMATION FOR SEQ ID NO:1500:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..193
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

aactccaage gecaceaate tegeetteeg aggaaaceea ecageeceace acagaecega 60 geggaagaag ceatgteegg gegeggeaag ggtggeaagg ggeteggeaa gggeggegeg 120 amkeacegga aggttetgeg egacaacate cagggeatea ecaageegge gateeggegn 180 etgggegagg agg

- (2) INFORMATION FOR SEQ ID NO:1501:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598214
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

Asn Ser Lys Arg His Gln Ser Arg Leu Pro Arg Lys Pro Thr Ser Pro

- (2) INFORMATION FOR SEQ ID NO:1502:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598215
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

Thr Pro Ser Ala Thr Asn Leu Ala Phe Arg Gly Asn Pro Pro Ala His 1 $$ 5 $$ 10 $$ 15

His Arg Pro Glu Arg Lys Lys Pro Cys Pro Gly Ala Ala Arg Val Ala 20 25 30

Arg Gly Ser Ala Arg Ala Ala Arg Xaa Thr Gly Arg Phe Cys Ala Thr 35 40 45

Thr Ser Arg Ala Ser Pro Ser Arg Arg Ser Gly Xaa Trp Ala Arg Arg 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1503:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

Leu Gln Ala Pro Pro Ile Ser Pro Ser Glu Glu Thr His Gln Pro Thr
1 5 10 15

Thr Asp Pro Ser Gly Arg Ser His Val Arg Ala Arg Gln Gly Trp Gln 20 25 30

Gly Ala Arg Gln Gly Arg Arg Xaa Xaa Pro Glu Gly Ser Ala Arg Gln 35 40 45

His Pro Gly His His Gln Ala Gly Asp Pro Ala Xaa Gly Arg Gly 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1504:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..123

480

(D) OTHER INFORMATION: / Ceres Seq. ID 1598217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504: gtttccctct tccccccact acccaaaccc aacaggcggc gcmrgcatcg ccaccaccgt 60 ccaaagatgg tgaagtteet caageeegge aaggeegtta teeteeteea gggeeggtte 120 (2) INFORMATION FOR SEQ ID NO:1505: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..41 (D) OTHER INFORMATION: / Ceres Seq. ID 1598218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505: Val Ser Leu Phe Pro Pro Leu Pro Lys Pro Asn Arg Arg Arg Xaa His 10 5 Arg His His Arg Pro Lys Met Val Lys Phe Leu Lys Pro Gly Lys Ala 25 Val Ile Leu Leu Gln Gly Arg Phe Ala 35 40 (2) INFORMATION FOR SEQ ID NO:1506: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..40 (D) OTHER INFORMATION: / Ceres Seq. ID 1598219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506: Phe Pro Leu Pro Pro Thr Thr Gln Thr Gln Gln Ala Ala Xaa Ala Ser 10 5 Pro Pro Pro Ser Lys Asp Gly Glu Val Pro Gln Ala Arg Gln Gly Arg 25 20 Tyr Pro Pro Pro Gly Pro Val Arg 35 (2) INFORMATION FOR SEQ ID NO:1507: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 485 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..485 (D) OTHER INFORMATION: / Ceres Seq. ID 1598224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507: ccactcccgg ccgccgcacc acttgctcgc ctttgcccct tccccttctg tcacccttcg 60 tecgtageag accaggaacg eccaaggset asgtetecaa gatggtgetg caaaacgaca 120 ttgacttact caatccaccg gcagagcttg agaagctaaa gcacaagaag aagcggctag 180 tccagtcccc caactccttc ttcatggatg tcaagtgcca gggctgtttc agcataacca 240 ctgtgttcag ccactcccag actgtggttg tgtgcccagg ctgccaaact gttctctgcc 300 aaccaaccgg tgggaaggcc aggctcaccg aggggtgctc cttccgtcgc aagggcgatt 360

aggtcctgct tctcttaacg tgagaagaga taaatttggt gttttgcaac tttctcagga tatgtgctgt gctcgggtga ggattntgtt aattattatr gctgttagcg tggcctgaca

atgct (2) INFORMATION FOR SEQ ID NO:1508: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..119 (D) OTHER INFORMATION: / Ceres Seq. ID 1598225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508: Thr Pro Gly Arg Arg Thr Thr Cys Ser Pro Leu Pro Leu Pro Leu Leu 10 Ser Pro Phe Val Arg Ser Arg Pro Gly Thr Pro Lys Xaa Xaa Val Ser 25 Lys Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu 40 Leu Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr 75 70 Val Phe Ser His Ser Gln Thr Val Val Val Cys Pro Gly Cys Gln Thr 90 Val Leu Cys Gln Pro Thr Gly Gly Lys Ala Arg Leu Thr Glu Gly Cys 105 100 Ser Phe Arg Arg Lys Gly Asp 115 (2) INFORMATION FOR SEQ ID NO:1509: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..86 (D) OTHER INFORMATION: / Ceres Seq. ID 1598226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509: Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu Leu 1.0 Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser 20 25 Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Val 40 Phe Ser His Ser Gln Thr Val Val Val Cys Pro Gly Cys Gln Thr Val 55 Leu Cys Gln Pro Thr Gly Gly Lys Ala Arg Leu Thr Glu Gly Cys Ser 70 Phe Arg Arg Lys Gly Asp 85 (2) INFORMATION FOR SEQ ID NO:1510: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510: 60 aattcgccac tgacgttcat tccgcttgct tgattgctcc aggtacctcc attcgcagtc ggccgtgtcc tcggagccgc gggagatggc ggatcaggag acagtagctg tggttgaggc 120 180 acctaccccg gttctagggg aacgatggac ctgatgactg ccctgcagct cgtcatgaag 240 aagtcaggtg ctcacgatgg ccttgtgaag ggtcttcgtg aggctgccaa agccatcgag aagcatgccg ctcagctctg cgtgcttgcc gaggactgcg accagcctga ttatgtcaag 300 360 ctggtgaagg ctctctgcgc tgagcacaat gtccacctgg ttactgtgcc tagcgccaaa actcttggag agtgggctgg gctttgcaag atcgactctg agggcaaagg cgaggaaggt 420 tgtaggctgc tcctgtgttg ttgtcaagga ctacggcgaa gaatctkaag gccttaac

- (2) INFORMATION FOR SEQ ID NO:1511:
 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..110
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511: Met Asp Leu Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Gly Ala 5 10 His Asp Gly Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu 25 20 Lys His Ala Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro 40 Asp Tyr Val Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His 55 Leu Val Thr Val Pro Ser Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu 75 70 Cys Lys Ile Asp Ser Glu Gly Lys Gly Glu Glu Gly Cys Arg Leu Leu 90 85 Leu Cys Cys Cys Gln Gly Leu Arg Arg Arg Ile Xaa Arg Pro 105 100
- (2) INFORMATION FOR SEQ ID NO:1512:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598229
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512: Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Gly Ala His Asp Gly 10 5 Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu Lys His Ala 25 20 Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro Asp Tyr Val 45 40 Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His Leu Val Thr 55 Val Pro Ser Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile 75 70 Asp Ser Glu Gly Lys Gly Glu Glu Gly Cys Arg Leu Leu Cys Cys

95 Cys Gln Gly Leu Arg Arg Arg Ile Xaa Arg Pro 100 (2) INFORMATION FOR SEQ ID NO:1513: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..100 (D) OTHER INFORMATION: / Ceres Seq. ID 1598230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513: Met Lys Lys Ser Gly Ala His Asp Gly Leu Val Lys Gly Leu Arg Glu 10 5 Ala Ala Lys Ala Ile Glu Lys His Ala Ala Gln Leu Cys Val Leu Ala 30 25 Glu Asp Cys Asp Gln Pro Asp Tyr Val Lys Leu Val Lys Ala Leu Cys 45 40 Ala Glu His Asn Val His Leu Val Thr Val Pro Ser Ala Lys Thr Leu 55 Gly Glu Trp Ala Gly Leu Cys Lys Ile Asp Ser Glu Gly Lys Gly Glu 75 70 Glu Gly Cys Arg Leu Leu Cys Cys Cys Gln Gly Leu Arg Arg 90 Ile Xaa Arg Pro 100 (2) INFORMATION FOR SEQ ID NO:1514: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..487 (D) OTHER INFORMATION: / Ceres Seq. ID 1598235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514: aaaaacccta acctegegae egtataaaeg agecaaceeg eecaceteee gegeegeege 60 cactcagege egegettgbt tteettetet eegetteeaa gatgtegaag egagggegtg 120 gaggttcggc tggtaacaag ttccggatgt cactgggtct accagtggca gctactgtga 180 240 actgtgccga taacactgga gccaagaacc tgtacatcat ttctgtgaag ggaatcaagg gtcgccttaa caggcttcct tctgcctgtg ttggtgacat ggttatggca accgtgaaga 300 360 agggaaagcc tgaccttaga aagaaggtga tgccagctgt tattgtgagg cagcgcaacc atggcgccga aaggatggtg tctacatgta ctttgaagac aatgctggag tgattgtgaa 420 cccaaaggag agatgaaagg ttctgccatc actgggccca tcggaaagga gtgtgctgat 480 ctctagc (2) INFORMATION FOR SEQ ID NO:1515: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515: Met Ser Lys Arg Gly Arg Gly Gly Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr 20 25 Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg 40 Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr 60 55 Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val 75 70 Ile Val Arg Gln Arg Asn His Gly Ala Glu Arg Met Val Ser Thr Cys 85 Thr Leu Lys Thr Met Leu Glu

- 100
- (2) INFORMATION FOR SEQ ID NO:1516:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598237
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn 10

Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly 25 20

Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala 40

Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala 55

Val Ile Val Arg Gln Arg Asn His Gly Ala Glu Arg Met Val Ser Thr 70

Cys Thr Leu Lys Thr Met Leu Glu 8.5

- (2) INFORMATION FOR SEQ ID NO:1517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..472
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

60 gaggggaaga cgagaggcag aagcgaagga aacagtagtt cttcagttag gcaggagggc 120 acaggaggag gaagatggcg tcgaagagga tccagaagga gctcaaggat cttcagaagg acceteceae etegtgeagt geaggteetg ttggtgaaga tatatteeae tggcaggeaa 180 caataatggg tccatctgat agcccatatt ctggtggagt tttcctagtt acaatccatt 240 ttcctcccga ttatcctttc aaaccaccaa aggkcattcc gcaccaaggt gttccatcca 300 aacatcaaca gcaacgggag catctgcctt gacatcctta aggaccagtg gagcccggcg 360 ctaaccatct ccaaggtgct gctgtccatc tgctccctgc tgaccgatcc gaaccccgac 420 gatectetgg teccegagat agegeaeatg tacaagaegg aceggaaeaa gt

- (2) INFORMATION FOR SEQ ID NO:1518:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..61
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598253
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

Glu Gly Lys Thr Arg Gly Arg Ser Glu Gly Asn Ser Ser Ser Val 1 5 10 15

Arg Gln Glu Gly Thr Gly Gly Gly Arg Trp Arg Arg Arg Gly Ser Arg 20 25 30

Arg Ser Ser Arg Ile Phe Arg Arg Thr Leu Pro Pro Arg Ala Val Gln 35 40 45

Val Leu Leu Val Lys Ile Tyr Ser Thr Gly Arg Gln Gln 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..51
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598254
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

Arg Gly Arg Arg Glu Ala Glu Ala Lys Glu Thr Val Val Leu Gln Leu 1 5 10 15

Gly Arg Arg Ala Gln Glu Glu Glu Asp Gly Val Glu Glu Asp Pro Glu 20 25 30

Gly Ala Gln Gly Ser Ser Glu Gly Pro Ser His Leu Val Gln Cys Arg 35 40 45

Ser Cys Trp

- (2) INFORMATION FOR SEQ ID NO:1520:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598255
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Met Ala Ser Lys Arg Ile Gln Lys Glu Leu Lys Asp Leu Gln Lys Asp

1 10 15

Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Gly Glu Asp Ile Phe His 20 25 30

Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly 35 40 45

Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro 50 55 60

Pro Lys Xaa Ile Pro His Gln Gly Val Pro Ser Lys His Gln Gln Gln 65 70 75 80

Arg Glu His Leu Pro

85

- (2) INFORMATION FOR SEQ ID NO:1521:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..426
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598257
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

(/	~ ~ .					
aacaacaaca	gcaacccgca	caagccctct	tcctcgattt	tbctcctccg	tccgcgtagt	60
tctcggtttc	gacgatatca	gggcgcggca	agggcggcaa	ggggctgggc	aagggcggcg	120
				tcacgaagcc		180
agctggccag	gaggggggg	atcaaacqca	tttctgggct	catctacgag	gaaacccgcg	240
gcgtgctcaa	gatcttcctc	gagaacgtca	tecqeqaeqe	cgtcacctac	accgagcacg	300
				gctcaagcgc		360
				ctttgatatn		420
tcggtt		5 5	, ,	-		
coggee						

- (2) INFORMATION FOR SEQ ID NO:1522:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

Asn Asn Asn Ser Asn Pro His Lys Pro Ser Ser Ser Ile Xaa Leu Leu 10 Arg Pro Arg Ser Ser Arg Phe Arg Arg Cys Arg Gly Ala Ala Arg Ala

25 Ala Arg Gly Trp Ala Arg Ala Ala Pro Ser Ala Pro Gln Xaa Leu Arg

40Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Ser Trp Pro Gly

55 Gly Ala Ala Ser Ser Ala Phe Leu Gly Ser Ser Thr Arg Lys Pro Ala

70 75 Ala Cys Ser Arg Ser Ser Ser Arg Thr Ser Ser Ala Thr Pro Ser Pro 90

Thr Pro Ser Thr Pro Ala Ala Arg Leu Ser Pro Pro Trp Met Ser Ser 105 110 100

Thr Arg Ser Ser Ala Arg Ala Gly Arg Ser Thr Ala Ser Ala Ala Arg 120 125 115

Xaa Ser Pro Ser Asp Ala Leu Ile Xaa Arg Pro Trp Ser Val 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1523:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1598259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523: Thr Thr Thr Ala Thr Arg Thr Ser Pro Leu Pro Arg Phe Xaa Ser Ser 10 5 Val Arg Val Val Leu Gly Phe Gly Asp Val Gly Ala Arg Gln Gly Arg 20 2.5 Gln Gly Ala Gly Gln Gly Arg Arg Gln Ala His Arg Lys Xaa Cys Ala 45 40 Thr Thr Ser Arg Ala Ser Arg Ser Arg Arg Ser Val Ala Gly Gln Glu 60 55 Gly Arg Arg Gln Ala His Phe Trp Ala His Leu Arg Gly Asn Pro Arg 75 70 Arg Ala Gln Asp Leu Pro Arg Glu Arg His Pro Arg Arg Arg His Leu 90 85 His Arg Ala Arg Pro Pro Gln Asp Cys His Arg His Gly Cys Arg Leu 105 110 Arg Ala Gln Ala Pro Gly Pro Asp Ala Leu Arg Leu Arg Leu Gly 120 Xaa Pro Leu Leu Met Leu 130 (2) INFORMATION FOR SEQ ID NO:1524: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 374 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..374 (D) OTHER INFORMATION: / Ceres Seq. ID 1598271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524: aacgcgcctc ctctcgccct cgctccgccg ccgccgccgc cgccgcatca agcacccgcc 60 120 ccqccqtcqc ctqaqqtaqa caccaatccq ccgccatggg gcgtatgcac agccgcggga 180 agggtatete ategteggeg etgeegtaca agaggaegee teetacetgg etcaagaeeg ctgcctccga cgtggaggag atgatcacaa aggcagcgaa gaagggacag atgccgtcgc 240 300 agatcggcgt cctgctccgt gaccagcacg gtatccccct tgtcaagagc gtcaccggca gcaagatcct ccgcatcctc aaggcccatg ggctggcacc agaaatcccc gaggacctgt 360 acttcctcat caag (2) INFORMATION FOR SEQ ID NO:1525: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..67 (D) OTHER INFORMATION: / Ceres Seq. ID 1598272 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525: Asn Ala Pro Pro Leu Ala Leu Ala Pro Pro Pro Pro Pro Pro Pro His 10 Gln Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro 25 2.0 Trp Gly Val Cys Thr Ala Ala Gly Arg Val Ser His Arg Arg Cys 40 Arg Thr Arg Gly Arg Leu Leu Pro Gly Ser Arg Pro Leu Pro Pro Thr 50 Trp Arg Arg

- (2) INFORMATION FOR SEQ ID NO:1526:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598273
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:
- Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu 1 5 10 15
- Pro Tyr Lys Arg Thr Pro Pro Thr Trp Leu Lys Thr Ala Ala Ser Asp 20 25 30
- Val Glu Glu Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser 35 40 45
- Gln Ile Gly Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys 50 60
- Ser Val Thr Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu 65 70 75 80
- Ala Pro Glu Ile Pro Glu Asp Leu Tyr Phe Leu Ile Lys 85 90
- (2) INFORMATION FOR SEQ ID NO:1527:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..90
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598274
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:
- Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu Pro Tyr Lys

 1 10 15
- Arg Thr Pro Pro Thr Trp Leu Lys Thr Ala Ala Ser Asp Val Glu Glu 20 25 30
- Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser Gln Ile Gly 35 40 45
- Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys Ser Val Thr 50 55 60
- Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu Ala Pro Glu 65 70 75 80
- Ile Pro Glu Asp Leu Tyr Phe Leu Ile Lys 85 90
- (2) INFORMATION FOR SEQ ID NO:1528:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..197
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598290
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

gtttcggcga tgtcggggcg cggcaagggc ggcaagggc tgggcaaggg cggcgcaagc 120 knaccgcaag gkctgcgcga caacatccag ggcatcacga agccggcgat ccgtagctgg 180 ccaggagggg cggcgtc

(2) INFORMATION FOR SEQ ID NO:1529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..65
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

Lys Thr Thr Thr Thr Arg Thr Thr Ala Arg Phe Xaa Ser Ser Val $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Arg Xaa Xaa Ser Val Ser Ala Met Ser Gly Arg Gly Lys Gly Gly Lys 20 25 30

Gly Leu Gly Lys Gly Gly Ala Ser Xaa Pro Gln Xaa Leu Arg Asp Asn 35 40 45

Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Ser Trp Pro Gly Gly Ala 50 60

Ala 65

- (2) INFORMATION FOR SEQ ID NO:1530:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..65
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598292
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Lys Gln Gln Gln Gln Pro Ala Gln Arg His Asp Ser Xaa Pro Pro Ser 1 5 10 15

Ala Xaa Ser Arg Phe Arg Arg Cys Arg Gly Ala Ala Arg Ala Ala Arg 20 25 30

Gly Trp Ala Arg Ala Ala Gln Xaa Xaa Arg Lys Xaa Cys Ala Thr Thr 35 40 45

Ser Arg Ala Ser Arg Ser Arg Ser Val Ala Gly Gln Glu Gly Arg
50 55 60

Arg

- (2) INFORMATION FOR SEQ ID NO:1531:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..57
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598293
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

Asn Asn Asn Asn Pro His Asn Gly Thr Ile Xaa Leu Leu Arg Pro

1 5 10 15

Arg Xaa Leu Gly Phe Gly Asp Val Gly Ala Arg Gln Gly Arg Gln Gly 20 25 30

Ala Gly Gln Gly Arg Arg Lys Xaa Thr Ala Arg Xaa Ala Arg Gln His 35 40 45

Pro Gly His His Glu Ala Gly Asp Pro 50 55

- (2) INFORMATION FOR SEQ ID NO:1532:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..517
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598318
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

60 acgacccaaa aaaggatcaa ggtgggagaw acaaaacaca aggyggcgtc cgcagcttcc 120 ccactccacg ttccgtgttt ccgactccgg tgactccacc accagcaacc cgtgcagcga gegeacteeg accategeea tgtegaggeg eggegaetgg gtetaegaga acaaeggegg 180 gacctgcgtg gccatcgccg gcgctgatta ctgtgtcgtc gctgcggaca cccgcctctc 240 300 tgtaggatac agtatcctca cgcgtgatca ctccaagatc tgcgacctgg ctgacaaatg 360 tgtactggca tcttctggct ttcaaggtga tattaaggct ctgcagaaga acctagctgc cagagaattg ctgtaccaac accagcataa taaaaggatg agctgccccg ccatggcaca 420 gctcctctcc aataccctgt actacaagcg attcttccca tattacgcct tcaatgtgct 480 cggtgggctt nacagcgakg ggaaaggatg cgttttc

- (2) INFORMATION FOR SEQ ID NO:1533:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..172
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598319
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

Arg Pro Lys Lys Gly Ser Arg Trp Glu Xaa Gln Asn Thr Arg Xaa Arg

1 10 15

10 15

Pro Gln Leu Pro His Ser Thr Phe Arg Val Ser Asp Ser Gly Asp Ser 20 25 30

Thr Thr Ser Asn Pro Cys Ser Glu Arg Thr Pro Thr Ile Ala Met Ser 35 40 45

Arg Arg Gly Asp Trp Val Tyr Glu Asn Asn Gly Gly Thr Cys Val Ala 50 55 60

Ile Ala Gly Ala Asp Tyr Cys Val Val Ala Ala Asp Thr Arg Leu Ser 65 70 75 80

Val Gly Tyr Ser Ile Leu Thr Arg Asp His Ser Lys Ile Cys Asp Leu 85 90 95

Ala Asp Lys Cys Val Leu Ala Ser Ser Gly Phe Gln Gly Asp Ile Lys
100 105 110

Ala Leu Gln Lys Asn Leu Ala Ala Arg Glu Leu Leu Tyr Gln His Gln
115 120 125

His Asn Lys Arg Met Ser Cys Pro Ala Met Ala Gln Leu Leu Ser Asn 130 135 140

Thr Leu Tyr Tyr Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn Val Leu 145 150 155 160

Gly Gly Leu Xaa Ser Xaa Gly Lys Gly Cys Val Phe 165 170

(2)	(i)	SEÇ (<i>P</i> (E (C	QUENC A) LE B) TY C) SI O) TO	E CH NGTH PE: RANI POLO	SEQ HARAC H: 12 amin DEDNE	TERI 6 am o ac SSS: line	STIC ino id ar	S:	ls							
			LECUI ATURE		PE:	pept	ide									
		(<i>F</i>	A) NA B) LO	ME/F	KEY:	11	.26									
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».«	(xi)) SEΩ	QUENC	CE DE	ESCRI Asp	PTIC	: N(C∈V	EQ J	D NC):15. Asn	34: Asn	Glv	Glv	Thr	Cvs	
1				5					10					15		
Val			20		Ala			25					30			
		35			Ser		40					45				
_	50				Cys	55					60					
Ile 65	Lys	Ala	Leu	Gln	Lys 70	Asn	Leu	Ala	Ala	Arg 75	Glu	Leu	Leu	Tyr	Gln 80	
His	Gln	His	Asn	Lys 85	Arg	Met	Ser	Cys	Pro 90	Ala	Met	Ala	Gln	Leu 95	Leu	
Ser	Asn	Thr	Leu 100		Tyr	Lys	Arg	Phe 105	Phe	Pro	Tyr	Tyr	Ala 110	Phe	Asn	
Val	Leu	Gly 115	Gly	Leu	Xaa	Ser	Xaa 120	Gly	Lys	Gly	Cys	Val 125	Phe			
(2)	(ii (ix) SE (((() MO () FE ((QUENA) L B) T C) S D) T LECU ATUR A) N B) L	CE C ENGT YPE: TRAN OPOL LE T E: AME/ OCAT	SEQ HARAGH: 1: nuc. DEDN: OGY: YPE: KEY: ION:	CTER 80 b leic ESS: lin DNA - 1 ORMA	ISTI ase aci sin ear (ge	CS: pair d gle nomi	c) Cere	s Se	eq. I	D 1 5	9832	.1		
aad	radat	att	cato	rtcct	ESCR gg c	atcc	gcac	a ga	.gttt	gttc	: cgt	ccag	gca	acca	aaaagc	60
at t	acco	acac	caco	rcada	iga a	gaag	agac	c ac	agga	ıggat	ngo	ıctcg	ŗtac	gaac	cagacc	120
gc:(2)					gag g R SEÇ					ıgcaç	g etc	gcca	ICCa	agge	ggcgag	100
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		i) M	OLEC	JLE :	rype:			€								
	•		(B) I	NAME, LOCA' DTHE!	/KEY: TION: R INE	: 1 FORM	.60 ATIO	N: /	Cere	es S	eq.	ID 1!	5983:	22		
	(x	i)_S	EQUE!	NCE	DESC	RIPT	: NOI	SEQ	ID 1	0:1	536:	e 17 =] Pr	0 90	r Ara	
1				5					10					TO	r Arg	
Gl			20					25					30		g Gly	
Gl	у Ха	a Al	a Ar	g Th	r Lys	s Gl	n Th	r Al	a Ar	g Ly	s Ph	e Hi	s Gl	y Ar	g Gln	

40 35 Gly Pro Pro Gln Ala Ala Arg His Gln Gly Gly Glu 55 (2) INFORMATION FOR SEQ ID NO:1537: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..59 (D) OTHER INFORMATION: / Ceres Seq. ID 1598323 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537: Thr Ala Ile Arg Val Leu Ala Ser Ala Glu Ser Leu Phe Arg Pro Gly 10 Asn Gln Lys Ala Leu Pro Arg Arg Ala Glu Lys Lys Arg Ala Glu Glu 25 20 Asp Xaa Leu Val Arg Ser Arg Pro Pro Ala Ser Ser Thr Gly Gly Lys 40 Ala Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala 55 (2) INFORMATION FOR SEQ ID NO:1538: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..59 (D) OTHER INFORMATION: / Ceres Seq. ID 1598324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538: Pro Leu Phe Val Ser Trp His Pro Gln Arg Val Cys Ser Val Gln Ala 10 Thr Lys Lys Arg Cys Pro Ala Ala Gln Arg Arg Glu Gln Arg Arg 20 25 Xaa Gly Ser Tyr Glu Ala Asp Arg Pro Gln Val Pro Arg Glu Ala Arg 40 35 Pro Pro Ala Ser Ser Ser Pro Pro Arg Arg 55 (2) INFORMATION FOR SEQ ID NO:1539: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..486 (D) OTHER INFORMATION: / Ceres Seq. ID 1598333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539: cttccaccac gcatcactcc cgggtcgccg ccgccgccgc cgccgccgcc gcgaaaaacc ctagcagget tegegetate acteetaggg gegegaceat ggtggeeaca aagaagaega agaaatccac ggacaacatc aacaacaagc tgcagcttgt tatgaagagt ggcaagtaca ctctcggcta caagaccgtc ctcaggactc tcaggaactc taagtcgaag ctagtgatca togotaataa otgooogooo ottogtaagt otgaaattga gtactatgot atgotggooa aggtcactgt ccaccacttc catagaaaca atgtctacct tggaactgcc tgtggtaaat actttcgggt ctgctgcctc agcattattg atcctggtga ttctgatatc atcaagacta caccgggtga gcagtaaaga agcccctgca gtagggggat cttactgcat ttgttcttct gtcttg

- (2) INFORMATION FOR SEQ ID NO:1540:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598334
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

Ser Thr Thr His His Ser Arg Val Ala Ala Ala Ala Ala Ala Ala Ala 10

Ala Lys Asn Pro Ser Arg Leu Arg Ala Ile Thr Pro Arg Gly Ala Thr 30 2.0 25

Met Val Ala Thr Lys Lys Thr Lys Lys Ser Thr Asp Asn Ile Asn Asn 45 40

Lys Leu Gln Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys 55

Thr Val Leu Arg Thr Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile 75 70

Ala Asn Asn Cys Pro Pro Leu Arg Lys Ser Glu Ile Glu Tyr Tyr Ala 90 8.5

Met Leu Ala Lys Val Thr Val His His Phe His Arg Asn Asn Val Tyr 105 110 100

Leu Gly Thr Ala Cys Gly Lys Tyr Phe Arg Val Cys Cys Leu Ser Ile 125 120 115

Ile Asp Pro Gly Asp Ser Asp Ile Ile Lys Thr Thr Pro Gly Glu Gln 135 130

- (2) INFORMATION FOR SEQ ID NO:1541:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598335
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

Met Val Ala Thr Lys Lys Thr Lys Lys Ser Thr Asp Asn Ile Asn Asn 10

Lys Leu Gln Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys 25

Thr Val Leu Arg Thr Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile 40

Ala Asn Asn Cys Pro Pro Leu Arg Lys Ser Glu Ile Glu Tyr Tyr Ala 55

Met Leu Ala Lys Val Thr Val His His Phe His Arg Asn Asn Val Tyr 75 70 Leu Gly Thr Ala Cys Gly Lys Tyr Phe Arg Val Cys Cys Leu Ser Ile

90

Ile Asp Pro Gly Asp Ser Asp Ile Ile Lys Thr Thr Pro Gly Glu Gln 105 100

(2) INFORMATION FOR SEQ ID NO:1542: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..91 (D) OTHER INFORMATION: / Ceres Seq. ID 1598336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542: Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Thr Val Leu Arg Thr 10 Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile Ala Asn Asn Cys Pro 30 25 20 Pro Leu Arg Lys Ser Glu Ile Glu Tyr Tyr Ala Met Leu Ala Lys Val 45 40 Thr Val His His Phe His Arg Asn Asn Val Tyr Leu Gly Thr Ala Cys 60 55 Gly Lys Tyr Phe Arg Val Cys Cys Leu Ser Ile Ile Asp Pro Gly Asp 75 70 Ser Asp Ile Ile Lys Thr Thr Pro Gly Glu Gln 85 (2) INFORMATION FOR SEQ ID NO:1543: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..460 (D) OTHER INFORMATION: / Ceres Seq. ID 1598414 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543: 60 agatccacaa caaatagcga aaccctagcy cawactcgac bkcctctgct ataagtagct ccactctctc tcctccaagc ytaccccagc ngccgccgcc gccaccgcca ccgccaccgy 120 yacytgenee agegegeege egeegeagee accatgggte gegteegeae caagacegtg 180 aagaagacct ccaggcaggt gatcgagaag tactactccc gcatgaccct cgacttccac 240 accaacaaga aggtgctgga ggaggtctcg attctgccct cgaagcgcct ccgcaacaag 300 gtggctggct tcagtaccca cctgatgcgc cgcatccagc gcggcccagt ccgcggcatc 360 tegeteaage tgeaggagga ggagegegas neggeatgga ettegtgeeg gagaagteeg 420 cgctcgaggt cgaagagatc cgcgtcgaca aggagaccat (2) INFORMATION FOR SEQ ID NO:1544: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..102 (D) OTHER INFORMATION: / Ceres Seq. ID 1598415 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544: Met Gly Arg Val Arg Thr Lys Thr Val Lys Lys Thr Ser Arg Gln Val

10

Ile Glu Lys Tyr Tyr Ser Arg Met Thr Leu Asp Phe His Thr Asn Lys

Client Docket No. 80146.003 20 25 Lys Val Leu Glu Glu Val Ser Ile Leu Pro Ser Lys Arg Leu Arg Asn 45 40 Lys Val Ala Gly Phe Ser Thr His Leu Met Arg Arg Ile Gln Arg Gly 55 Pro Val Arg Gly Ile Ser Leu Lys Leu Gln Glu Glu Glu Arg Xaa Xaa 70 75 Ala Trp Thr Ser Cys Arg Arg Ser Pro Arg Ser Arg Ser Lys Arg Ser 90 Ala Ser Thr Arg Arg Pro 100 (2) INFORMATION FOR SEQ ID NO:1545: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..79 (D) OTHER INFORMATION: / Ceres Seq. ID 1598416 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545: Met Thr Leu Asp Phe His Thr Asn Lys Lys Val Leu Glu Glu Val Ser 5 10 Ile Leu Pro Ser Lys Arg Leu Arg Asn Lys Val Ala Gly Phe Ser Thr 25 20 His Leu Met Arg Arg Ile Gln Arg Gly Pro Val Arg Gly Ile Ser Leu 40 Lys Leu Gln Glu Glu Glu Arg Xaa Xaa Ala Trp Thr Ser Cys Arg Arg 55 Ser Pro Arg Ser Arg Ser Lys Arg Ser Ala Ser Thr Arg Arg Pro 70 (2) INFORMATION FOR SEQ ID NO:1546: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 477 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..477 (D) OTHER INFORMATION: / Ceres Seq. ID 1598417 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546: 60 aggacacaat caagggctaa aagcactaca ggcccaaatt cagcccatac ccactctccc atccacgaga ccacaagcca caccaaaccc gcgttcatcg acggacgagc tcgccggcga gagagegact gagatggagg eggeggeasg geggeeggeg tggagetggg etettegaag ccccagatcg cgacgcaggc ggagatggcg gaggcccggg tgccgctcgc ctaccgcgac cagtgcgcgc acctcctcat cccgctcaac aagtgccgcg tcgccgagtt ctacctcccc tggaagtgcg agcccgagcg ccacgcctac gagaagtgcc agtacgagct cgtcatggag

120 180 240 300 360 420 cggatgctcc agatgcagaa gatccgcgag gcgcaggaga ccaaggtcaa gggcggcgct ccattggcct catcccggcc accgccaage tegectgata egggteccag eccgate

- (2) INFORMATION FOR SEQ ID NO:1547:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

Pro Thr Leu Pro Ser Thr Arg Pro Gln Ala Thr Pro Asn Pro Arg Ser 20 25 30

Ser Thr Asp Glu Leu Ala Gly Glu Arg Ala Thr Glu Met Glu Ala Ala 35 40 45

Ala Xaa Arg Pro Ala Trp Ser Trp Ala Leu Arg Ser Pro Arg Ser Arg 50 55 60

Arg Arg Arg Trp Arg Arg Pro Gly Cys Arg Ser Pro Thr Ala Thr 65 70 75 80

Ser Ala Arg Thr Ser Ser Ser Arg Ser Thr Ser Ala Ala Ser Pro Ser 85 90 95

Ser Thr Ser Pro Gly Ser Ala Ser Pro Ser Ala Thr Pro Thr Arg Ser 100 105 110

Ala Ser Thr Ser Ser Ser Trp Ser Gly Cys Ser Arg Cys Arg Arg Ser 115 120 125

Ala Arg Arg Arg Pro Arg Ser Arg Ala Ala Leu His Trp Pro His 130 135 140

Pro Gly His Arg Gln Ala Arg Leu Ile Arg Val Pro Ala Arg 145 150 155

- (2) INFORMATION FOR SEQ ID NO:1548:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598419
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

Met Glu Ala Ala Ala Xaa Arg Pro Ala Trp Ser Trp Ala Leu Arg Ser 1 10 15 15

Pro Arg Ser Arg Arg Arg Arg Trp Arg Arg Pro Gly Cys Arg Ser 20 25 30

Pro Thr Ala Thr Ser Ala Arg Thr Ser Ser Ser Arg Ser Thr Ser Ala 35 40 45

Ala Ser Pro Ser Ser Thr Ser Pro Gly Ser Ala Ser Pro Ser Ala Thr 50 55 60

Pro Thr Arg Ser Ala Ser Thr Ser Ser Ser Trp Ser Gly Cys Ser Arg 65 70 75 80

Cys Arg Arg Ser Ala Arg Arg Arg Pro Arg Ser Arg Ala Ala Leu 85 90 95 His Trp Pro His Pro Gly His Arg Gln Ala Arg Leu Ile Arg Val Pro

105

Ala Arq

(2) INFORMATION FOR SEQ ID NO:1549:

100

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met Ala Glu Ala Arg Val Pro Leu Ala Tyr Arg Asp Gln Cys Ala His

Leu Leu Ile Pro Leu Asn Lys Cys Arg Val Ala Glu Phe Tyr Leu Pro 20 25 30

Trp Lys Cys Glu Pro Glu Arg His Ala Tyr Glu Lys Cys Gln Tyr Glu 35 40 45

Leu Val Met Glu Arg Met Leu Gln Met Gln Lys Ile Arg Glu Ala Gln 50 55 60

Glu Thr Lys Val Lys Gly Gly Ala Pro Leu Ala Ser Ser Arg Pro Pro 65 70 75 80

Pro Ser Ser Pro Asp Thr Gly Pro Ser Pro Ile 85 90

- (2) INFORMATION FOR SEQ ID NO:1550:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..499
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550: agcgtcagac attccagtgc gtgcctggca agtggcaaac tcgagctgtc tagtcctcgg 60 ttcgcgaatc ttccacagag atgcagacgg caggactcgc ttcaagctcc tcatctcgcg 120 cagggggggt cgcctgagat cacagcgaca atggtgaagg cagttgctgt cctcgccggc 180 240 actgatgtca agggcaccat cttctttca caggaggggg atggtccgac caccgtgact ggaagtatet etggeeteaa geeagggete eatgggttee atgtgeaege gettggegae 300 accaccaacg gctgcatgtc gactgggcca cacttcaatc ctgttggcaa ggagcatggc 360 gcaccggaag atgaggaccg ccatgccggt gatcttggga atgtgacagc gggagaagat 420 ggtgttgtta atgtcaatat tactgacagc cagatacctc ttgctggacc ccactcgatc 480 attggccgag ctgttttgt
- (2) INFORMATION FOR SEQ ID NO:1551:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598426
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

Ser Val Arg His Ser Ser Ala Cys Leu Ala Ser Gly Lys Leu Glu Leu 1 5 10 15

Ser Ser Pro Arg Phe Ala Asn Leu Pro Gln Arg Cys Arg Arg Gln Asp

Ser Leu Gln Ala Pro His Leu Ala Gln Gly Gly Ser Pro Glu Ile Thr 35 40 45

Ala Thr Met Val Lys Ala Val Ala Val Leu Ala Gly Thr Asp Val Lys 50 55 60

Gly Thr Ile Phe Phe Ser Gln Glu Gly Asp Gly Pro Thr Thr Val Thr 65 70 75 80

Gly Ser Ile Ser Gly Leu Lys Pro Gly Leu His Gly Phe His Val His 85 90 95

Ala Leu Gly Asp Thr Thr Asn Gly Cys Met Ser Thr Gly Pro His Phe

105 100 Asn Pro Val Gly Lys Glu His Gly Ala Pro Glu Asp Glu Asp Arg His 120 115 Ala Gly Asp Leu Gly Asn Val Thr Ala Gly Glu Asp Gly Val Val Asn 135 140 Val Asn Ile Thr Asp Ser Gln Ile Pro Leu Ala Gly Pro His Ser Ile 150 155 Ile Gly Arg Ala Val Leu 165 (2) INFORMATION FOR SEQ ID NO:1552: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..116 (D) OTHER INFORMATION: / Ceres Seq. ID 1598427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552: Met Val Lys Ala Val Ala Val Leu Ala Gly Thr Asp Val Lys Gly Thr 10 Ile Phe Phe Ser Gln Glu Gly Asp Gly Pro Thr Thr Val Thr Gly Ser Ile Ser Gly Leu Lys Pro Gly Leu His Gly Phe His Val His Ala Leu 40 Gly Asp Thr Thr Asn Gly Cys Met Ser Thr Gly Pro His Phe Asn Pro 55 Val Gly Lys Glu His Gly Ala Pro Glu Asp Glu Asp Arg His Ala Gly 7.0 Asp Leu Gly Asn Val Thr Ala Gly Glu Asp Gly Val Val Asn Val Asn 90 8.5 Ile Thr Asp Ser Gln Ile Pro Leu Ala Gly Pro His Ser Ile Ile Gly 105 100 Arg Ala Val Leu 115 (2) INFORMATION FOR SEQ ID NO:1553: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..472 (D) OTHER INFORMATION: / Ceres Seq. ID 1598452 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553: agegetttee tgteegacte ecageegteg tetgetgegt acteegeete eaatttggte tgtttcttgc aagttgctct tgcggtagtt cccccwactg tcaccatgca gaacgaggag 120 ggtaagactg tggacctcta tgttcccagg aagtgctcgg ccacanacag gatcatcact 180 240 qccaaqqacc atgcctctgt ccagatcaac attggccact tggatgcgaa tggcctgtat 300 gatggtcact tcacaacatt tgctctctct gggtttgtcc gtgctcaggg cgatgcagac 360 agctccttgg acaggctgtg gcagaagaag aaggctgata tcaagcagta gattttacat ctagtttacc aagaattgga cactgcctta gctatgtttt gaattcatgt cactatatgc 420 aatgttgtga tttcagctgg taccttaaat ctgaagattt agtatctttg tt (2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:
- Ser Ala Phe Leu Ser Asp Ser Gln Pro Ser Ser Ala Ala Tyr Ser Ala 1 5 10 15
- Ser Asn Leu Val Cys Phe Leu Gln Val Ala Leu Ala Val Val Pro Xaa 20 25 30
- Thr Val Thr Met Gln Asn Glu Glu Gly Lys Thr Val Asp Leu Tyr Val 35 40 45
- Pro Arg Lys Cys Ser Ala Thr Xaa Arg Ile Ile Thr Ala Lys Asp His 50 55
- Ala Ser Val Gln Ile Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr 65 70 75 80
- Asp Gly His Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln 85 90 95
- Gly Asp Ala Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala 100 105 110

Asp Ile Lys Gln 115

- (2) INFORMATION FOR SEQ ID NO:1555:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598454
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:
- Met Gln Asn Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg Lys 1 10 15
- Cys Ser Ala Thr Xaa Arg Ile Ile Thr Ala Lys Asp His Ala Ser Val 20 25 30
- Gln Ile Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly His
- Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp Ala 50 55 60
- Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile Lys 65 70 75 80
- (2) INFORMATION FOR SEQ ID NO:1556:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..74
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598455
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:
- Met Phe Pro Gly Ser Ala Arg Pro Xaa Thr Gly Ser Ser Leu Pro Arg

Client Docket No. 80146.003 5 10 Thr Met Pro Leu Ser Arg Ser Thr Leu Ala Thr Trp Met Arg Met Ala 25 Cys Met Met Val Thr Ser Gln His Leu Leu Ser Leu Gly Leu Ser Val 45 40 Leu Arg Ala Met Gln Thr Ala Pro Trp Thr Gly Cys Gly Arg Arg Arg 55 Arg Leu Ile Ser Ser Ser Arg Phe Tyr Ile 70 (2) INFORMATION FOR SEQ ID NO:1557: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 470 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..470
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557: akgaacccta gcgccccgcc cgttcctgcc gccgccgcag ccgccatcgc acggccatgg 60 gtatcgatct cgtagccggc ggccgcaaca agaagaccaa gcgcacggcg sccaagtccg 120 180 acgatgtcta cctcaagctc ctcgtcaagc tctaccgctt ccttgtgcgc aggacaaaga 240 gcaacttcaa cgccgtgatc ctcaagcgcc tcttcatgag caagaccaac cgcccgccgc 300 tctcgatgcg ccgcctcgtc aggttcatgg aggggaaggg tgatcagatc gccgtgattg tgggcaccgt gaccgacgac aagaggatca gcgaggtgcc ggcgatgaag gtctgcgcgc 360 tcaggttcac tgagacagcg agggccagga tcatcaatgc tggcggagac gcgtcctgct 420 gaccgcttag gtccttttgc atcttgtttc aactatctgc gctaagaaat
- (2) INFORMATION FOR SEQ ID NO:1558:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598457
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

Xaa Thr Leu Ala Pro Arg Pro Phe Leu Pro Pro Pro Gln Pro Pro Ser 10

His Gly His Gly Tyr Arg Ser Arg Ser Arg Pro Gln Gln Glu Asp 25

Gln Ala His Gly Xaa Gln Val Arg Arg Cys Leu Pro Gln Ala Pro Arg 40

Gln Ala Leu Pro Leu Pro Cys Ala Gln Asp Lys Glu Gln Leu Gln Arg 55 60 Arg Asp Pro Gln Ala Pro Leu His Glu Gln Asp Gln Pro Pro Ala Ala

75 70 Leu Asp Ala Pro Pro Arg Gln Val His Gly Gly Glu Gly 85

- (2) INFORMATION FOR SEQ ID NO:1559:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg 1 5 10 15

Thr Ala Xaa Lys Ser Asp Asp Val Tyr Leu Lys Leu Leu Val Lys Leu 20 25 30

Tyr Arg Phe Leu Val Arg Arg Thr Lys Ser Asn Phe Asn Ala Val Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Leu Ser Met 50 55 60

Arg Arg Leu Val Arg Phe Met Glu Gly Lys Gly Asp Gln Ile Ala Val 65 70 75 80

Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Ser Glu Val Pro Ala 85 90 95

Met Lys Val Cys Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile 100 105 110

Ile Asn Ala Gly Gly Asp Ala Ser Cys 115 120

- (2) INFORMATION FOR SEQ ID NO:1560:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..68
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598459
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

Met Ser Lys Thr Asn Arg Pro Pro Leu Ser Met Arg Arg Leu Val Arg 1 5 10 15

Phe Met Glu Gly Lys Gly Asp Gln Ile Ala Val Ile Val Gly Thr Val 20 25 30 Thr Asp Asp Lys Arg Ile Ser Glu Val Pro Ala Met Lys Val Cys Ala

35 40 45
Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Ile Asn Ala Gly Gly

Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Ile Ash Ala Gly Gl 50 55 60

Asp Ala Ser Cys

65

- (2) INFORMATION FOR SEQ ID NO:1561:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..235
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598463
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

taweceteae ceaeceaace tteggeagty cecatectet eteetgtggg egeteeetet 60 eeceegeece caaateateg egeeteeete geeaegeete ayagggeegg ttegegtasg 120 agaaakgaga aasgaaggag gggakgeggt ektegggega katgagegae teettetgee 180 eegaetgeaa gaageataeg gaggtggegt tegaeeaete ggeggkggae atggt

- (2) INFORMATION FOR SEQ ID NO:1562:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..54
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:
- Xaa Pro Ser Pro Thr Gln Pro Ser Ala Xaa Pro Ile Leu Ser Pro Val
 1
 5
 10
 15
- Gly Ala Pro Ser Pro Pro Pro Pro Asn His Arg Ala Ser Leu Ala Thr 20 25 30
- Pro Xaa Arg Ala Gly Ser Arg Xaa Arg Xaa Glu Lys Xaa Arg Arg Gly 35 40 45
- Xaa Gly Xaa Arg Ala Xaa 50
- (2) INFORMATION FOR SEQ ID NO:1563:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598465
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:
- Xaa Pro His Pro Pro Asn Leu Arg Gln Xaa Pro Ser Ser Leu Leu Trp 1 5 10 15
- Ala Leu Pro Leu Pro Arg Pro Gln Ile Ile Ala Pro Pro Ser Pro Arg 20 25 30
- Leu Xaa Gly Pro Val Arg Val Xaa Glu Xaa Arg Xaa Glu Gly Gly Xaa 35 40 45
- Ala Val Xaa Gly Arg Xaa Glu Arg Leu Leu Pro Arg Leu Gln Glu 50 55 60
- Ala Tyr Gly Gly Gly Val Arg Pro Leu Gly Xaa Gly His Gly 65 70 75
- (2) INFORMATION FOR SEQ ID NO:1564:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598466
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:
- Xaa Leu Thr His Pro Thr Phe Gly Ser Xaa His Pro Leu Ser Cys Gly
 1 5 10 15
- Arg Ser Leu Ser Pro Ala Pro Lys Ser Ser Arg Leu Pro Arg His Ala 20 25 30
- Ser Xaa Gly Arg Phe Ala Xaa Glu Lys Xaa Glu Xaa Lys Glu Gly Xaa 35 40 45
- Arg Xaa Ser Gly Xaa Met Ser Asp Ser Phe Cys Pro Asp Cys Lys Lys 50 55 60
- His Thr Glu Val Ala Phe Asp His Ser Ala Xaa Asp Met

180 240

300

360

420

- (2) INFORMATION FOR SEQ ID NO:1565: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 477 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..477 (D) OTHER INFORMATION: / Ceres Seq. ID 1598469 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565: aaactggctt acctcttcgg aaagggaaaa cgccaccaca cgcggatcga attaggctct ccgagtctcc ggttccctcc tctcggcggc ggctcaggtc cctctccatc tccggcgtgg cgcttggcgt ctgacctcaa caagcaagaa agcaaatggc aggcggcagg gttgcgcatg ccaccetcaa gggcccgagt gtggtgaagg agatetteat tggactgace etgggtetga tcgcgggagg catgtggaag atgcaccact ggaacgagca gaggaagact aggtccttct atgacatgct tgacaagggc cagatcagcg ttgtcgtcga ggagtaaaga gttcttccca gttattttca aagaactctc tcgagagcat gacaaagtga ttgcttgctg tggagatttg tcctggaaat aagcacaacc atttgggaac accagatttt gtcgaatttt cctttcc (2) INFORMATION FOR SEQ ID NO:1566: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..68 (D) OTHER INFORMATION: / Ceres Seq. ID 1598470 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566: Lys Leu Ala Tyr Leu Phe Gly Lys Gly Lys Arg His His Thr Arg Ile 10 Glu Leu Gly Ser Pro Ser Leu Arg Phe Pro Pro Leu Gly Gly Ser 20 25 Gly Pro Ser Pro Ser Pro Ala Trp Arg Leu Ala Ser Asp Leu Asn Lys 40 Gln Glu Ser Lys Trp Gln Ala Ala Gly Leu Arg Met Pro Pro Ser Arg 55 Ala Arg Val Trp (2) INFORMATION FOR SEQ ID NO:1567: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..63 (D) OTHER INFORMATION: / Ceres Seq. ID 1598471 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:
- Met Ala Gly Gly Arg Val Ala His Ala Thr Leu Lys Gly Pro Ser Val 10 Val Lys Glu Ile Phe Ile Gly Leu Thr Leu Gly Leu Ile Ala Gly Gly 25 30 Met Trp Lys Met His His Trp Asn Glu Gln Arg Lys Thr Arg Ser Phe 35 40

Tyr Asp Met Leu Asp Lys Gly Gln Ile Ser Val Val Glu Glu

60 50 55 (2) INFORMATION FOR SEQ ID NO:1568: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1598472 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568: Met Thr Cys Leu Thr Arg Ala Arg Ser Ala Leu Ser Ser Arg Ser Lys 5 10 Glu Phe Phe Pro Val Ile Phe Lys Glu Leu Ser Arg Glu His Asp Lys 25 Val Ile Ala Cys Cys Gly Asp Leu Ser Trp Lys 35 40 (2) INFORMATION FOR SEQ ID NO:1569: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..333 (D) OTHER INFORMATION: / Ceres Seq. ID 1598480 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569: aaaccaggaa agcaaagygs tttcgcaagc acaggcagtg atcggcaacc aaatccggac 60 120 agtettgage tetetcagte teageattte agtteecaga tteacatage eccageecea caagtagcga aatggcagct gctccgttcg cgattgcygg ccggctctcc cccgttgcgc 180 gcctcccggt ccgcgcctgg aggccggcgc acgggtttgc gtcgtccggg agagcccgct 240 cgctcgccgt ggcgtccgcg gcgcaggaga acagggacaa cagtgtcgac gtacaggtta 300 gccagaacgg cggcaacagg cagcagggca acg (2) INFORMATION FOR SEQ ID NO:1570: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..111 (D) OTHER INFORMATION: / Ceres Seq. ID 1598481 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570: Lys Pro Gly Lys Gln Xaa Xaa Phe Ala Ser Thr Gly Ser Asp Arg Gln 10 Pro Asn Pro Asp Ser Leu Glu Leu Ser Gln Ser Gln His Phe Ser Ser 20 25 Gln Ile His Ile Ala Pro Ala Pro Gln Val Ala Lys Trp Gln Leu Leu 40 Arg Ser Arg Leu Xaa Ala Gly Ser Pro Pro Leu Arg Ala Ser Arg Ser 55 Ala Pro Gly Gly Arg Arg Thr Gly Leu Arg Arg Pro Gly Glu Pro Ala 70 75 Arg Ser Pro Trp Arg Pro Arg Arg Arg Thr Gly Thr Thr Val Ser 90

Thr Tyr Arg Leu Ala Arg Thr Ala Ala Thr Gly Ser Arg Ala Thr 105 100 (2) INFORMATION FOR SEQ ID NO:1571: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..67 (D) OTHER INFORMATION: / Ceres Seq. ID 1598482 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571: Met Ala Ala Pro Phe Ala Ile Xaa Gly Arg Leu Ser Pro Val Ala 10 Arg Leu Pro Val Arg Ala Trp Arg Pro Ala His Gly Phe Ala Ser Ser 30 25 Gly Arg Ala Arg Ser Leu Ala Val Ala Ser Ala Ala Gln Glu Asn Arg 45 40 Asp Asn Ser Val Asp Val Gln Val Ser Gln Asn Gly Gly Asn Arg Gln 55 50 Gln Gly Asn (2) INFORMATION FOR SEQ ID NO:1572: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 493 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..493 (D) OTHER INFORMATION: / Ceres Seq. ID 1598487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572: 60 ctctcgagcc tgacccttac gccttcgctc gcnccgccgc cgccgccgcc gctacgcccc 120 qcacctcqct tcatttcqtq tcqccaagat gacgaagcgc actaagaagg caggaattgt tggcaaatat ggaaccaggt atggtgctag cttgcgtaas aatcaagaag atggaggtat 180 ctcagcattc caagtacttt tgcgagttct gtgggaagtt tgctgtgaag aggaaagcag 240 ttggaatttg ggggtgcaag gactgtggga aggtgaaggc tggtggtgct tacaccatga 300 acactgctag tgcggtggtc gtggaggcta cggcggcggt gggggatacg gtggtgcaaa 360 ccgcggcggc gtctacggca acaacgacgg gaactggagg aactnagcgg tggggtccgc 420 tgaggcctag ttatcttgtt tcgcttctgc taccgtgttc accctagtct agagggggtt 480 tatcttcgtc tgt (2) INFORMATION FOR SEQ ID NO:1573: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..112 (D) OTHER INFORMATION: / Ceres Seq. ID 1598488 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

Met Glu Pro Gly Met Val Leu Ala Cys Val Xaa Ile Lys Lys Met Glu

1 5 10 15

Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala
20 25 30

 Val
 Lys
 Arg
 Lys
 Ala
 Val
 Gly
 Ile
 Trp
 Gly
 Cys
 Lys
 Asp
 Cys
 Gly
 Lys

 Val
 Lys
 Ala
 Gly
 Gly
 Ala
 Tyr
 Thr
 Met
 Asp
 Thr
 Ala
 Ser
 Ala
 Val
 Val

 Val
 Gly
 Ala
 Ala
 Val
 Gly
 Asp
 Thr
 Val
 Gly
 Thr
 Ala
 Ala
 Ala

 Ala
 Ser
 Thr
 Ala
 Thr
 Thr
 Gly
 Thr
 Val
 Val
 Gly
 Thr
 Ala
 Ala
 Ala

 Ala
 Ser
 Thr
 Ala
 Thr
 Thr
 Gly
 Thr
 Val
 Gly
 Thr
 Xaa
 Arg
 Trp
 Gly

 Ala
 Ser
 Thr
 Thr
 Thr
 Thr
 Gly
 Thr
 Thr
 Xaa
 Arg
 Trp
 Gly

 Pro
 Leu
 Arg
 Pro
 Ser
 Tyr
 Leu
 Val
 Ser
 Leu
 Leu
 L

- (2) INFORMATION FOR SEQ ID NO:1574:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

Met Val Leu Ala Cys Val Xaa Ile Lys Lys Met Glu Val Ser Gln His

Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Arg Lys 20 25 30

Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys Ala Gly 35 40

Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Val Glu Ala Thr 50 55 60

Ala Ala Val Gly Asp Thr Val Val Gln Thr Ala Ala Ala Ser Thr Ala 65 70 75 80

Thr Thr Gly Thr Gly Gly Thr Xaa Arg Trp Gly Pro Leu Arg Pro 85 90 95

Ser Tyr Leu Val Ser Leu Leu Leu Pro Cys Ser Pro 100 105

- (2) INFORMATION FOR SEQ ID NO:1575:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598490
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys

Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys
20 25 30

Gly Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala 35 40 45

Val Val Val Glu Ala Thr Ala Ala Val Gly Asp Thr Val Val Gln Thr
50 55 60

Ala Ala Ala Ser Thr Ala Thr Thr Thr Gly Thr Gly Gly Thr Xaa Arg 65 70 75 80

Trp Gly Pro Leu Arg Pro Ser Tyr Leu Val Ser Leu Leu Pro Cys

85 90 95

Ser Pro

- (2) INFORMATION FOR SEQ ID NO:1576:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..486
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598509
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

aaaagagcca gtccctgcgt ttccttactt cctggtaaag aaagaagcga mrcaggtact tgttgttgag cgcggagaga ggagaggcgc agagcatcga cgatggcgag cggcacatga 120 agaggagat cagcgagacc cacgacaccc tccgcttcgg cctcaatgcc ggcgtcaagg 180 ccgacctcgc kccgccgcac ccgctccagt ccagcatcca atcggaggcc aagttctggg 240 cggacaagaa gaagtttggg acagaggcca tctacggatc cgccttgaac atccgcaaga 300 tctcgatgcc caaatcctct caaggttcca aaggccccct ggtgctttgc catcatctct 360 gcttggatat gaggcactga caggttccct agatgatttt ggttttgaag attatcttaa 420 catgcctcaa gattctgaag gtttccgtca acctgacatg caccacggaa tggaggttcg 480 ccttgg

- (2) INFORMATION FOR SEQ ID NO:1577:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598510
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

Lys Glu Pro Val Pro Ala Phe Pro Tyr Phe Leu Val Lys Lys Glu Ala 1 5 10 15

Xaa Gl
n Val Leu Val Val Glu Arg Gly Glu Arg Arg Gly Ala Glu His
 $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30 \hspace{1.5cm}$

Arg Arg Trp Arg Ala Ala His Glu Glu Gly Asp Gln Arg Asp Pro Arg 35 40 45

His Pro Pro Leu Arg Pro Gln Cys Arg Arg Gln Gly Arg Pro Arg Xaa 50 55 60
Ala Ala Pro Ala Pro Val Gln His Pro Ile Gly Gly Gln Val Leu Gly

65 70 75 80

Gly Gln Glu Val Trp Asp Arg Gly His Leu Arg Ile Arg Leu Glu 85 90 95 His Pro Gln Asp Leu Asp Ala Gln Ile Leu Ser Arg Phe Gln Arg Pro

100 105 110
Pro Gly Ala Leu Pro Ser Ser Leu Leu Gly Tyr Glu Ala Leu Thr Gly

115 120 125

Ser Leu Asp Asp Phe Gly Phe Glu Asp Tyr Leu Asn Met Pro Gln Asp

130 135 140
Ser Glu Gly Phe Arg Gln Pro Asp Met His His Gly Met Glu Val Arg

145 150 155 160 Leu

- (2) INFORMATION FOR SEQ ID NO:1578:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids

(C) STRANDEDNESS:

(B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..87 (D) OTHER INFORMATION: / Ceres Seq. ID 1598511 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578: Met Lys Arg Glu Ile Ser Glu Thr His Asp Thr Leu Arg Phe Gly Leu 10 Asn Ala Gly Val Lys Ala Asp Leu Xaa Pro Pro His Pro Leu Gln Ser 20 25 Ser Ile Gln Ser Glu Ala Lys Phe Trp Ala Asp Lys Lys Phe Gly 40 Thr Glu Ala Ile Tyr Gly Ser Ala Leu Asn Ile Arg Lys Ile Ser Met 55 60 Pro Lys Ser Ser Gln Gly Ser Lys Gly Pro Leu Val Leu Cys His His 70 Leu Cys Leu Asp Met Arg His 85 (2) INFORMATION FOR SEQ ID NO:1579: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..242 (D) OTHER INFORMATION: / Ceres Seq. ID 1598512 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579: atctttttt cgactttcga gcgcagaaac gagagggccg gagcagccgc agtcccggcg 60 120 atcocgccgc cggtcgccct catacttcct cgtcactgcc ttcgtttctc tttccaacaa 180 tcaabatgag ccgtggcgnt acgcgggtgg tggtcaaagt tctctgggtt acctctttgg aagcsgtgag ccccccaaac cagcagtggc accagctgta agtgctccac ctgctgctgc 240 (2) INFORMATION FOR SEQ ID NO:1580: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..42 (D) OTHER INFORMATION: / Ceres Seq. ID 1598513 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580: Ile Phe Phe Ser Thr Phe Glu Arg Arg Asn Glu Arg Ala Gly Ala Ala 10 Ala Val Pro Ala Ile Pro Pro Pro Val Ala Leu Ile Leu Pro Arg His 20 25 Cys Leu Arg Phe Ser Phe Gln Gln Ser Xaa (2) INFORMATION FOR SEQ ID NO:1581: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 80 amino acids (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598514
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

Ser Phe Phe Arg Leu Ser Ser Ala Glu Thr Arg Gly Pro Glu Gln Pro 1 10 15

Gln Ser Arg Arg Ser Arg Arg Ser Pro Ser Tyr Phe Leu Val Thr 20 25 30

Gly Gly Gln Ser Ser Leu Gly Tyr Leu Phe Gly Ser Xaa Glu Pro 50 55 60

Pro Lys Pro Ala Val Ala Pro Ala Val Ser Ala Pro Pro Ala Ala Ala 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:1582:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..72
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598515
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

Leu Phe Phe Asp Phe Arg Ala Gln Lys Arg Glu Gly Arg Ser Ser Arg

10 15

Ser Pro Gly Asp Pro Ala Ala Gly Arg Pro His Thr Ser Ser Leu 20 25 30

Pro Ser Phe Leu Phe Pro Thr Ile Xaa Met Ser Arg Gly Xaa Thr Arg 35 40 45

Val Val Val Lys Val Leu Trp Val Thr Ser Leu Glu Xaa Val Ser Pro 50 55 60

Pro Asn Gln Gln Trp His Gln Leu 65 70

- (2) INFORMATION FOR SEQ ID NO:1583:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

tttt

- (A) NAME/KEY: -
- (B) LOCATION: 1..424
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

ctagacgcac ccettcetcg tttegeegee teegeegaea cegaetgeet aceteagetg 60 cegtegeeat gggeagaagg etgetagatg etategeeag ateaagaaca agecatacee 120 taagteeagg tactgeegg gtgteeetga eeceaagate aggatetaeg atgttgggat 180 gaagaggaag ggtgttgatg agtteeeta ttgtgtgeae ettgtetett gggagaagga 240 gaatgtetee agtgaggege ttgaggetge eegeattgee tgeaacaagt acatgaceaa 300 gtetgeagga aaggatgett teeacettag ggteegggtt eacegtteea tgteeteegt 360 ateaacaaga tgetttegtg tgetggget gataggetee agaetggaat taggggtgee 420

- Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:1584: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..59 (D) OTHER INFORMATION: / Ceres Seq. ID 1598517 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584: Arg Arg Thr Pro Ser Ser Phe Arg Arg Leu Arg Arg His Arg Leu Pro 1.0 5 Thr Ser Ala Ala Val Ala Met Gly Arg Arg Leu Leu Asp Ala Ile Ala 30 25 20 Arg Ser Arg Thr Ser His Thr Leu Ser Pro Gly Thr Ala Val Val Ser 40 Leu Thr Pro Arg Ser Gly Ser Thr Met Leu Gly 55 (2) INFORMATION FOR SEQ ID NO:1585: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..82 (D) OTHER INFORMATION: / Ceres Seq. ID 1598518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585: Met Lys Arg Lys Gly Val Asp Glu Phe Pro Tyr Cys Val His Leu Val 10 Ser Trp Glu Lys Glu Asn Val Ser Ser Glu Ala Leu Glu Ala Ala Arg 25 20 Ile Ala Cys Asn Lys Tyr Met Thr Lys Ser Ala Gly Lys Asp Ala Phe 45 40 35 His Leu Arg Val Arg Val His Arg Ser Met Ser Ser Val Ser Thr Arg 60 55 Cys Phe Arg Val Leu Gly Leu Ile Gly Ser Arg Leu Glu Leu Gly Val 70 65 Pro Phe (2) INFORMATION FOR SEQ ID NO:1586: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..44 (D) OTHER INFORMATION: / Ceres Seq. ID 1598519 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:
 - Met Thr Lys Ser Ala Gly Lys Asp Ala Phe His Leu Arg Val Arg Val 10 His Arg Ser Met Ser Ser Val Ser Thr Arg Cys Phe Arg Val Leu Gly 25 Leu Ile Gly Ser Arg Leu Glu Leu Gly Val Pro Phe

60

120

180

240

300 360

420

480

160

40 35 (2) INFORMATION FOR SEQ ID NO:1587: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 509 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..509 (D) OTHER INFORMATION: / Ceres Seq. ID 1598528 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587: tccaccagcg gcatctatag caaccggtcc agcactttca cgctcagctc cagcaatggc tgcctccacc atggcgatct cctccacggc gatggccggc acccccatca aggtgggctc cttcggcgag ggccgcatca ccatgcgcaa gaccgtgggc aagcccaagg tggcggcgtc cggcagcccc tggtacggcc ccgaccgcgt caagtacctc ggccccttct ccggcgagcc cccgagctac ctcaccggcg agttccccgg cgactacggc tgggacaccg ccgggctgtc cgccgacccc gagaccttcg ccaagaaccg cgagctggag gtgatccact cccgctgggc catgctcggc gcgctcggct gcgtcttccc cgagctgctc tcccgcaacg gcgtcaagtt cggcgaggcc gtctggttca aggccggctc ccagatcttc agcgagggcg ggctggacta cctcggcaac cccagcctga tccacgcgc (2) INFORMATION FOR SEQ ID NO:1588: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..169 (D) OTHER INFORMATION: / Ceres Seq. ID 1598529 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588: Ser Thr Ser Gly Ile Tyr Ser Asn Arg Ser Ser Thr Phe Thr Leu Ser 10 Ser Ser Asn Gly Cys Leu His His Gly Asp Leu Leu His Gly Asp Gly 25 Arg His Pro His Gln Gly Gly Leu Leu Arg Arg Gly Pro His His His 40 Ala Gln Asp Arg Gly Gln Ala Gln Gly Gly Gly Val Arg Gln Pro Leu 60 55 Val Arg Pro Arg Pro Arg Gln Val Pro Arg Pro Leu Leu Arg Arg Ala 75 70 Pro Glu Leu Pro His Arg Arg Val Pro Arg Arg Leu Arg Leu Gly His 90 85 Arg Arg Ala Val Arg Arg Pro Arg Asp Leu Arg Gln Glu Pro Arg Ala 110 105 100 Gly Gly Asp Pro Leu Pro Leu Gly His Ala Arg Arg Ala Arg Leu Arg 125 120 115 Leu Pro Arg Ala Ala Leu Pro Gln Arg Arg Gln Val Arg Arg Gly Arg 140 135 Leu Val Gln Gly Arg Leu Pro Asp Leu Gln Arg Gly Arg Ala Gly Leu

155

165
(2) INFORMATION FOR SEQ ID NO:1589:

Pro Arg Gln Pro Gln Pro Asp Pro Arg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..169
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:
- Pro Pro Ala Ala Ser Ile Ala Thr Gly Pro Ala Leu Ser Arg Ser Ala 1 5 10 15
- Pro Ala Met Ala Ser Thr Met Ala Ile Ser Ser Thr Ala Met Ala 20 25 30
- Gly Thr Pro Ile Lys Val Gly Ser Phe Gly Glu Gly Arg Ile Thr Met 35 40 45
- Arg Lys Thr Val Gly Lys Pro Lys Val Ala Ala Ser Gly Ser Pro Trp 50 55 60
- Tyr Gly Pro Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly Glu Pro 65 70 75 80
- Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp Asp Thr 85 90 95
- Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg Glu Leu 100 105 110
- Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly Cys Val 115 120 125
- Phe Pro Glu Leu Leu Ser Arg Asn Gly Val Lys Phe Gly Glu Ala Val 130 135 140
- Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu Asp Tyr 145 150 155 160
- Leu Gly Asn Pro Ser Leu Ile His Ala 165
- (2) INFORMATION FOR SEQ ID NO:1590:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..151
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598531
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:
- Met Ala Ala Ser Thr Met Ala Ile Ser Ser Thr Ala Met Ala Gly Thr
- Pro Ile Lys Val Gly Ser Phe Gly Glu Gly Arg Ile Thr Met Arg Lys 20 25 30
- Thr Val Gly Lys Pro Lys Val Ala Ala Ser Gly Ser Pro Trp Tyr Gly 35 40 45
- Pro Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly Glu Pro Pro Ser 50 55 60

 Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp Asp Thr Ala Gly
- 65 70 75 80
 Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg Glu Leu Glu Val
- 85 90 95

 Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly Cys Val Phe Pro
- 100 105 110
 Glu Leu Leu Ser Arg Asn Gly Val Lys Phe Gly Glu Ala Val Trp Phe
- 115 120 125 Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu Asp Tyr Leu Gly
- 130 135 Asn Pro Ser Leu Ile His Ala
- 145 150

- (2) INFORMATION FOR SEQ ID NO:1591:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..481
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598535
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

 accecttaaa ceetegteaa aacegetget cactgaatat tteeatttt accettteet 60

 cgeecetaee eegecaeeg eegecgeegt egecgeagee atggegtege ggegetgtet 120

 ceteegette etetegatee geetegttee teagagatet caacetettg egecgatete 180

 gaetgegaee eggaceetaa eetetttyte egaggeeete ggeteeeag eteeeggge 240

 cetegeetee eeeeggetgt actaceeete gegetgeeae ttegegaeee geteeteegg 300

 cgaegaggae gaeggagaag acgaagaaga geactaegae gatgaggga gegatggga 360

 atgggggae gatgaggag tggtggegge gaagaaaeeg agegggaaga eegaagaga 420

 gaaggtageg gaggegggg agateggeta caaggtyttg ggaeegeteg aggetgaega 480
- (2) INFORMATION FOR SEQ ID NO:1592:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598536
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592: Pro Leu Lys Pro Ser Ser Lys Pro Leu Leu Thr Glu Tyr Phe His Phe
- 1 5 10 15 Tyr Pro Phe Leu Ala Pro Thr Pro Ala Thr Ala Ala Ala Val Ala Ala 20 25 30
- Ala Met Ala Ser Arg Arg Cys Leu Leu Arg Phe Leu Ser Ile Arg Leu
 35 40 45
- Val Pro Gln Arg Ser Gln Pro Leu Ala Pro Ile Ser Thr Ala Thr Arg
 50 55 60
- Thr Leu Thr Ser Leu Ser Glu Ala Leu Gly Ser Pro Ala Pro Arg Ala 65 70 75 80
- Leu Ala Ser Pro Arg Leu Tyr Tyr Pro Ser Arg Cys His Phe Ala Thr 85 90 95
- Arg Ser Ser Gly Asp Glu Asp Gly Glu Asp Glu Glu His Tyr
 100 105 110
- Asp Asp Glu Gly Ser Asp Gly Glu Trp Gly Asp Asp Glu Glu Val Val 115 120 125
- Ala Ala Lys Lys Pro Ser Gly Lys Thr Glu Glu Glu Lys Val Ala Glu 130 135 140
- Ala Ala Glu Ile Gly Tyr Lys Val Leu Gly Pro Leu Glu Ala Asp Asp 145 150 155
- (2) INFORMATION FOR SEQ ID NO:1593:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..127 (D) OTHER INFORMATION: / Ceres Seq. ID 1598537 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593: Met Ala Ser Arg Arg Cys Leu Leu Arg Phe Leu Ser Ile Arg Leu Val 10 Pro Gln Arg Ser Gln Pro Leu Ala Pro Ile Ser Thr Ala Thr Arg Thr 25 20 Leu Thr Ser Leu Ser Glu Ala Leu Gly Ser Pro Ala Pro Arg Ala Leu 45 40 Ala Ser Pro Arg Leu Tyr Tyr Pro Ser Arg Cys His Phe Ala Thr Arg 60 55 Ser Ser Gly Asp Glu Asp Asp Gly Glu Asp Glu Glu Glu His Tyr Asp 75 70 Asp Glu Gly Ser Asp Gly Glu Trp Gly Asp Asp Glu Glu Val Val Ala 90 85 Ala Lys Lys Pro Ser Gly Lys Thr Glu Glu Glu Lys Val Ala Glu Ala 110 105 100 Ala Glu Ile Gly Tyr Lys Val Leu Gly Pro Leu Glu Ala Asp Asp 120 115 (2) INFORMATION FOR SEQ ID NO:1594: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 473 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..473 (D) OTHER INFORMATION: / Ceres Seq. ID 1598551 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594: ctttttctcg agcctgaccc ttacgccttc gctcgcgccg ccgccgccgc cgccgctacg 60 ccccgcacct cgcttcattt cgtgtcgcca agatgacgaa gcgcactaag aaggcaggaa 120 ttgttggcaa atatggaacc aggtatggtg ctagcttgcg taasaaaatc aagaagatgg 180 aggtatetea geatteeaag taettttgeg agttetgtgg gaagtttget gtgaagagga 240 aagcagttgg aatttggggg tgcaaggact gtgggaaggt gaaggctggt ggtgcttaca 300 ccatgaacac tgctagtgcg gtcaccgtca gagcacgatc cgccgcctga gggagcagac 360 tgaagcatga tatagctctt tatattattg gggtttcctg tagttgctct tgtcaggcat 420 gttgtggggg ccttatctag tggaaatgtg gaatcactgt actggctgtt ttg (2) INFORMATION FOR SEQ ID NO:1595: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..85 (D) OTHER INFORMATION: / Ceres Seq. ID 1598552 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595: Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 10 Arg Tyr Gly Ala Ser Leu Arg Xaa Lys Ile Lys Lys Met Glu Val Ser 30 25 20 Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys 40 Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys

60 50 55 Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Val Arg 75 70 Ala Arg Ser Ala Ala 85 (2) INFORMATION FOR SEQ ID NO:1596: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..57 (D) OTHER INFORMATION: / Ceres Seq. ID 1598553 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596: Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys 10 Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys 30 25 Gly Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala 40 Val Thr Val Arg Ala Arg Ser Ala Ala 55 50 (2) INFORMATION FOR SEQ ID NO:1597: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 507 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..507 (D) OTHER INFORMATION: / Ceres Seq. ID 1598560 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597: acgecteaaa tegeteeetg cetetgeeet etggteacet egetteeget eeeggeteee 60 ctccggccac ccagacatcg tccgttcgct cgccaagaga caggaccgga gaccatggcg 120 gaccagetea ecgaegacea gategeegag tteaaggagg cetteageet ettegaeaag 180 240 gacggcgacg gttgcatcac aaccaaggag ctcggaactg tcatgcgatc actgggtcag 300 aacccaaccg aggctgagct ccaggacatg atcaacgagg tcgatgcgga cggcaacggc 360 accatcgact teccggagtt ceteaaeete atggeeegta agatgaagga caeegaetee gaggaggagc tcaaggaggc gttcagggtg ttcgacaagg accagaacgg cttcatctct 420 480 geggeggast cegeacgtga tgaccaacet eggegagaag etgacegaeg aggaggtega tgagatgatc cgcgagccga cgtcgat (2) INFORMATION FOR SEQ ID NO:1598: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1598561 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598: Thr Pro Gln Ile Ala Pro Cys Leu Cys Pro Leu Val Thr Ser Leu Pro

10

Leu Pro Ala Pro Leu Arg Pro Pro Arg His Arg Pro Phe Ala Arg Gln

20 25 Glu Thr Gly Pro Glu Thr Met Ala Asp Gln Leu Thr Asp Asp Gln Ile 35 40 Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln 75 70 Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala 90 8.5 Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala 100 105 110 Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe 120 125 115 Arg Val Phe Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Xaa Ser 140 130 135 Ala Arg Asp Asp Gln Pro Arg Arg Glu Ala Asp Arg Arg Gly Gly Arg 150

- (2) INFORMATION FOR SEQ ID NO:1599:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

Arg Leu Lys Ser Leu Pro Ala Ser Ala Leu Trp Ser Pro Arg Phe Arg 1 5 10 15

Ser Arg Leu Pro Ser Gly His Pro Asp Ile Val Arg Ser Leu Ala Lys 20 25 30

Arg Gln Asp Arg Arg Pro Trp Arg Thr Ser Ser Pro Thr Thr Arg Ser

Pro Ser Ser Arg Arg Pro Ser Ala Ser Ser Thr Arg Thr Ala Thr Val 50 55 60

Ala Ser Gln Pro Arg Ser Ser Glu Leu Ser Cys Asp His Trp Val Arg
65 70 75 80

Thr Gln Pro Arg Leu Ser Ser Arg Thr 85

- (2) INFORMATION FOR SEQ ID NO:1600:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598563
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala
1 5 10 15

Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu 20 25 30

Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu

60

120

180

240

300

360 420

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LeuGlnAspMetIleAspGluValAspAlaAspGlyAspGlyThrIleAspPheProGluPheLeuAspLeuMetAlaArgLysMetLysAspThrAspSerGluGluLeuLysGluAlaPheArgValPheAspLysAspGlnAspGluPheIleSerAlaAlaXaaSerAlaArgAspAspAspGluPro105LysAspAspAspIleProIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIl
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Arg Arg Glu Ala Asp Arg Arg Gly Gly Arg 115 120

- (2) INFORMATION FOR SEQ ID NO:1601:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..478
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

 gtttatetet tetteeaetg cetececaee acttegteet egeeggeteg caacteettg atggeggea eggegagtet cactaceaet geteceteee etceagetet ecteaaagea teageteett tgettatete etttegeeee gteteeegee actgeaagaa ectgegeate eagaaceaagg ceacagaaaa tgateagtet getaaaaage ateagaaggt gaaagageatt etttgeeagg actgegaagg aaatggggea ategtatgea ecaaatgtga aggaaatggg gtaaateetg ttgaetattt tgaaggeega tttaaagetg gatetttatg etggttgtge agaggeaage gtgaaateet atgtgggaae tgtaatggtg etggettett gggtggattt etaageactt tegatgaaae tgegeaatag teateggttt ageacttteg atgaaagt (2) INFORMATION FOR SEQ ID NO:1602:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..149
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598565
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

Arg Asn Ser Leu Met Ala Ala Thr Ala Ser Leu Thr Thr Thr Ala Pro
20 25 30

Ser Pro Pro Ala Leu Leu Lys Ala Ser Ala Pro Leu Leu Ile Ser Phe 35 40 45

Arg Pro Val Ser Arg His Cys Lys Asn Leu Cys Ile Lys Thr Lys Ala
50 55 60

Thr Glu Asn Asp Gln Ser Ala Lys Lys His Gln Lys Val Lys Ser Ile 65 70 75 80
Leu Cys Gln Asp Cys Glu Gly Asn Gly Ala Ile Val Cys Thr Lys Cys

85 90 95
Glu Gly Asn Gly Val Asn Ser Val Asp Tyr Phe Glu Gly Arg Phe Lys
100 105 110

Ala Gly Ser Leu Cys Trp Leu Cys Arg Gly Lys Arg Glu Ile Leu Cys
115 120 125

Gly Asn Cys Asn Gly Ala Gly Phe Leu Gly Gly Phe Leu Ser Thr Phe 130 135 140

Asp Glu Thr Ala Gln

145 (2) INFORMATION FOR SEQ ID NO:1603: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..129 (D) OTHER INFORMATION: / Ceres Seq. ID 1598566 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603: Met Ala Ala Thr Ala Ser Leu Thr Thr Thr Ala Pro Ser Pro Pro Ala 10 Leu Leu Lys Ala Ser Ala Pro Leu Leu Ile Ser Phe Arg Pro Val Ser 30 25 2.0 Arg His Cys Lys Asn Leu Cys Ile Lys Thr Lys Ala Thr Glu Asn Asp 40 45 Gln Ser Ala Lys Lys His Gln Lys Val Lys Ser Ile Leu Cys Gln Asp 55 Cys Glu Gly Asn Gly Ala Ile Val Cys Thr Lys Cys Glu Gly Asn Gly 75 70 Val Asn Ser Val Asp Tyr Phe Glu Gly Arg Phe Lys Ala Gly Ser Leu 85 Cys Trp Leu Cys Arg Gly Lys Arg Glu Ile Leu Cys Gly Asn Cys Asn 105 100 Gly Ala Gly Phe Leu Gly Gly Phe Leu Ser Thr Phe Asp Glu Thr Ala 120 115 Gln (2) INFORMATION FOR SEQ ID NO:1604: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..162 (D) OTHER INFORMATION: / Ceres Seq. ID 1598578 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604: cacgccacgc tetecaacre cacagettge geoegeaatg geactegtet eegecteete 60 gtectecace accgeegtea egsetteece aggaatggge agegggegte gteeteette 120 ctcggcggca agacgctgct gagacaggcc gaggcggccg gc (2) INFORMATION FOR SEQ ID NO:1605: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

His Ala Thr Leu Ser Asn Xaa Thr Ala Cys Ala Arg Asn Gly Thr Arg

1 5 10 15

Leu Arg Leu Leu Val Leu His His Arg Arg His Xaa Phe Pro Arg Asn

(D) OTHER INFORMATION: / Ceres Seq. ID 1598579

Crience Bookee No. 001111111	
20 25 30	
Gly Gln Arg Ala Ser Ser Ser Phe Leu Gly Gly Lys Thr Leu Leu Arg 35 40 45	
Gln Ala Glu Ala Ala Gly 50	
(2) INFORMATION FOR SEQ ID NO:1606: (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 46 amino acids	
(B) TYPE: amino acid (C) STRANDEDNESS:	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide (ix) FEATURE:	
(A) NAME/KEY: peptide	
(B) LOCATION: 146 (D) OTHER INFORMATION: / Ceres Seq. ID 1598580	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606: Thr Pro Arg Ser Pro Xaa Pro Gln Leu Ala Pro Ala Met Ala Leu Val	
1 10 15	
Ser Ala Ser Ser Ser Ser Thr Thr Ala Val Thr Xaa Ser Pro Gly Met 20 25 30	
Gly Ser Gly Arg Arg Pro Pro Ser Ser Ala Ala Arg Arg Cys 35 40 45	
(2) INFORMATION FOR SEQ ID NO:1607: (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 53 amino acids	
(B) TYPE: amino acid (C) STRANDEDNESS:	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide (ix) FEATURE:	
(A) NAME/KEY: peptide (B) LOCATION: 153	
(D) OTHER INFORMATION: / Ceres Seq. ID 1598581	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607: Arg His Ala Leu Gln Xaa His Ser Leu Arg Pro Gln Trp His Ser Ser	
1 5 10 15 Pro Pro Pro Arg Pro Pro Pro Pro Pro Ser Xaa Leu Pro Gln Glu Trp	
20 25 30 Ala Ala Gly Val Val Leu Leu Pro Arg Arg Gln Asp Ala Ala Glu Thr	
35 40 45 Gly Arg Gly Gly Arg	
50	
(2) INFORMATION FOR SEQ ID NO:1608: (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 180 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
(ix) FEATURE: (A) NAME/KEY: -	
(B) LOCATION: 1180	
(D) OTHER INFORMATION: / Ceres Seq. ID 1598598 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:	
cacaccaaga atcacaatac gaaacgaatt aatccccaat caacacagca agtcagcanc	60 20
aannaaanna uudauuuday ayaatyacyo yaggatyeey gagaaagaaa	80
(2) INFORMATION FOR SEQ ID NO:1609: (i) SEQUENCE CHARACTERISTICS:	
(T) ODSODNOD OWNERSTANDED	

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

His Thr Glu Asn His Asn Thr Lys Arg Ile Asn Pro Gln Ser Thr Gln 1 5 10 15

Gln Val Ser Xaa Lys Gln Ser Ser Asp Pro Arg Asp Gly Arg Glu Asp 20 25 30

Val Arg Ala Gly Asp Pro Pro Gly Gly Gly Ala Ala Ser Pro Ala Gly 35 40 45

Arg Ala Arg Arg Gln Gly Gly Arg Arg Arg Thr 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1610:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598600
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

Thr Pro Arg Ile Thr Ile Arg Asn Glu Leu Ile Pro Asn Gln His Ser

Lys Ser Ala Xaa Ser Lys Ala Ala Thr Arg Glu Met Asp Ala Arg Met 20 25 30

Phe Gly Leu Glu Thr Pro Arg Val Ala Ala Leu His His Leu Leu Asp 35 40 45

- Val Pro Asp Gly Asp Lys Ala Gly Gly Ala 50
- (2) INFORMATION FOR SEQ ID NO:1611:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..32
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598601
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

Met Asp Ala Arg Met Phe Gly Leu Glu Thr Pro Arg Val Ala Ala Leu 1 5 10 15

His His Leu Leu Asp Val Pro Asp Gly Asp Lys Ala Gly Gly Gly Ala 20 25 30

- (2) INFORMATION FOR SEQ ID NO:1612:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..498
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598610
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612: caagaaggca gtggagaact ctcctttcct ggagaagctg aagaagaggg gctacgaggt 60 cctgtacatg gttgatgcca ttgatgagta tgctgttggt cagctcaagg agtttgaggg 120 caagaagett gteteggeea eeaaggaggg tetgaagett gatgagaeeg aggatgagaa 180 gaagaggaag gaggagctga aggagaagtt tgagggtctg tgcaagatca tcaaggaggt 240 tctgggcgac aaggttgaga aggttgtggt gtctgaccgt gtcgtggact caccgtgctg 300 360 ccttgtcact ggtgagtatg gctggacagc aacatggaga ggatcatgaa ggcgcaggcc ctgagggact ctagcatgtc ggggtacatg tcgagcaaaa agactatgga aatcaacccg 420 gagaacccaa tcatggatga gctccgtaag cgcgccgagg ctgacaggaa tgacaagtca 480 gtcaaggatc ttgtgatg
- (2) INFORMATION FOR SEQ ID NO:1613:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598611

Glu Gly Leu Lys Leu Asp Glu Thr Glu Asp Glu Lys Lys Arg Lys Glu
50 55 60

Glu Leu Lys Glu Lys Phe Glu Gly Leu Cys Lys Ile Ile Lys Glu Val 65 70 75 80

Leu Gly Asp Lys Val Glu Lys Val Val Val Ser Asp Arg Val Val Asp 85 90 95

85 90 95

Ser Pro Cys Cys Leu Val Thr Gly Glu Tyr Gly Trp Thr Ala Thr Trp
100 105 110

Arg Gly Ser

- (2) INFORMATION FOR SEQ ID NO:1614:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598612
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:
- Met Val Asp Ala Ile Asp Glu Tyr Ala Val Gly Gln Leu Lys Glu Phe 1 5 10 15
- Glu Gly Lys Lys Leu Val Ser Ala Thr Lys Glu Gly Leu Lys Leu Asp 20 25 30 Glu Thr Glu Asp Glu Lys Lys Arg Lys Glu Glu Leu Lys Glu Lys Phe

60

120

180

240

300

360

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 4.5 40 35 Glu Gly Leu Cys Lys Ile Ile Lys Glu Val Leu Gly Asp Lys Val Glu 60 55 Lys Val Val Val Ser Asp Arg Val Val Asp Ser Pro Cys Cys Leu Val 75 70 Thr Gly Glu Tyr Gly Trp Thr Ala Thr Trp Arg Gly Ser 85 (2) INFORMATION FOR SEQ ID NO:1615: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..375 (D) OTHER INFORMATION: / Ceres Seq. ID 1598623 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615: aggtgtactg tactgtagta ggttggttct ccattcatca ttcagctcac aggtccctcc gcctccgccg tatcggaggg agaggaagcg gaaggcttgg aaggagaaga gaatggcggg gcggcgcgcg gaggaggagt acgactacct gttcaaggtg gtgctgatcg gggactcggg cgtcggcaag tccaacctcc tctcccgctt cacccgcaac gagttctgcc tcgagtccaa gtccaccatc ggcgtcgagt tcgccacacg gacactccat gttgagggca agatcatcaa ggcgcagatc tgggacacgg caggccagga gcggtaccgg gcgatcacca gcgcctacta tcgcggggcg ctggg (2) INFORMATION FOR SEQ ID NO:1616: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..124 (D) OTHER INFORMATION: / Ceres Seq. ID 1598624 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616: Gly Val Leu Tyr Cys Ser Arg Leu Val Leu His Ser Ser Phe Ser Ser 5

Gln Val Pro Pro Pro Pro Tyr Arg Arg Glu Arg Lys Arg Lys Ala 25 2.0 Trp Lys Glu Lys Arg Met Ala Gly Arg Arg Ala Glu Glu Tyr Asp 40 Tyr Leu Phe Lys Val Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser 55 Asn Leu Leu Ser Arg Phe Thr Arg Asn Glu Phe Cys Leu Glu Ser Lys 75 7.0 Ser Thr Ile Gly Val Glu Phe Ala Thr Arg Thr Leu His Val Glu Gly 90 85 Lys Ile Ile Lys Ala Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr 105 Arg Ala Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Leu

- (2) INFORMATION FOR SEQ ID NO:1617:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

Met Ala Gly Arg Arg Ala Glu Glu Glu Tyr Asp Tyr Leu Phe Lys Val 10

Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Asn Leu Leu Ser Arg 25

Phe Thr Arg Asn Glu Phe Cys Leu Glu Ser Lys Ser Thr Ile Gly Val 40

Glu Phe Ala Thr Arg Thr Leu His Val Glu Gly Lys Ile Ile Lys Ala 55

Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg Ala Ile Thr Ser 70

Ala Tyr Tyr Arg Gly Ala Leu 85

- (2) INFORMATION FOR SEQ ID NO:1618:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..470
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598631
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618: gtcctgtctc ctcccaccct tgcctccgag tcacctcctc ccttggtctc cgccgtcgct 60 gcctccttgc cggaacccta aatggacccc ggcgccggcg cacactactc cgtccgtacc 120 geggaggagg tttteegega etteegegee geegegeggg catgateaag geeeteacea 180 acqatgtgga gaagttctac cagctgtgtg accccgaaaa ggaaaacttg tgcctttatg 240 gctaccccaa cgaaacatgg gaagtaactt tgccagcaga ggaagttcct ccagagatcc 300 ctgaaccagc tttgggtata aactttgcta gggatggcat gaatgagaag gattggttag 360 420 cgctagttgc tgtccacagc gattcctggt tactagcagt tgcattctac tttgcagccc ggtttgggtt tgacaaagag tccagacggc ggctcttcaa catgataaat
- (2) INFORMATION FOR SEQ ID NO:1619:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..156
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598632
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

Pro Val Ser Ser His Pro Cys Leu Arg Val Thr Ser Ser Leu Gly Leu 10 5

Arg Arg Arg Cys Leu Leu Ala Gly Thr Leu Asn Gly Pro Arg Arg Arg 25 20

Arg Thr Leu Leu Arg Pro Tyr Arg Gly Gly Gly Phe Pro Arg Leu Pro 40

Arg Arg Arg Ala Gly Met Ile Lys Ala Leu Thr Asn Asp Val Glu Lys 60

Phe Tyr Gln Leu Cys Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly 75 70

Tyr Pro Asn Glu Thr Trp Glu Val Thr Leu Pro Ala Glu Glu Val Pro 85 90

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Pro Glu Ile Pro Glu Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly
                               105
           100
Met Asn Glu Lys Asp Trp Leu Ala Leu Val Ala Val His Ser Asp Ser
                                               125
                           120
       115
Trp Leu Leu Ala Val Ala Phe Tyr Phe Ala Ala Arg Phe Gly Phe Asp
                                           140
                       135
   130
Lys Glu Ser Arg Arg Arg Leu Phe Asn Met Ile Asn
                   150
(2) INFORMATION FOR SEQ ID NO:1620:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 103 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..103
          (D) OTHER INFORMATION: / Ceres Seq. ID 1598633
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:
Met Ile Lys Ala Leu Thr Asn Asp Val Glu Lys Phe Tyr Gln Leu Cys
                5
                                   10
Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly Tyr Pro Asn Glu Thr
                                                   30
                                25
            20
Trp Glu Val Thr Leu Pro Ala Glu Glu Val Pro Pro Glu Ile Pro Glu
                                                45
                            40
Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp
                        55
                                            60
Trp Leu Ala Leu Val Ala Val His Ser Asp Ser Trp Leu Leu Ala Val
                                       75
                    70
Ala Phe Tyr Phe Ala Ala Arg Phe Gly Phe Asp Lys Glu Ser Arg Arg
                                    90
                85
Arg Leu Phe Asn Met Ile Asn
            100
(2) INFORMATION FOR SEQ ID NO:1621:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 476 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..476
           (D) OTHER INFORMATION: / Ceres Seq. ID 1598634
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:
 getgacacat tecacecace cateacecet teetteettt ceattetetg tegeettege
                                                                       60
 ccctccaagg ttctctgatt ccagacgcaa ccctgcggct gcggggtcaa ggagccaggg
                                                                      120
 ggtgcacage gategttetg eeggagateg aaaceeteag etagggtetg aggegeeggg
                                                                      180
 ctgcggccgc cgagatgtcg acgccggcga ggaagcggct gatgcgggac ttcaggcgcc
                                                                      240
 tgcagcagga cccgcccgcc ggatcaccgg cgcgccgcac gacaacaaca tcatgctctg
                                                                      300
                                                                      360
 gaacgccgtc atattcgggc cggatgatac gccttgggac ggaggcacgt tcaagcttac
 420
 gtttcatcca aacatatatg ctgatggaag catctgcttg gatatcctac agaacc
 (2) INFORMATION FOR SEQ ID NO:1622:
      (i) SEQUENCE CHARACTERISTICS:
```

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..158
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598635
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:
- Leu Thr His Ser Thr His Pro Ser Pro Leu Pro Ser Phe Pro Phe Ser 1 5 10 15
- Val Ala Phe Ala Pro Pro Arg Phe Ser Asp Ser Arg Arg Asn Pro Ala 20 25 30
- Ala Ala Gly Ser Arg Ser Gln Gly Val His Ser Asp Arg Ser Ala Gly 35 40 45
- Asp Arg Asn Pro Gln Leu Gly Ser Glu Ala Pro Gly Cys Gly Arg Arg 50 55 60
- Asp Val Asp Ala Gly Glu Glu Ala Ala Asp Ala Gly Leu Gln Ala Pro 65 70 75 80
- Ala Ala Gly Pro Ala Arg Arg Ile Thr Gly Ala Pro His Asp Asn Asn 85 90 95
- Ile Met Leu Trp Asn Ala Val Ile Phe Gly Pro Asp Asp Thr Pro Trp 100 105 110
- Asp Gly Gly Thr Phe Lys Leu Thr Leu Gln Phe Thr Glu Asp Tyr Pro 115 120 125
- Asn Lys Pro Pro Thr Val Arg Phe Val Ser Arg Met Phe His Pro Asn 130 135 140
- Ile Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn 145 150 155
- (2) INFORMATION FOR SEQ ID NO:1623:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598636
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623: Met Ser Thr Pro Ala Arg Lys Arg Leu Met Arg Asp Phe Arg Arg Leu
- 1 5 10 15 Gln Gln Asp Pro Pro Ala Gly Ser Pro Ala Arg Arg Thr Thr Thr Thr 20 25 30
- Ser Cys Ser Gly Thr Pro Ser Tyr Ser Gly Arg Met Ile Arg Leu Gly
- Thr Glu Ala Arg Ser Ser Leu Pro Cys Ser Leu Gln Lys Ile Thr Gln
 50 55 60
- Thr Ser His Gln Leu Phe Gly Ser Ser Leu Gly Cys Phe Ile Gln Thr 65 70 75 80
- Tyr Met Leu Met Glu Ala Ser Ala Trp Ile Ser Tyr Arg Thr 85 90
- (2) INFORMATION FOR SEQ ID NO:1624:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598637
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

Met Arg Asp Phe Arg Arg Leu Gln Gln Asp Pro Pro Ala Gly Ser Pro 10 Ala Arg Arg Thr Thr Thr Ser Cys Ser Gly Thr Pro Ser Tyr Ser 25 Gly Arg Met Ile Arg Leu Gly Thr Glu Ala Arg Ser Ser Leu Pro Cys 40 Ser Leu Gln Lys Ile Thr Gln Thr Ser His Gln Leu Phe Gly Ser Ser 55 Leu Gly Cys Phe Ile Gln Thr Tyr Met Leu Met Glu Ala Ser Ala Trp 75 Ile Ser Tyr Arg Thr

(2) INFORMATION FOR SEQ ID NO:1625:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..480
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625: aacataaaaa actcaccggg aagaaggaag gagaagctaa ccggcacgtc gtgaagctaa 60 120 ccgggaagca gagacgtccg cccgtccccc gtcgtccgtc gtcatggccg ccgtggaggt gtgcgtgaag gccgccacgg ggaagcccga cacgctcggc gactgcccgt tctcgcagag 180 ggtgctgctc acgctggagg agaagaaggt cccctacgag gtgaagctcg tcgacctcga 240 300 caacaagece gaatggttte tgaagateag eecagagggt aaggtgeetg tgttcaaegg 360 tggtgatggc aaatgcatcg ctgattctga tgtaatcacc caaaccattg aggagaagtt cccaactcca tctctggtca ctcctgtaga atatgcatca gtgggatcaa agattttccc 420 480 agectteate acattettga agageaagga tgetagtgat ggtteegaga aggegettet
- (2) INFORMATION FOR SEQ ID NO:1626:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Ala Ala Val Glu Val Cys Val Lys Ala Ala Thr Gly Lys Pro Asp 10 Thr Leu Gly Asp Cys Pro Phe Ser Gln Arg Val Leu Leu Thr Leu Glu 25 20

Glu Lys Lys Val Pro Tyr Glu Val Lys Leu Val Asp Leu Asp Asn Lys 40

Pro Glu Trp Phe Leu Lys Ile Ser Pro Glu Gly Lys Val Pro Val Phe 55

Asn Gly Gly Asp Gly Lys Cys Ile Ala Asp Ser Asp Val Ile Thr Gln 75 70

Thr Ile Glu Glu Lys Phe Pro Thr Pro Ser Leu Val Thr Pro Val Glu 90

Tyr Ala Ser Val Gly Ser Lys Ile Phe Pro Ala Phe Ile Thr Phe Leu 105

Lys Ser Lys Asp Ala Ser Asp Gly Ser Glu Lys Ala Leu 120

(2)	INFORMATION FOR SEQ ID NO:1627: (i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
	(ix) FEATURE: (A) NAME/KEY: -
	(B) LOCATION: 1152
	(D) OTHER INFORMATION: / Ceres Seq. ID 1598640
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:
aaac	aacage gaacacatet cetegeattn ntteccatee gateeecet tegeaaccaa 60
aacc	ccaact egecycgcat egatygegee caaggeegag aagaaaooog oggogaagaa
kcyg	geggag gaggageeeg eggeegakaa gg INFORMATION FOR SEQ ID NO:1628:
(2)	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 49 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS:
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: peptide (ix) FEATURE:
	(A) NAME/KEY: peptide
	(B) LOCATION: 149
	(D) OTHER INFORMATION: / Ceres Seq. ID 1598641
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:
Lys	Gln Gln Arg Thr His Leu Leu Ala Xaa Xaa Pro Ile Arg Ser Pro
1	5 10 15 Arg Asn Gln Asn Pro Asn Ser Xaa Arg Ile Asp Gly Ala Gln Gly
Leu	arg Asn Gin Asn Pio Asn Sei Add Arg Tie Asp Giy Ard Gin
Ara	Glu Glu Thr Arg Gly Glu Glu Xaa Gly Gly Gly Ala Arg Gly
5	35 40 45
Arg	
(0)	TATODMETON FOR GEO ID NO.162Q.
(2)	INFORMATION FOR SEQ ID NO:1629: (i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 50 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS:
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: peptide
	(ix) FEATURE: (A) NAME/KEY: peptide
	(B) LOCATION: 150
	(D) OTHER INFORMATION: / Ceres Seq. ID 1598642
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:
Asn	Asn Ser Glu His Ile Ser Ser His Xaa Phe Pro Ser Asp Pro Pro
1	5 10 15 Ala Thr Lys Thr Pro Thr Arg Xaa Ala Ser Met Ala Pro Lys Ala
Phe	20 25 30
Glu	Lys Lys Pro Ala Ala Lys Xaa Xaa Ala Glu Glu Pro Ala Ala
GIU	35 40 45
Xaa	Lys
	50
(2)	INFORMATION FOR SEQ ID NO:1630:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS:
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..50 (D) OTHER INFORMATION: / Ceres Seq. ID 1598643 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630: Thr Thr Ala Asn Thr Ser Pro Arg Ile Xaa Ser His Pro Ile Pro Pro 10 Ser Gln Pro Lys Pro Gln Leu Ala Xaa His Arg Trp Arg Pro Arg Pro 30 25 20 Arg Arg Asn Pro Arg Arg Arg Xaa Xaa Arg Arg Arg Ser Pro Arg Pro 40 Xaa Arq 50 (2) INFORMATION FOR SEQ ID NO:1631: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 435 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..435 (D) OTHER INFORMATION: / Ceres Seq. ID 1598644 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631: acaagcgtcc acagcttcca ctagagaccg aagtaccgaa cagatagaga ttggagaacc 60 atgatgagat ccggccttct ctcgctatgt ttccacctag ccctggccat cacactggct 120 gcaagtkttc ctggccttgc tcgtagtagg gtaatcgaca tcgaaccgca actcaaaccg 180 acgctgcaac tagaaccaaa gcatggtgta tctcaaccag acagaaacca atgaacccaa 240 accgacacca caacctgagc caaaaccgga gcctaaaccg gaaccaaaac ctgcaccaca 300 atcagacacc aaatcagacc ctaaacccgc accacagtca gacccaaaac ctgcaccaca 360 accggaccta aaaccagaac ccaaacctac accacagcca gacccaaaac cttcaccaca 420 accagaccca gagcc (2) INFORMATION FOR SEQ ID NO:1632: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..57 (D) OTHER INFORMATION: / Ceres Seq. ID 1598645 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632: Met Met Arg Ser Gly Leu Leu Ser Leu Cys Phe His Leu Ala Leu Ala 5 1.0 Ile Thr Leu Ala Ala Ser Xaa Pro Gly Leu Ala Arg Ser Arg Val Ile 30 25 Asp Ile Glu Pro Gln Leu Lys Pro Thr Leu Gln Leu Glu Pro Lys His 40 Gly Val Ser Gln Pro Asp Arg Asn Gln 55 50 (2) INFORMATION FOR SEQ ID NO:1633: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 amino acids (B) TYPE: amino acid

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..56 (D) OTHER INFORMATION: / Ceres Seq. ID 1598646 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633: Met Arg Ser Gly Leu Leu Ser Leu Cys Phe His Leu Ala Leu Ala Ile 10 5 Thr Leu Ala Ala Ser Xaa Pro Gly Leu Ala Arg Ser Arg Val Ile Asp 25 Ile Glu Pro Gln Leu Lys Pro Thr Leu Gln Leu Glu Pro Lys His Gly 40 Val Ser Gln Pro Asp Arg Asn Gln (2) INFORMATION FOR SEQ ID NO:1634: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..77 (D) OTHER INFORMATION: / Ceres Seq. ID 1598647 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634: Met Val Tyr Leu Asn Gln Thr Glu Thr Asn Glu Pro Lys Pro Thr Pro 15 10 Gln Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Ala Pro 30 25 2.0 Gln Ser Asp Thr Lys Ser Asp Pro Lys Pro Ala Pro Gln Ser Asp Pro 45 40 35 Lys Pro Ala Pro Gln Pro Asp Leu Lys Pro Glu Pro Lys Pro Thr Pro 55 Gln Pro Asp Pro Lys Pro Ser Pro Gln Pro Asp Pro Glu 70 (2) INFORMATION FOR SEQ ID NO:1635: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 173 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..173 (D) OTHER INFORMATION: / Ceres Seq. ID 1598661 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635: accgccgccg acttctgatt ctaccaccac ccgcctcctc tcgagttcga tctgtttgct 60 ccccagaca tgtcgggccg cggcaaggga ggcaagggcc tgggtaaggg cggcgcgaaa 120 cgcaccgcaa gtcttccgcg acaacatcca gggcatcacg aagccggcca tcc (2) INFORMATION FOR SEQ ID NO:1636: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..57
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598662

60

120

180

240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636: Pro Pro Pro Thr Ser Asp Ser Thr Thr Thr Arg Leu Leu Ser Ser 10 Ile Cys Leu Leu Pro Gln Thr Cys Arg Ala Ala Ala Arg Glu Ala Arg 2.5 Ala Trp Val Arg Ala Arg Asn Ala Pro Gln Val Phe Arg Asp Asn 4.0 Ile Gln Gly Ile Thr Lys Pro Ala Ile 50 55 (2) INFORMATION FOR SEQ ID NO:1637: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..34 (D) OTHER INFORMATION: / Ceres Seq. ID 1598663 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637: Arg Arg Arg Leu Leu Ile Leu Pro Pro Pro Ala Ser Ser Arg Val Arg 10 Ser Val Cys Ser Pro Arg His Val Gly Pro Arg Gln Gly Arg Gln Gly 25 Pro Gly (2) INFORMATION FOR SEQ ID NO:1638: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..34 (D) OTHER INFORMATION: / Ceres Seq. ID 1598664 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638: Met Ser Gly Arg Gly Lys Gly Lys Gly Leu Gly Lys Gly Ala 5 10 Lys Arg Thr Ala Ser Leu Pro Arg Gln His Pro Gly His His Glu Ala 25 Gly His (2) INFORMATION FOR SEQ ID NO:1639: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..450 (D) OTHER INFORMATION: / Ceres Seq. ID 1598668 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639: aatogageeg eegeegeege egeegeagtt gtetteggte tteegtgete acettegaga

gatcaagttg ctgctgcggt agtccccaac catcatcatg cagaacgagg agggtaagac

ggtggacctc tacgtcccca ggaagtgctc ggccacgaat aggatcatca ctgccaagga

tcatgcctct gtccagatca acattggcca cttggatgcg aatggcctgt acgatggtca

cttcaccacg tttgctctct ctgggtttgt ccgtgctcag ggtgatgctg acagttcgtt 300 ggacaggctg tggcagaaga agaaggctga gatcaagcag taggtctttg cacgtagttc 360 caccggtaat ggactcttga gggatactgc tctagctaat gctttagctg ggggggggg 420 antgattckg atgtttggct gtycgtttgt

- (2) INFORMATION FOR SEQ ID NO:1640:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598669
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

Ser Ser Arg Arg Arg Arg Arg Ser Cys Leu Arg Ser Ser Val Leu
1 10 15

Thr Phe Glu Arg Ser Ser Cys Cys Cys Gly Ser Pro Gln Pro Ser Ser 20 25 30

Cys Arg Thr Arg Arg Val Arg Arg Trp Thr Ser Thr Ser Pro Gly Ser

Ala Arg Pro Arg Ile Gly Ser Ser Leu Pro Arg Ile Met Pro Leu Ser 50 60

Arg Ser Thr Leu Ala Thr Trp Met Arg Met Ala Cys Thr Met Val Thr 65 70 75 80

Ser Pro Arg Leu Leu Ser Leu Gly Leu Ser Val Leu Arg Val Met Leu 85 90 95

Thr Val Arg Trp Thr Gly Cys Gly Arg Arg Arg Arg Leu Arg Ser Ser 100 105 110

Ser Arg Ser Leu His Val Val Pro Pro Val Met Asp Ser 115 120 125

- (2) INFORMATION FOR SEQ ID NO:1641:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Gln Asn Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg Lys

1 5 10 15

15 15 16 Thr Ala Lys Asp His Ala Ser Val

Cys Ser Ala Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser Val
20
25
30

Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp Ala
50
60
Asp Ser Ser Leu Asp Arg Leu Tro Gln Lys Lys Ala Glu Ile Lys

Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Glu Ile Lys 65 70 75 80

Gln

- (2) INFORMATION FOR SEQ ID NO:1642:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..65 (D) OTHER INFORMATION: / Ceres Seq. ID 1598671 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642: Met Pro Leu Ser Arg Ser Thr Leu Ala Thr Trp Met Arg Met Ala Cys 10 Thr Met Val Thr Ser Pro Arg Leu Leu Ser Leu Gly Leu Ser Val Leu 20 Arg Val Met Leu Thr Val Arg Trp Thr Gly Cys Gly Arg Arg Arg 40 Leu Arg Ser Ser Ser Arg Ser Leu His Val Val Pro Pro Val Met Asp Ser 65 (2) INFORMATION FOR SEQ ID NO:1643: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..451 (D) OTHER INFORMATION: / Ceres Seq. ID 1598689 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643: actoccactt tactoctato cactgoggoo tggacgogtg ckagakgott gaccaagcag 60 cagcagggat ggcgcctctg aagctgtacg ggatgccgct gtcccccaac gtggtgcgcg 120 tggccaccgt gctcaacgag aagggcctcg acttcgagat cgtccccgtc gacctcacca 180 ceggegeeca caageageec gaetteeteg ceetcaacee ttteggeeag ateceggete 240 togtogacgg agacgaayct ottogagtoc ogtgogatoa accggtacat ogccagcaag 300 tacgcgtcgg agggcacgga cctgctcccc gcgacggcgt cggcgcgaac gtggaaggtg 360 tggctagagg tggagtcgca ccacttctac ccgaacgcgt cgccgctggt gttccagctg 420 ctcqtqaqqc cgctcctggg cgcgccccga c (2) INFORMATION FOR SEQ ID NO:1644: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..149 (D) OTHER INFORMATION: / Ceres Seq. ID 1598690 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644: Ser His Phe Thr Pro Ile His Cys Gly Leu Asp Ala Cys Xaa Xaa Leu 10 Asp Gln Ala Ala Ala Gly Met Ala Pro Leu Lys Leu Tyr Gly Met Pro 25 Leu Ser Pro Asn Val Val Arg Val Ala Thr Val Leu Asn Glu Lys Gly 40 Leu Asp Phe Glu Ile Val Pro Val Asp Leu Thr Thr Gly Ala His Lys 60 Gln Pro Asp Phe Leu Ala Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu 70 7.5 Val Asp Gly Asp Glu Xaa Leu Arg Val Pro Cys Asp Gln Pro Val His

Arg Gln Gln Val Arg Val Gly Gly His Gly Pro Ala Pro Arg Asp Gly 100 105 110

Val Gly Ala Asn Val Glu Gly Val Ala Arg Gly Gly Val Ala Pro Leu 115 120 125

Leu Pro Glu Arg Val Ala Ala Gly Val Pro Ala Ala Arg Glu Ala Ala 130 135 140

Pro Gly Arg Ala Pro

145

- (2) INFORMATION FOR SEQ ID NO:1645:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598691
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

Met Ala Pro Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val 1 5 10 15

Arg Val Ala Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val 20 25 30

Pro Val Asp Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Ala 35 40 45

Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa 50 55 60

Leu Arg Val Pro Cys Asp Gln Pro Val His Arg Gln Gln Val Arg Val 65 70 75 80 Gly Gly His Gly Pro Ala Pro Arg Asp Gly Val Gly Ala Asn Val Glu

85 90 95
Gly Val Ala Arg Gly Gly Val Ala Pro Leu Leu Pro Glu Arg Val Ala

100 105 110 Ala Gly Val Pro Ala Ala Arg Glu Ala Ala Pro Gly Arg Ala Pro

- 115 120 (2) INFORMATION FOR SEQ ID NO:1646:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

Met Pro Leu Ser Pro Asn Val Val Arg Val Ala Thr Val Leu Asn Glu
1 5 10 15

Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp Leu Thr Thr Gly Ala 20 25 30

His Lys Gln Pro Asp Phe Leu Ala Leu Asn Pro Phe Gly Gln Ile Pro 35 40 45

Ala Leu Val Asp Gly Asp Glu Xaa Leu Arg Val Pro Cys Asp Gln Pro 50 55 60

Val His Arg Gln Gln Val Arg Val Gly Gly His Gly Pro Ala Pro Arg 65 70 75 80

Asp Gly Val Gly Ala Asn Val Glu Gly Val Ala Arg Gly Gly Val Ala 85 90 95 Pro Leu Leu Pro Glu Arg Val Ala Ala Gly Val Pro Ala Ala Arg Glu Client Docket No. 80146.003 110 105 100 Ala Ala Pro Gly Arg Ala Pro 115 (2) INFORMATION FOR SEQ ID NO:1647: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 467 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..467 (D) OTHER INFORMATION: / Ceres Seq. ID 1598693 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647: 60 qcttctggga tggctgcatt tatgcaggca cactgctgcc ggcagccacg actggttgga aggagggagg ggtagtagta aaaccaggta ggtgtggctg gctcgtgcag cggcgacagg 120 cqqcaqtqaq agcqatgagc gcggcgtcga cgagctcggt caccaagttc atcaagtgcg 180 240 tcacggtcgg cgatggggcc gtcgggaaga cctgcatgct catctgctac acctgcaaca 300 agttocccac ggattatate eccaceqtat tegacaactt cagegecaat gteteegtgg 360 qtqqqaqcat cqtcaacttq qqcctctqgg acacgqcagg ccaggaggat tacagcaggt 420 tgaggcctct cagctacagg ggtgctgatg tgttcatcct ctccttctcc ctggtcagca gggcgagcta tgagaacgtc ctcaagaagt ggatgccaga gcttcgc (2) INFORMATION FOR SEQ ID NO:1648: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..155 (D) OTHER INFORMATION: / Ceres Seq. ID 1598694 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648: Phe Trp Asp Gly Cys Ile Tyr Ala Gly Thr Leu Leu Pro Ala Ala Thr 10 Thr Gly Trp Lys Glu Gly Gly Val Val Lys Pro Gly Arg Cys Gly 25 Trp Leu Val Gln Arg Arg Gln Ala Ala Val Arg Ala Met Ser Ala Ala 40 Ser Thr Ser Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp 55 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Cys Asn Lys 70 75 Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn 8.5 90 Val Ser Val Gly Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala

105

Gly Gln Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala 120

Asp Val Phe Ile Leu Ser Phe Ser Leu Val Ser Arg Ala Ser Tyr Glu

110

125

140

150 (2) INFORMATION FOR SEQ ID NO:1649:

- (i) SEQUENCE CHARACTERISTICS:

Asn Val Leu Lys Lys Trp Met Pro Glu Leu Arg

(A) LENGTH: 111 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..111
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598695
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:
- Met Ser Ala Ala Ser Thr Ser Ser Val Thr Lys Phe Ile Lys Cys Val

 1 10 15

 15 10 15 Cys Tyr
- Thr Val Gly Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr 20 25 30
- Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn 35 40 45
- Phe Ser Ala Asn Val Ser Val Gly Gly Ser Ile Val Asn Leu Gly Leu 50 55 60
- Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser 65 70 75 80
- Tyr Arg Gly Ala Asp Val Phe Ile Leu Ser Phe Ser Leu Val Ser Arg 85 90 95
- Ala Ser Tyr Glu Asn Val Leu Lys Lys Trp Met Pro Glu Leu Arg $100 \hspace{1.5cm} 105 \hspace{1.5cm} 105$
- (2) INFORMATION FOR SEQ ID NO:1650:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598696
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:
- Met Leu Ile Cys Tyr Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro 1 5 10 15
- Thr Val Phe Asp Asn Phe Ser Ala Asn Val Ser Val Gly Gly Ser Ile 20 25 30
- Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg
 35 40 45
- Leu Arg Pro Leu Ser Tyr Arg Gly Ala Asp Val Phe Ile Leu Ser Phe 50 55 60
- Ser Leu Val Ser Arg Ala Ser Tyr Glu Asn Val Leu Lys Lys Trp Met 65 70 75 80
- Pro Glu Leu Arg
- (2) INFORMATION FOR SEQ ID NO:1651:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..496
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598730
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:
- acatcacggt accattcacc ggagatgact gttgtgagta tcatgtggtc gttagtgcag 60 gtgcaggtgc tggtggcggt ggcattagca tttctggtag gcggtgctgg tgtggtcctc ccaaggttcc cccgggtaag aacatcacag ccaaatatgg tagtgattgg ctagatgcca 180 ggtacaagga cgtgaataag gcccctttca atagcatggg cgcgtgtggc aacgtccca 300

tcttcaagga cggtctaggt tgtggatcct gcttcgagat caagtgtgac aagccagcgg 360 agtgctctgg caagcccgtg gtggtgtaca ttacggacat gaactacgag cccattgcgg 420 cataccactt cgacctagcg ggcacggcgt tcggtgccat ggctaagaag ggtgaggagg 480 agaagttgcg caaggc

- (2) INFORMATION FOR SEQ ID NO:1652:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..164
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598731
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

Ile Thr Val Pro Phe Thr Gly Asp Asp Cys Cys Glu Tyr His Val Val 1 10 15

Val Ser Ala Gly Ala Gly Ala Gly Gly Gly Ile Ser Ile Ser Gly 20 25 30

Arg Arg Cys Trp Cys Gly Pro Pro Lys Val Pro Pro Gly Lys Asn Ile

Thr Ala Lys Tyr Gly Ser Asp Trp Leu Asp Ala Lys Ala Thr Trp Tyr 50 60

Gly Lys Pro Thr Gly Ala Gly Pro Asp Asp Asp Gly Gly Gly Cys Gly 65 70 75 80

Tyr Lys Asp Val Asn Lys Ala Pro Phe Asn Ser Met Gly Ala Cys Gly
85 90 95

Asn Val Pro Ile Phe Lys Asp Gly Leu Gly Cys Gly Ser Cys Phe Glu
100 105 110

Ile Lys Cys Asp Lys Pro Ala Glu Cys Ser Gly Lys Pro Val Val Val 115 120 125

Tyr Ile Thr Asp Met Asn Tyr Glu Pro Ile Ala Ala Tyr His Phe Asp 130 135 140

Leu Ala Gly Thr Ala Phe Gly Ala Met Ala Lys Lys Gly Glu Glu 145 150 155 160

Lys Leu Arg Lys

- (2) INFORMATION FOR SEQ ID NO:1653:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..429
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598732
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

- (2) INFORMATION FOR SEQ ID NO:1654:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..72
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598733
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:
- Glu Phe Pro Phe Asp Pro Ile His Phe Ser Val Leu Thr Ser Ile Ser 1 10 15
- Arg Glu Ala Xaa Arg Arg Arg Arg Val Arg Gly Asp Arg Glu Gln Pro 20 25 30
- Glu Pro Glu Pro Xaa Leu Glu Asp Glu Asp Val Arg Pro Val Ala Gly 35 40 45
- Ile Leu Pro Pro Gly Val Glu Ala Gln Leu Ala Leu Pro His Gly Val 50 60
- Arg His His Arg Leu His His His 65 70
- (2) INFORMATION FOR SEQ ID NO:1655:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..39
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598734
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:
- Ile Ser Ile Arg Pro His Pro Leu Leu Ser Ser His Leu Asn Leu Ala
 1 10 15
- Arg Ser Glu Xaa Glu Glu Glu Gly Ala Arg Arg Ser Arg Ala Ala Gly 20 25 30
- Ala Gly Ala Gly Xaa Arg Arg 35
- (2) INFORMATION FOR SEQ ID NO:1656:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598735
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:
- Met Lys Thr Phe Asp Pro Trp Pro Val Phe Phe Arg Arg Glu Trp Lys
 1 10 15
- Arg Asn Trp Pro Phe Leu Thr Gly Phe Ala Ile Thr Gly Phe Ile Ile 20 25 30
- Thr Lys Met Thr Ala Asn Phe Thr Glu Glu Asp Leu Lys Asn Ser Lys 35 40 45
- Phe Val Gln Glu His Lys Lys Arg
- (2) INFORMATION FOR SEQ ID NO:1657:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..505
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598744
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657: ttaacaaaat tatcgatatt aattactatc ctgttgagac agcaaaagag gtcaatatgc gtcacaggcc aattggcata ggtgttcaag gcctggcaga tacttttata ttactgggca 120 tgccgtttga ttcaccagag gctcaacagt tgaataagga tatattcgaa actatctact 180 atcatgetet gaaagettet getgaacteg etgetaaaga aggteeetat gaaaegtatg 240 aagggageee tgteageaag ggeattetee aacetgacat gtgggatgta gtgeeateta 300 acagatggaa ctggccatct ctaagggaga ccatttcaaa agttgggata agaaattctc 360 ttcttgttgc tccaatgccc actgcttcca ctagtcagat tcttggcaac aatgagtgtt 420 ttgaacccta cacgtctaat atatacagtc gacgtgttct aagtggggaa tttgttgtgg 480 gtaacaagca tcttcttcat gatct
- (2) INFORMATION FOR SEQ ID NO:1658:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..167
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598745
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:
- Asn Lys Ile Ile Asp Ile Asn Tyr Tyr Pro Val Glu Thr Ala Lys Glu

 1 10 15 15
- Val Asn Met Arg His Arg Pro Ile Gly Ile Gly Val Gln Gly Leu Ala 20 25 30
- Asp Thr Phe Ile Leu Leu Gly Met Pro Phe Asp Ser Pro Glu Ala Gln 35 40 45
- Gln Leu Asn Lys Asp Ile Phe Glu Thr Ile Tyr Tyr His Ala Leu Lys 50 55 60
- Ala Ser Ala Glu Leu Ala Ala Lys Glu Gly Pro Tyr Glu Thr Tyr Glu 65 70 75 80
- Gly Ser Pro Val Ser Lys Gly Ile Leu Gln Pro Asp Met Trp Asp Val 85 90 95
- Val Pro Ser Asn Arg Trp Asn Trp Pro Ser Leu Arg Glu Thr Ile Ser 100 105 110
- Lys Val Gly Ile Arg Asn Ser Leu Leu Val Ala Pro Met Pro Thr Ala 115 120 125
- Ser Thr Ser Gln Ile Leu Gly Asn Asn Glu Cys Phe Glu Pro Tyr Thr 130 135 140
- Ser Asn Ile Tyr Ser Arg Arg Val Leu Ser Gly Glu Phe Val Val Gly 145 150 155 160
- Asn Lys His Leu Leu His Asp

- (2) INFORMATION FOR SEQ ID NO:1659:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1598746 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659: Met Arg His Arg Pro Ile Gly Ile Gly Val Gln Gly Leu Ala Asp Thr 10 Phe Ile Leu Leu Gly Met Pro Phe Asp Ser Pro Glu Ala Gln Gln Leu 20 25 Asn Lys Asp Ile Phe Glu Thr Ile Tyr Tyr His Ala Leu Lys Ala Ser 40 Ala Glu Leu Ala Ala Lys Glu Gly Pro Tyr Glu Thr Tyr Glu Gly Ser 55 Pro Val Ser Lys Gly Ile Leu Gln Pro Asp Met Trp Asp Val Val Pro 75 70 Ser Asn Arg Trp Asn Trp Pro Ser Leu Arg Glu Thr Ile Ser Lys Val 90 85 Gly Ile Arg Asn Ser Leu Leu Val Ala Pro Met Pro Thr Ala Ser Thr 100 105 110 Ser Gln Ile Leu Gly Asn Asn Glu Cys Phe Glu Pro Tyr Thr Ser Asn 115 120 125 Ile Tyr Ser Arg Arg Val Leu Ser Gly Glu Phe Val Val Gly Asn Lys 135 His Leu Leu His Asp

nis Leu Leu His Asp

- (2) INFORMATION FOR SEQ ID NO:1660:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598747 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:
- Met
 Pro
 Phe
 Asp
 Ser
 Pro
 Glu
 Ala
 Gln
 Gln
 Leu
 Asn
 Lys
 Asp
 Ile
 Phe

 Glu
 Thr
 Ile
 Tyr
 Tyr
 His
 Ala
 Leu
 Lys
 Ala
 Ser
 Ala
 Glu
 Leu
 Ala
 Ala
- Trp Pro Ser Leu Arg Glu Thr Ile Ser Lys Val Gly Ile Arg Asn Ser 65 70 75 80
 Leu Leu Val Ala Pro Met Pro Thr Ala Ser Thr Ser Gln Ile Leu Gly
- 85 90 95
 Asn Asn Glu Cys Phe Glu Pro Tyr Thr Ser Asn Ile Tyr Ser Arg Arg
- Asn Asn Glu Cys Phe Glu Pro Tyr Thr Ser Asn Ile Tyr Ser Arg Arg

 100 105 110
- Val Leu Ser Gly Glu Phe Val Val Gly Asn Lys His Leu Leu His Asp 115 120 125
- (2) INFORMATION FOR SEQ ID NO:1661:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598752
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

actcgagcca gccagccage cagcaagccg cttgggcgc atctctag agcttcgtac 60 cctcgaagaa gatccggcg ggcccaataa acacccggct tactacagac tcgcagatgg 120 ccgcagcccag gatgaagtte gtcgcegtcg ccgcagtgc cgccgcgctc gtggcgtccg 180 ccgcagcgcg ctccctcgcc gccgcgctc tcggtacctc ttctgctaga tccgcgctgg atacgtggtt cctgctcaa aatatgatte gtctggtctg gcgcgctga gtccagctcg 300 tgtgtcgtgc gtgtctctgt gttagtgtcc gttctacctt tggattaggt gttggtaccc ctgttgttcc ctttggttgc tcccgctatg aaacgagacg agagaagaat

- (2) INFORMATION FOR SEQ ID NO:1662:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

Leu Glu Pro Ala Ser Gln Pro Ala Ser Arg Leu Gly Ala Ile Ser Leu 1 5 10 15

Glu Leu Arg Thr Leu Glu Glu Asp Pro Ala Arg Pro Asn Lys His Pro 20 25 30

Ala Tyr Tyr Arg Leu Ala Asp Gly Arg Pro Gln Asp Glu Val Arg Arg 35 40 45

Arg Arg Arg His Gly Arg Arg Ala Arg Gly Val Arg Arg Ser Arg Arg 50 55 60

Gly Pro Arg Pro Gly Ser Arg Val Arg Arg Arg Gly Arg Arg Thr Pro 65 70 75 80

Arg Arg Gly Leu Pro Arg Arg Arg Arg Leu Arg Tyr Leu Phe Cys 85 90 95

- (2) INFORMATION FOR SEQ ID NO:1663:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

Met Ala Gly Leu Arg Met Lys Phe Val Ala Val Ala Ala Met Ala Ala 1 5 10 15

Ala Leu Val Ala Ser Ala Ala Ala Ala Glu Ala Pro Ala Pro 20 25 30

Ala Ser Asp Ala Ala Ala Ala Val Pro Leu Ala Ala Ala Ser Leu Ala 35 40 45

Ala Ala Ala Phe Gly Thr Ser Ser Ala Arg Ser Ala Leu Asp Thr Trp 50 55 60

Phe Leu Leu Gln Asn Met Ile Arg Leu Val Trp Arg Ala 65 70 75

- (2) INFORMATION FOR SEQ ID NO:1664:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..72 (D) OTHER INFORMATION: / Ceres Seq. ID 1598755 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664: Met Lys Phe Val Ala Val Ala Ala Met Ala Ala Ala Leu Val Ala Ser 10 Ala Ala Ala Ala Glu Ala Pro Ala Pro Ala Pro Ala Ser Asp Ala Ala 25 30 2.0 Ala Ala Val Pro Leu Ala Ala Ala Ser Leu Ala Ala Ala Ala Phe Gly 45 40 Thr Ser Ser Ala Arg Ser Ala Leu Asp Thr Trp Phe Leu Leu Gln Asn 55 Met Ile Arg Leu Val Trp Arg Ala 70 (2) INFORMATION FOR SEQ ID NO:1665: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 485 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..485 (D) OTHER INFORMATION: / Ceres Seq. ID 1598764 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665: aacaacagcg aacacatctg cttcgcattt cttcccatcc cccttcgcaa cccaaacccc 60 120 aactcqctnn catcgatggc gcccaaggcc gagaagaagc ccgcggcrna gaagccggcg gaggaggage eegeggetga gaaggegeee geegngaaga ageegamgta tgaagegggt 180 240 cccqctqqn caagtccqct gccaaggagg gcggcgaggg caagaggggc aggaagaagg 300 gcaagaagag cgtggagacc tacaagatct acatcttcaa ggtgctgaag caggtgcacc 360 cggacattgg catctcctcc aaggccatgt cgatcatgaa ctccttcatt aacgatatct 420 tegagaaget agetgetgag geegecaage tegegegeta taacaagaag ecaaccatea cctcccgtga gatacagact tccgtgcgcc tcgtccttcc cggggagctc gaatttyagg 480 tgaag (2) INFORMATION FOR SEQ ID NO:1666: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..95 (D) OTHER INFORMATION: / Ceres Seq. ID 1598765 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666: Asn Asn Ser Glu His Ile Cys Phe Ala Phe Leu Pro Ile Pro Leu Arg 10 Asn Pro Asn Pro Asn Ser Xaa Xaa Ser Met Ala Pro Lys Ala Glu Lys 25

Lys Pro Ala Xaa Xaa Lys Pro Ala Glu Glu Pro Ala Ala Glu Lys 35 40 45
Ala Pro Ala Xaa Lys Lys Pro Xaa Tyr Glu Ala Gly Pro Arg Trp Xaa

Ser Pro Leu Pro Arg Arg Ala Ala Arg Ala Arg Gly Ala Gly Arg Arg

75

55

Client Docket No. 80146.003 Ala Arg Arg Ala Trp Arg Pro Thr Arg Ser Thr Ser Ser Arg Cys 90 8.5 (2) INFORMATION FOR SEQ ID NO:1667: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..116 (D) OTHER INFORMATION: / Ceres Seq. ID 1598766 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667: Thr Thr Ala Asn Thr Ser Ala Ser His Phe Phe Pro Ser Pro Phe Ala 10 5 Thr Gln Thr Pro Thr Arg Xaa His Arg Trp Arg Pro Arg Pro Arg Arg 30 25 20 Ser Pro Arg Xaa Arg Ser Arg Arg Arg Ser Pro Arg Leu Arg Arg 45 40 35 Arg Pro Pro Xaa Arg Ser Arg Xaa Met Lys Arg Val Pro Ala Xaa Gln 60 55 Val Arg Cys Gln Gly Gly Arg Arg Gly Gln Glu Gly Gln Glu Gly 70 75 Gln Glu Glu Arg Gly Asp Leu Gln Asp Leu His Leu Gln Gly Ala Glu 90 8.5 Ala Gly Ala Pro Gly His Trp His Leu Leu Gln Gly His Val Asp His 105 100 Glu Leu Leu His 115 (2) INFORMATION FOR SEQ ID NO:1668: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..70 (D) OTHER INFORMATION: / Ceres Seq. ID 1598767 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668: Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Xaa Xaa Lys Pro Ala Glu 10 Glu Glu Pro Ala Ala Glu Lys Ala Pro Ala Xaa Lys Lys Pro Xaa Tyr 20 25 Glu Ala Gly Pro Arg Trp Xaa Ser Pro Leu Pro Arg Arg Ala Ala Arg 40 Ala Arg Gly Ala Gly Arg Arg Ala Arg Arg Ala Trp Arg Pro Thr Arg 50 Ser Thr Ser Ser Arg Cys 70 (2) INFORMATION FOR SEQ ID NO:1669: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 495 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -

(B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1598768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669: 60 aagacggccg ccatctcccc tgttcggttt taggagacct gcgccgctcc tccggccacg cgagcacgcc gaaatggtcg cccacaggtt ccatcagtac caggtggtgg gtcgcgcgct 120 gccgaccccg accgatgagc accccaagat ctaccgcatg aagctctggg ccactaacga 180 ggttcgcgcc aagtcgaagt tctggtactt cctgagaaag ctgaagaagg tgaagaagag 240 caatggccag atgctcgcca tcaacgagat cttcgagcgc aaccctacca ccatcaagaa 300 ctacggcatc tggctgcggt accagagcag gacggggtac acaacatgta caaggagtac 360 420 cgcgacacga ccctgaacgg cgccgtggag cagatgtaca acgagatggc ctcgcgccac cgcgtgaggt ccccctgcat ccagatcatc aagactgcka cggtccactt caagctgtgc 480 aagakggaca acacq

- (2) INFORMATION FOR SEQ ID NO:1670:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670: Arg Arg Pro Pro Ser Pro Leu Phe Gly Phe Arg Arg Pro Ala Pro Leu 10 Leu Arg Pro Arg Glu His Ala Glu Met Val Ala His Arg Phe His Gln 30 25 20 Tyr Gln Val Val Gly Arg Ala Leu Pro Thr Pro Thr Asp Glu His Pro 40 45 Lys Ile Tyr Arg Met Lys Leu Trp Ala Thr Asn Glu Val Arg Ala Lys 55 Ser Lys Phe Trp Tyr Phe Leu Arg Lys Leu Lys Lys Val Lys Lys Ser 75 70 Asn Gly Gln Met Leu Ala Ile Asn Glu Ile Phe Glu Arg Asn Pro Thr 90 85 Thr Ile Lys Asn Tyr Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr Gly 110 105 100 Tyr Thr Thr Cys Thr Arg Ser Thr Ala Thr Arg Pro

120

- (2) INFORMATION FOR SEQ ID NO:1671:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

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- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

Met Val Ala His Arg Phe His Gln Tyr Gln Val Val Gly Arg Ala Leu

1 10 15 15

Pro Thr Pro Thr Asp Glu His Pro Lys Ile Tyr Arg Met Lys Leu Trp 20 25 30

Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp Tyr Phe Leu Arg 35 40 45

Lys Leu Lys Lys Val Lys Lys Ser Asn Gly Gln Met Leu Ala Ile Asn 50 55 60

Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn Tyr Gly Ile Trp

75 65 7.0 Leu Arg Tyr Gln Ser Arg Thr Gly Tyr Thr Thr Cys Thr Arg Ser Thr 90 Ala Thr Arg Pro 100 (2) INFORMATION FOR SEQ ID NO:1672: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..84 (D) OTHER INFORMATION: / Ceres Seq. ID 1598771 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672: Met Ala Arg Cys Ser Pro Ser Thr Arg Ser Ser Ser Ala Thr Leu Pro 5 10 Pro Ser Arg Thr Thr Ala Ser Gly Cys Gly Thr Arg Ala Gly Arg Gly 25 20 Thr Gln His Val Gln Gly Val Pro Arg His Asp Pro Glu Arg Arg Arg 35 Gly Ala Asp Val Gln Arg Asp Gly Leu Ala Pro Pro Arg Glu Val Pro 55 Leu His Pro Asp His Gln Asp Cys Xaa Gly Pro Leu Gln Ala Val Gln 75 Xaa Gly Gln His (2) INFORMATION FOR SEQ ID NO:1673: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..336 (D) OTHER INFORMATION: / Ceres Seq. ID 1598781 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673: agtaaccege ateceacate acteatecae agetegeage egtatteetg tetegaatee 60 tetetegeeg eteegatgge eegeacgaag caaacagcaa ggaagtegae eggeggeaag 120 gececegga ageagetgge caetaagget gegegeaagt eggeeeegge caeeggegge 180 gtgaagaage eccaeegett etgeeeegge acegtegege teegsagate egcaagtace 240 agaagagcac tgagctgctc atccgcaagc tccccttcca gcgcctcgtc cgcgagatcg 300 cgcaggactt caagactgat ctgaggttcc agtcct (2) INFORMATION FOR SEQ ID NO:1674: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1598782 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674: Ser Asn Pro His Pro Thr Ser Leu Ile His Ser Ser Gln Pro Tyr Ser

Cys Leu Glu Ser Ser Leu Ala Ala Pro Met Ala Arg Thr Lys Gln Thr 20 25 30

Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Thr 35 40 45

Lys Ala Ala Arg Lys Ser Ala Pro Ala Thr Gly Gly Val Lys Lys Pro
50 55 60

His Arg Phe Cys Pro Gly Thr Val Ala Leu Xaa Arg Ser Ala Ser Thr 65 70 75 80

Arg Arg Ala Leu Ser Cys Ser Ser Ala Ser Ser Pro Ser Ser Ala Ser 85 90 95

Ser Ala Arg Ser Arg Arg Thr Ser Arg Leu Ile 100 105

- (2) INFORMATION FOR SEQ ID NO:1675:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598783
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

Val Thr Arg Ile Pro His His Ser Ser Thr Ala Arg Ser Arg Ile Pro
1 10 15

Val Ser Asn Pro Leu Ser Pro Leu Arg Trp Pro Ala Arg Ser Lys Gln 20 25 30

Gln Gly Ser Arg Pro Ala Ala Arg Pro Pro Gly Ser Ser Trp Pro Leu 35 40 45

Arg Leu Arg Ala Ser Arg Pro Arg Pro Pro Ala Ala 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1676:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 - MOLECULE EVDE: poptide
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala
1 5 10 15

Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Ala 20 25 30

Thr Gly Gly Val Lys Lys Pro His Arg Phe Cys Pro Gly Thr Val Ala 35 40 45

Leu Xaa Arg Ser Ala Ser Thr Arg Arg Ala Leu Ser Cys Ser Ser Ala
50 55 60

Ser Ser Pro Ser Ser Ala Ser Ser Ala Arg Ser Arg Arg Thr Ser Arg 65 70 75 80

Leu Ile

- (2) INFORMATION FOR SEQ ID NO:1677:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..198 (D) OTHER INFORMATION: / Ceres Seq. ID 1598795 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677: gegatacaac gactteetge agteetgege tgegeeeete ettteegeet eeaeggetee acqctgccga cgtccaccac acagcacggt ckwgtcaccc gatccctcca tggcggcggc agtggcggcg gtcgcggctg ccacgacggc ggaggacgag gcgcgcctgc tgcgtctgga ggagcaggcg gacacggc (2) INFORMATION FOR SEQ ID NO:1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..66 (D) OTHER INFORMATION: / Ceres Seq. ID 1598796 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678: Ala Ile Gln Arg Leu Pro Ala Val Leu Arg Cys Ala Pro Pro Phe Arg 10 Leu His Gly Ser Thr Leu Pro Thr Ser Thr Thr Gln His Gly Xaa Val 2.5 20 Thr Arg Ser Leu His Gly Gly Gly Ser Gly Gly Gly Arg Gly Cys His 40 Asp Gly Gly Arg Gly Ala Pro Ala Ala Ser Gly Gly Ala Gly Gly 55 50 His Gly (2) INFORMATION FOR SEQ ID NO:1679: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..65 (D) OTHER INFORMATION: / Ceres Seq. ID 1598797 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679: Arg Tyr Asn Asp Phe Leu Gln Ser Cys Ala Ala Pro Leu Leu Ser Ala 10 Ser Thr Ala Pro Arg Cys Arg Arg Pro Pro His Ser Thr Val Xaa Ser 25 Pro Asp Pro Ser Met Ala Ala Ala Val Ala Ala Val Ala Ala Ala Thr 40 Thr Ala Glu Asp Glu Ala Arg Leu Leu Arg Leu Glu Glu Gln Ala Asp 55 50 Thr 65 (2) INFORMATION FOR SEQ ID NO:1680:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

Gly Ala Leu Leu

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..65 (D) OTHER INFORMATION: / Ceres Seq. ID 1598798 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680: Asp Thr Thr Thr Ser Cys Ser Pro Ala Leu Arg Pro Ser Phe Pro Pro 10 Pro Arg Leu His Ala Ala Asp Val His His Thr Ala Arg Xaa Xaa His 30 25 20 Pro Ile Pro Pro Trp Arg Arg Gln Trp Arg Arg Ser Arg Leu Pro Arg 40 Arg Arg Arg Thr Arg Arg Ala Cys Cys Val Trp Arg Ser Arg Arg Thr 55 Arg 65 (2) INFORMATION FOR SEQ ID NO:1681: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..349 (D) OTHER INFORMATION: / Ceres Seq. ID 1598802 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681: akagcacgag acacccaata aacacacaca cacaagckak wdagcactac ctgttggttg 60 gattetette agtetageta etegateggt eeettgteea eagttaagtt teagacaeat 120 ggggagcatt ggcagaggca cggccaactg ckccaccgtg ccgcagccgc cgccgtcgac 180 agggaagete atcacgatee tgageatega tggeggegge atcegeggee ttatecegge 240 gaccatcatt gcgtacctcg aggccaagct ccaggagctg gacggcccgg acgctcggat 300 cgccgactac ttcgatgtga ttgccgggac gagcaccggc gccctgctc (2) INFORMATION FOR SEQ ID NO:1682: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..116 (D) OTHER INFORMATION: / Ceres Seq. ID 1598803 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682: Xaa His Glu Thr Pro Asn Lys His Thr His Thr Ser Xaa Xaa Ala Leu 5 10 Pro Val Gly Trp Ile Leu Phe Ser Leu Ala Thr Arg Ser Val Pro Cys 20 25 Pro Gln Leu Ser Phe Arg His Met Gly Ser Ile Gly Arg Gly Thr Ala 40 Asn Cys Xaa Thr Val Pro Gln Pro Pro Pro Ser Thr Gly Lys Leu Ile 60 Thr Ile Leu Ser Ile Asp Gly Gly Gly Ile Arg Gly Leu Ile Pro Ala 75 Thr Ile Ile Ala Tyr Leu Glu Ala Lys Leu Gln Glu Leu Asp Gly Pro 90 Asp Ala Arg Ile Ala Asp Tyr Phe Asp Val Ile Ala Gly Thr Ser Thr

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(2) INF	ORMATION	FOR	SEQ	ID	NO:1683:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1...77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

Met Gly Ser Ile Gly Arg Gly Thr Ala Asn Cys Xaa Thr Val Pro Gln 10

Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly 25

Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu 45

Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr 55

Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu 70

- (2) INFORMATION FOR SEQ ID NO:1684:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..479
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598805
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684: ggcaccagag tcatcgcggc gtgttcaaat cccacaatct tcttgtagca caccactgtc 120 ttcgtccaac tcggcggcga tgtctgggcg cggcaagggc ggcaaggggc tgggcaaggg tggtgcgaaa cgccaccgta agttctccgc gacaacatcc agggtatcac gaagccggca 180 atccggagct ggcgaggagg ggcggcgtga agcgtatctc cgggcttatc tacgaggaga 240 cccgcggcgt gctcaagatc ttcctcgaga atgtcatccg cgacgstnca cctacaccga 300 360 gcacgctcgc cgcaagaccg tcaccgccat ggatgttgtg tacgccctca agcgccaggg cegcactetg taegggtteg gtggttgage geatetette cetegtetge ageggetgee 420 ggtggcgttt cctcagttcc ctctgccttg cttggcttga tgtagagagt tatcagatt
- (2) INFORMATION FOR SEQ ID NO:1685:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:
- Ala Pro Glu Ser Ser Arg Arg Val Gln Ile Pro Gln Ser Ser Cys Ser 10

Thr Pro Leu Ser Ser Ser Asn Ser Ala Ala Met Ser Gly Arg Gly Lys 25 20

Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg His Arg Lys Phe 40

 Ser
 Ala
 Thr
 Thr
 Ser
 Arg
 Val
 Ser
 Arg
 Ser
 Arg
 Gln
 Ser
 Gln
 Ser
 Gln
 Ser
 Gln
 Ser
 Gln
 Ser
 Gln
 Ser
 Gln
 Gln
 Gln
 Gln
 Arg
 Gln
 Arg
 Arg
 Ala
 Tyr
 Leu
 Arg
 Glu
 Cys
 His
 Pro
 Arg
 Xaa
 Xaa
 Xaa
 Yaa
 Arg
 Arg
 Leu
 Arg
 Lys
 Thr
 Val
 Thr
 Ala
 Met
 Asp
 Val

 Thr
 Tyr
 Ala
 Leu
 Lys
 Arg
 Lys
 Thr
 Val
 Thr
 Ala
 Met
 Asp
 Val

 Val
 Tyr
 Ala
 Leu
 Lys
 Arg
 Arg
 Lys
 Thr
 Val
 Thr
 Ala
 Met
 Asp
 Val

 Val
 Tyr
 Ala
 Leu
 Lys
 Arg
 Arg
 Thr
 Leu
 Tyr
 Gly
 Phe
 Gly
 Gly
 Fr
 Leu
 Tyr
 Leu
 Ly

- (2) INFORMATION FOR SEQ ID NO:1686:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

His Gln Ser His Arg Gly Val Phe Lys Ser His Asn Leu Leu Val Ala 1 5 10 15

His His Cys Leu Arg Pro Thr Arg Arg Arg Cys Leu Gly Ala Arg 20 25 30

Ala Ala Arg Gly Trp Ala Arg Val Val Arg Asn Ala Thr Val Ser Ser 40 45

Pro Arg Gln His Pro Gly Tyr His Glu Ala Gly Asn Pro Glu Leu Ala 50 55 60

Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr Glu Glu Thr 65 70 75 80

Arg Gly Val Leu Lys Ile Phe Leu Glu Asn Val Ile Arg Asp Xaa Xaa 85 90 95

Pro Thr Pro Ser Thr Leu Ala Ala Arg Pro Ser Pro Pro Trp Met Leu 100 105 110

Cys Thr Pro Ser Ser Ala Arg Ala Ala Leu Cys Thr Gly Ser Val Val 115 120 125

Glu Arg Ile Ser Ser Leu Val Cys Ser Gly Cys Arg Trp Arg Phe Leu 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1687:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598808
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Ala 1 10 15

Lys Arg His Arg Lys Phe Ser Ala Thr Thr Ser Arg Val Ser Arg Ser 20 25 30

Arg Gln Ser Gly Ala Gly Glu Glu Gly Arg Arg Glu Ala Tyr Leu Arg

Leu Tyr Gly Phe Gly Gly 100

- (2) INFORMATION FOR SEQ ID NO:1688:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..454
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598847
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688: 60 actgacgttc attccgtttc cttgcttgct ccaggtactc ccatcgctat cgaccgggtc ctcgagcgcg ggagatggcg gatcaggaga ccccagttgc agttgaggcc cctaccccgg 120 tccttgggga gccgatggac ctgatgactg ctctgcrctt gtcatgaaga agtcgggtgc 180 tcatgatggc cttgttaagg gtcttcgtga ggctgccaaa gccattgaga agcatgctgc 240 tcagctttgc gtgcttgcgg aggactgtga ccagcctgat tatgtcaagc tggtgaaggc 300 360 tetttgetet gageacaaeg tteaectggt taetgtgeet agegetaaaa etettggega 420 atggtctggg ctttgcaaga ttgattctka gggcaaggcg aggaaggttg tgggttgctc ctgtgttgtc gtcaaggact atggcgaaga atct
- (2) INFORMATION FOR SEQ ID NO:1689:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598848
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

Met Lys Lys Ser Gly Ala His Asp Gly Leu Val Lys Gly Leu Arg Glu

1 5 10 15

Ala Ala Lys Ala Ile Glu Lys His Ala Ala Gln Leu Cys Val Leu Ala

Ala Ala Lys Ala lie Glu Lys His Ala Ala Gli Hed Cys Val Led Hid 20 25 30

Glu Asp Cys Asp Gln Pro Asp Tyr Val Lys Leu Val Lys Ala Leu Cys
35 40 45

Ser Glu His Asn Val His Leu Val Thr Val Pro Ser Ala Lys Thr Leu 50 55 60
Gly Glu Trp Ser Gly Leu Cys Lys Ile Asp Ser Xaa Gly Lys Ala Arg

65 70 75 80

Lys Val Val Gly Cys Ser Cys Val Val Val Lys Asp Tyr Gly Glu Glu
85 90 95

Ser

- (2) INFORMATION FOR SEQ ID NO:1690:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..502
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598874
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690: aaaccctaat cgtgaccgcc gcgccnncag cawctgaagt ttcgtcctcg cggccttctc 60 tecetecaet egaacegege egacgagega egacaacegt tgetgeatte tteaatggeg 120 actgtgccag ttaacccaaa acctttcctg aacaacctga cggggaagcc tgtaattgtc 180 aaactcaagt ggggtatgga gtacaaaggt tatcttgctt cggtggactc ctatatgaat 240 ctccagcttg ccaacactga ggagtacatt gatgggcaat tctctggaaa cctgggagag 300 attctgatca ggtgcaacaa cgttatgtat ctccgaggcg ttccagagga tgcagagata 360 gaggatgcag aatgagaaga tgtgaatgta atttgattct gacatgtatg tttgaatatg 420 ceggtgacaa ctagacctat eggatettag ttatgateag tagggettga ggtgetgtte 480
- (2) INFORMATION FOR SEQ ID NO:1691:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

aaactgagaa aggaatatca cg

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598875
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691: Met Ala Thr Val Pro Val Asn Pro Lys Pro Phe Leu Asn Asn Leu Thr
- 1 5 10 15 Gly Lys Pro Val Ile Val Lys Leu Lys Trp Gly Met Glu Tyr Lys Gly 20 25 30
- 20 25 30

 Tyr Leu Ala Ser Val Asp Ser Tyr Met Asn Leu Gln Leu Ala Asn Thr
 35 40 45
- Glu Glu Tyr Ile Asp Gly Gln Phe Ser Gly Asn Leu Gly Glu Ile Leu 50 55 60
- Ile Arg Cys Asn Asn Val Met Tyr Leu Arg Gly Val Pro Glu Asp Ala 65 70 75 80
- Glu Ile Glu Asp Ala Glu
- (2) INFORMATION FOR SEQ ID NO:1692:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598876
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:
- Met Glu Tyr Lys Gly Tyr Leu Ala Ser Val Asp Ser Tyr Met Asn Leu
 1 10 15
- Gln Leu Ala Asn Thr Glu Glu Tyr Ile Asp Gly Gln Phe Ser Gly Asn 20 25 30
- Leu Gly Glu Ile Leu Ile Arg Cys Asn Asn Val Met Tyr Leu Arg Gly 35 40 45
- Val Pro Glu Asp Ala Glu Ile Glu Asp Ala Glu
 50 55
- (2) INFORMATION FOR SEQ ID NO:1693:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..46
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598877
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

Met Asn Leu Gln Leu Ala Asn Thr Glu Glu Tyr Ile Asp Gly Gln Phe 1 5 10 15

Ser Gly Asn Leu Gly Glu Ile Leu Ile Arg Cys Asn Asn Val Met Tyr 20 25 30

Leu Arg Gly Val Pro Glu Asp Ala Glu Ile Glu Asp Ala Glu 35 40 45

- (2) INFORMATION FOR SEQ ID NO:1694:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..488
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598878
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694: acccagcac aagcaacctc gtccccaaac aagcaaccac cgcctccccg atctcgtcga gaggaagcc aatcccgaaa ccgccgccct attccaatgg cgcccaaggc cgagaagaag

gaggaagccc aatcccgaaa ccgccgcct attccaatgg cgcccaaggc cgagaagaag 120 cccgccgcca agaagcctgc ggaggaggag ccggcgsgna gaaggccacg gcggggaaga 180 agcccaaggc tgagaagcgg ctccccgcgg caagtccgca gcaaggaggg tggcgaaga 240 aaggggaaga agaaggcaaa gaagtcggtg gagacgtaca agatctacat cttcaaggtg ctgaagcagg tgcacccgga cattggcatc tcgtccaagg ccatgtccat catgaactcc tcatcaacg acatcttcga gaagctggcg gcggaggcgg ccaagctggc gcggtacaac 420 aagaagccta ccattacgtc ccgcgagatc cagacctccg ttcgcctcgt cctccccggc 480

- gagctcgc
 (2) INFORMATION FOR SEQ ID NO:1695:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

Thr Gln Gln Gln Ala Thr Ser Ser Pro Asn Lys Gln Pro Pro Pro 1 5 10 15

Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Ala Lys Lys Pro Ala Glu 35 40 45

Glu Glu Pro Ala Xaa Arg Arg Pro Arg Arg Gly Arg Ser Pro Arg Leu 50 60

Arg Ser Gly Ser Pro Arg Gln Val Arg Ser Lys Glu Gly Gly Glu Lys 65 70 75 80

Lys Gly Lys Lys Lys Ala Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr 85 90 95 Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser 100 105 110

Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys 115 120 125

Leu Ala Ala Glu Ala Ala Lys Leu Ala Arg Tyr Asn Lys Lys Pro Thr 130 135 140

Ile Thr Ser Arg Glu Ile Gln Thr Ser Val Arg Leu Val Leu Pro Gly 145 150 155 160 Glu Leu

GIU Leu

- (2) INFORMATION FOR SEQ ID NO:1696:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598880
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Pro Ala Thr Ser Asn Leu Val Pro Lys Gln Ala Thr Thr Ala Ser Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Ile Ser Ser Arg Gly Ser Pro Ile Pro Lys Pro Pro Pro Tyr Ser Asn 20 25 30

Gly Ala Gln Gly Arg Glu Glu Ala Arg Arg Gln Glu Ala Cys Gly Gly 35 40 45

Gly Ala Gly Xaa Xaa Lys Ala Thr Ala Gly Lys Lys Pro Lys Ala Glu 50 55 60

Lys Arg Leu Pro Ala Ala Ser Pro Gln Gln Gly Gly Trp Arg Glu Glu 65 70 75 80

Gly Glu Glu Gly Lys Glu Val Gly Gly Asp Val Gln Asp Leu His
85 90 95

Leu Gln Gly Ala Glu Ala Gly Ala Pro Gly His Trp His Leu Val Gln 100 105 110

Gly His Val His His Glu Leu Leu His Gln Arg His Leu Arg Glu Ala
115
120
125

Gly Gly Gly Gly Gln Ala Gly Ala Val Gln Gln Glu Ala Tyr His 130 135 140

Tyr Val Pro Arg Asp Pro Asp Leu Arg Ser Pro Arg Pro Pro Arg Arg 145 150 155 160

Ala Arg

- (2) INFORMATION FOR SEQ ID NO:1697:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598881
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Ala Lys Lys Pro Ala Glu
1 10 15

Glu Glu Pro Ala Xaa Arg Arg Pro Arg Arg Gly Arg Ser Pro Arg Leu 20 25 30

Arg Ser Gly Ser Pro Arg Gln Val Arg Ser Lys Glu Gly Gly Glu Lys

Lys Gly Lys Lys Lys Lys Ala Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr 50

Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser 70

Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys 95

Leu Ala Ala Glu Ala Ala Lys Leu Ala Arg Tyr Asn Lys Lys Pro Thr 100

Ile Thr Ser Arg Glu Ile Gln Thr Ser Val Arg Leu Val Leu Pro Gly 115

Glu Leu 130

- (2) INFORMATION FOR SEQ ID NO:1698:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..491
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598884
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698: ccggtcccgt ctgcktgcgt gcgatcgacg cagaggcgcg ggcgctcgca ccaagccgat 60 ccgatggcct tcatgcgctc ccgctcaaat gcatcttctg gcatgggagt tgctcctaac 120 attagggaga cgtttgtcga gctccaaatg aagaagacat tccgatatgt tatcttcaaa 180 atcgaagaaa agcaaaagca ggtagttgtg gagaagacag gggccactac tgaaagctat 240 gatgattttb tggcctctct cccagagaat gactgccgat atgcgctgta tgattttgat 300 tttgtcaccg gggagaatgt gcagaaaagc aagattttgc ttcattgcct ggtccccgtc 360 gacatcccgc atccgtgcca agatgcttta ctccacctcg aaggaccgca tcaagtatga 420 ggctcgacgg gttccactac gagatccagg cgaccgaccc atccgaggcg gacattragg 480 ttctgcggga c
- (2) INFORMATION FOR SEQ ID NO:1699:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..139
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699: Pro Val Pro Ser Xaa Cys Val Arg Ser Thr Gln Arg Arg Gly Arg Ser 10 His Gln Ala Asp Pro Met Ala Phe Met Arg Ser Arg Ser Asn Ala Ser 25 20 Ser Gly Met Gly Val Ala Pro Asn Ile Arg Glu Thr Phe Val Glu Leu 40 Gln Met Lys Lys Thr Phe Arg Tyr Val Ile Phe Lys Ile Glu Glu Lys 60 55 Gln Lys Gln Val Val Glu Lys Thr Gly Ala Thr Thr Glu Ser Tyr 75 70 Asp Asp Phe Xaa Ala Ser Leu Pro Glu Asn Asp Cys Arg Tyr Ala Leu 90 85 Tyr Asp Phe Asp Phe Val Thr Gly Glu Asn Val Gln Lys Ser Lys Ile 105 100 Leu Leu His Cys Leu Val Pro Val Asp Ile Pro His Pro Cys Gln Asp

125 120 Ala Leu Leu His Leu Glu Gly Pro His Gln Val 130 135 (2) INFORMATION FOR SEQ ID NO:1700: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..118 (D) OTHER INFORMATION: / Ceres Seq. ID 1598886 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700: Met Ala Phe Met Arg Ser Arg Ser Asn Ala Ser Ser Gly Met Gly Val 10 Ala Pro Asn Ile Arg Glu Thr Phe Val Glu Leu Gln Met Lys Lys Thr 25 Phe Arg Tyr Val Ile Phe Lys Ile Glu Glu Lys Gln Lys Gln Val Val 40 Val Glu Lys Thr Gly Ala Thr Thr Glu Ser Tyr Asp Asp Phe Xaa Ala 55 Ser Leu Pro Glu Asn Asp Cys Arg Tyr Ala Leu Tyr Asp Phe Asp Phe 70 Val Thr Gly Glu Asn Val Gln Lys Ser Lys Ile Leu Leu His Cys Leu 90 85 Val Pro Val Asp Ile Pro His Pro Cys Gln Asp Ala Leu Leu His Leu 105 100 Glu Gly Pro His Gln Val 115 (2) INFORMATION FOR SEQ ID NO:1701: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..115 (D) OTHER INFORMATION: / Ceres Seq. ID 1598887 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701: Met Arg Ser Arg Ser Asn Ala Ser Ser Gly Met Gly Val Ala Pro Asn 10 Ile Arg Glu Thr Phe Val Glu Leu Gln Met Lys Lys Thr Phe Arg Tyr 25 20 Val Ile Phe Lys Ile Glu Glu Lys Gln Lys Gln Val Val Val Glu Lys 40 Thr Gly Ala Thr Thr Glu Ser Tyr Asp Asp Phe Xaa Ala Ser Leu Pro 55 Glu Asn Asp Cys Arg Tyr Ala Leu Tyr Asp Phe Asp Phe Val Thr Gly 70 75 Glu Asn Val Gln Lys Ser Lys Ile Leu Leu His Cys Leu Val Pro Val 85 90 Asp Ile Pro His Pro Cys Gln Asp Ala Leu Leu His Leu Glu Gly Pro 105 100 His Gln Val

- (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..481
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702: adacgettee eegacgeetg actecaaace etttegeete egeegeegee geegeegeet 60 gatageteca gegecetege egteggetge eeggetgeeg teeteeeget aegagetagg 120 180 catctccttc gccgatccag catgggtaag acacgtggta tgggagctkg gcgcaastca 240 akacccacag gaggaaccag aggtgggctg acaaagccta caagaagagc catcttggca 300 acgagtggaa gaaaccettt getggateat eteacgeaaa ggggategte etegaaaaga 360 teggeatega ggccaageag cetaactetg etateegtaa gtgtgetegt gtteagetgt tgaagaacgg taagaagatt gccgcctttg tgccgaacga cggctgcttg aactacatcg 420 aggaaaacga tgaggtgctg atcgcggggt tcggtcgtaa gggtcacgcc gtgggagata 480
- (2) INFORMATION FOR SEQ ID NO:1703:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598889
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:
- Xaa Ala Ser Pro Thr Pro Asp Ser Lys Pro Phe Arg Leu Arg Arg 1 5 10 15

Arg Arg Arg Leu Ile Ala Pro Ala Pro Ser Pro Ser Ala Ala Arg Leu 20 25 30

Pro Ser Ser Arg Tyr Glu Leu Gly Ile Ser Phe Ala Asp Pro Ala Trp 35 40 45

Val Arg His Val Val Trp Glu Xaa Gly Ala Xaa Gln Xaa Pro Gln Glu 50 55 60

Glu Pro Glu Val Gly

- (2) INFORMATION FOR SEQ ID NO:1704:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..73
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598890
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:
- Met Gly Lys Thr Arg Gly Met Gly Ala Xaa Arg Xaa Ser Xaa Pro Thr
- Gly Gly Thr Arg Gly Gly Leu Thr Lys Pro Thr Arg Arg Ala Ile Leu 20 25 30
- Ala Thr Ser Gly Arg Asn Pro Leu Leu Asp His Leu Thr Gln Arg Gly 35 40 45
- Ser Ser Ser Lys Arg Ser Ala Ser Arg Pro Ser Ser Leu Thr Leu Leu 50 55 60

Ser Val Ser Val Leu Val Phe Ser Cys 70 (2) INFORMATION FOR SEQ ID NO:1705: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..67 (D) OTHER INFORMATION: / Ceres Seq. ID 1598891 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705: Met Gly Ala Xaa Arg Xaa Ser Xaa Pro Thr Gly Gly Thr Arg Gly Gly 10 Leu Thr Lys Pro Thr Arg Arg Ala Ile Leu Ala Thr Ser Gly Arg Asn 25 20 Pro Leu Leu Asp His Leu Thr Gln Arg Gly Ser Ser Ser Lys Arg Ser 4.0 Ala Ser Arg Pro Ser Ser Leu Thr Leu Leu Ser Val Ser Val Leu Val 55 50 Phe Ser Cys (2) INFORMATION FOR SEQ ID NO:1706: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..466 (D) OTHER INFORMATION: / Ceres Seq. ID 1598896 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706: 60 agtctttccc tgccacagtc atcagccgcc gtaggagcag gagtgaggga gcgcgatggc 120 ggagaagaag cagcgcccag gagggtccag gaaggacgag gtggttaccc gcgagtacac catcaacctc cacaagcgcc tccacggatg caccttcaag aagaaagccc ccaatgctat 180 caaggaaatc aggaagtttg cacagaaggc aatgggcacc actgacatca ggattgatgt 240 300 gaaactcaac aagcacatct ggagcagtgg tatccggagt gtgccgaggc gtgtccgtgt caggatogca ogcaagagga acgatgagga agacgocaag gaagagottt actotottgt 360 taccgttgct gagattcccc cagaaggcct gaagggtctg ggtacaaggt tgtggaggac 420 gacgagtaga tctgcctggg tactgatctg tgtcaactgt caaatc (2) INFORMATION FOR SEQ ID NO:1707: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..79 (D) OTHER INFORMATION: / Ceres Seq. ID 1598897 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707: Ser Phe Pro Ala Thr Val Ile Ser Arg Arg Arg Ser Arg Ser Glu Gly 15 10 Ala Arg Trp Arg Arg Arg Ser Ser Ala Gln Glu Gly Pro Gly Arg Thr

25

Arg Trp Leu Pro Ala Ser Thr Pro Ser Thr Ser Thr Ser Ala Ser Thr

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 35 40 45 Asp Ala Pro Ser Arg Arg Lys Pro Pro Met Leu Ser Arg Lys Ser Gly 50 55 60 Ser Leu His Arg Arg Gln Trp Ala Pro Leu Thr Ser Gly Leu Met 70 (2) INFORMATION FOR SEQ ID NO:1708: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..137 (D) OTHER INFORMATION: / Ceres Seq. ID 1598898 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708: Met Ala Glu Lys Lys Gln Arg Pro Gly Gly Ser Arg Lys Asp Glu Val 10 Val Thr Arg Glu Tyr Thr Ile Asn Leu His Lys Arg Leu His Gly Cys 25 Thr Phe Lys Lys Lys Ala Pro Asn Ala Ile Lys Glu Ile Arg Lys Phe Ala Gln Lys Ala Met Gly Thr Thr Asp Ile Arg Ile Asp Val Lys Leu 55 Asn Lys His Ile Trp Ser Ser Gly Ile Arg Ser Val Pro Arg Arg Val 70 Arg Val Arg Ile Ala Arg Lys Arg Asn Asp Glu Glu Asp Ala Lys Glu 90 85 Glu Leu Tyr Ser Leu Val Thr Val Ala Glu Ile Pro Pro Glu Gly Leu 100 105 Lys Gly Leu Gly Thr Arg Leu Trp Arg Thr Thr Ser Arg Ser Ala Trp 115 120 Val Leu Ile Cys Val Asn Cys Gln Ile 130 135 (2) INFORMATION FOR SEQ ID NO:1709: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..85 (D) OTHER INFORMATION: / Ceres Seq. ID 1598899 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

Met Gly Thr Thr Asp Ile Arg Ile Asp Val Lys Leu Asn Lys His Ile 1 5 10 15

Trp Ser Ser Gly Ile Arg Ser Val Pro Arg Arg Val Arg Val Arg Ile
20 25 30

Ala Arg Lys Arg Asn Asp Glu Glu Asp Ala Lys Glu Glu Leu Tyr Ser 35 40 45

Leu Val Thr Val Ala Glu Ile Pro Pro Glu Gly Leu Lys Gly Leu Gly 50 55 60

Thr Arg Leu Trp Arg Thr Thr Ser Arg Ser Ala Trp Val Leu Ile Cys 65 70 75 80

Val Asn Cys Gln Ile 85

- (2) INFORMATION FOR SEQ ID NO:1710:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..479
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710: aggaccqqtc actcqqcaqt cggcacgcag gctagcagca cagcagcagc cagagccatc 60 ccctctcctc gctacgcttc gcttcctcgg cgccgattcc tcctcctcct cctccaccct 120 cgtccgtccc gttccggcgc gcgactcgcc cagagatggc gaacsagaga tcgggtgtcg 180 ctgtgaacga tgagtgcatg ctgaagtttg gcgagctgca gtcgaagagg ctgcaccgct 240 tcataacttt caagatggac gacaagttca aggagatagt tgtggaccag gtcggggatc 300 gegetaceag etacgatgae tteacaaaea geeteeetga gaatgaetge egataegega 360 tctatgattt cgactttgtt actgcagagg atgtccagaa gagcaggatc ttctatatcc 420 tatggtcccc atcctccgcc aaggtgaaga gcaagatgct ttatgcaagc tcaaaccag
- (2) INFORMATION FOR SEQ ID NO:1711:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598905
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:
- Met Ala Asn Xaa Arg Ser Gly Val Ala Val Asn Asp Glu Cys Met Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Lys Phe Gly Glu Leu Gln Ser Lys Arg Leu His Arg Phe Ile Thr Phe 20 25 30

Lys Met Asp Asp Lys Phe Lys Glu Ile Val Val Asp Gln Val Gly Asp 35 40 45

Arg Ala Thr Ser Tyr Asp Asp Phe Thr Asn Ser Leu Pro Glu Asn Asp 50 55 60
Cys Arg Tyr Ala Ile Tyr Asp Phe Asp Phe Val Thr Ala Glu Asp Val

Cys Arg Tyr Ala IIe Tyr Asp Phe Asp Phe Val Thr Ala Giu Asp Val 65 70 75 80 Gln Lys Ser Arg Ile Phe Tyr Ile Leu Trp Ser Pro Ser Ser Ala Lys

85 90
Val Lys Ser Lys Met Leu Tyr Ala Ser Ser Asn Gln
100 105

- (2) INFORMATION FOR SEQ ID NO:1712:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598906
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

Met Leu Lys Phe Gly Glu Leu Gln Ser Lys Arg Leu His Arg Phe Ile
1 5 10 15

Thr Phe Lys Met Asp Asp Lys Phe Lys Glu Ile Val Val Asp Gln Val 20 25 30

Gly Asp Arg Ala Thr Ser Tyr Asp Asp Phe Thr Asn Ser Leu Pro Glu

35 40 4.5 Asn Asp Cys Arg Tyr Ala Ile Tyr Asp Phe Asp Phe Val Thr Ala Glu 55 60 Asp Val Gln Lys Ser Arg Ile Phe Tyr Ile Leu Trp Ser Pro Ser Ser 75 70 Ala Lys Val Lys Ser Lys Met Leu Tyr Ala Ser Ser Asn Gln 90 (2) INFORMATION FOR SEQ ID NO:1713: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..75 (D) OTHER INFORMATION: / Ceres Seq. ID 1598907 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713: Met Asp Asp Lys Phe Lys Glu Ile Val Val Asp Gln Val Gly Asp Arg 10 Ala Thr Ser Tyr Asp Asp Phe Thr Asn Ser Leu Pro Glu Asn Asp Cys 25 20 Arg Tyr Ala Ile Tyr Asp Phe Asp Phe Val Thr Ala Glu Asp Val Gln 40 Lvs Ser Arg Ile Phe Tyr Ile Leu Trp Ser Pro Ser Ser Ala Lys Val 55 Lys Ser Lys Met Leu Tyr Ala Ser Ser Asn Gln 70 (2) INFORMATION FOR SEQ ID NO:1714: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..450 (D) OTHER INFORMATION: / Ceres Seq. ID 1598914 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714: 60 ctcttcacta caccetttcc teegtgeege eccaetttte teeteeegeg ecceteegeg 120 agetecetae ecetegeget caegeeggeg acaagtttee gecagagtta ggtagateag 180 qtqctqcqcc ggcagccgtg gaagggatgg aggacctcgc gagttcgcgt ggcggcgggg gatgcggtgg tcttgatgcg cagatcgaac agctcatgga gtgccgcccg ctcccagaga 240 300 cggaggttaa aacactgtgt gagaaggcca aggagatatt aatggaggaa agcaatgttc agccagttaa aagccctgtg acgatttgtg gtgatattca tggccaattc catgatcttt 360 420 tagaactttt ccggattggt ggggaagtgt ccagatacaa attatttgtt tatgggtgat tatgtggatc gtggctatta ctctgttgag (2) INFORMATION FOR SEQ ID NO:1715: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..138 (D) OTHER INFORMATION: / Ceres Seq. ID 1598915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

```
Leu His Tyr Thr Leu Ser Ser Val Pro Pro His Phe Ser Pro Pro Ala
                                   1.0
Pro Leu Arg Glu Leu Pro Thr Pro Arg Ala His Ala Gly Asp Lys Phe
                                                    30
                               25
Pro Pro Glu Leu Gly Arg Ser Gly Ala Ala Pro Ala Ala Val Glu Gly
Met Glu Asp Leu Ala Ser Ser Arg Gly Gly Gly Cys Gly Gly Leu
                        55
                                            60
Asp Ala Gln Ile Glu Gln Leu Met Glu Cys Arg Pro Leu Pro Glu Thr
                                        75
                    70
Glu Val Lys Thr Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Glu Glu
                                    90
                85
Ser Asn Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile
                                                  110
                               105
            100
His Gly Gln Phe His Asp Leu Leu Glu Leu Phe Arg Ile Gly Glu
                                                125
                           120
       115
Val Ser Arg Tyr Lys Leu Phe Val Tyr Gly
                       135
    130
(2) INFORMATION FOR SEQ ID NO:1716:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 90 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..90
          (D) OTHER INFORMATION: / Ceres Seq. ID 1598916
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:
Met Glu Asp Leu Ala Ser Ser Arg Gly Gly Gly Cys Gly Gly Leu
                                    1.0
Asp Ala Gln Ile Glu Gln Leu Met Glu Cys Arg Pro Leu Pro Glu Thr
                                25
           2.0
Glu Val Lys Thr Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Glu Glu
                            40
Ser Asn Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile
                        55
His Gly Gln Phe His Asp Leu Leu Glu Leu Phe Arg Ile Gly Glu
                    70
Val Ser Arg Tyr Lys Leu Phe Val Tyr Gly
                85
 (2) INFORMATION FOR SEQ ID NO:1717:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 534 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..534
           (D) OTHER INFORMATION: / Ceres Seq. ID 1598921
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:
 awagttgtgc tgatacgatg tgcaattctt gctctttctt ctctagaatg ttcctgccga
                                                                        60
 tgcttttata agagaaggtt gctctttctt ctctagagtg tctagctgag aacatggtga
                                                                       120
 cctcaagcaa gggcaaggta tatgtaaccg gggcctcagg ctttgttgcc tcttggctta
                                                                       180
 tcaaacggct cctcgagtct ggatatcatg tggtagggac tgtcagggac ccaggaaatc
                                                                       240
                                                                       300
 accaaaaaac agcccacctt tggaaattac ctggcgctaa agagaggctg caaatcgtgc
                                                                       360
 gagctgatct gttggaagaa gggagcttcg acagcgccgt gatggcctgt gagggtgtat
```

tecacactge atececegte etegetaaac eegactetae tageaaggag gaaacgeteg

ttcctgcggt gaacggtact ctgaacgtgc tgagatcgtg caagaagaac cccttcctga 480 aaaggtcgtc ctttacgtct tcgtcgtctg cggtgaggat cagggacgaa tggt

- (2) INFORMATION FOR SEQ ID NO:1718:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids(B) TYPE: amino acid
 - (B) IIIE. amino ac
 - (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598922
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

Met Val Thr Ser Ser Lys Gly Lys Val Tyr Val Thr Gly Ala Ser Gly

Phe Val Ala Ser Trp Leu Ile Lys Arg Leu Leu Glu Ser Gly Tyr His 20 25 30

Val Val Gly Thr Val Arg Asp Pro Gly Asn His Gln Lys Thr Ala His

Leu Trp Lys Leu Pro Gly Ala Lys Glu Arg Leu Gln Ile Val Arg Ala 50 55 60

Asp Leu Leu Glu Glu Gly Ser Phe Asp Ser Ala Val Met Ala Cys Glu 65 70 75 80

Gly Val Phe His Thr Ala Ser Pro Val Leu Ala Lys Pro Asp Ser Thr 85 90 95

Ser Lys Glu Glu Thr Leu Val Pro Ala Val Asn Gly Thr Leu Asn Val 100 105 110

Leu Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Ser Ser Phe Thr 115 120 125

Ser Ser Ser Ser Ala Val Arg Ile Arg Asp Glu Trp 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1719:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..447
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598927
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

aaagagcac cagcacactc gtcttttcc tctacggccg ccaccatcgc ctcgcggccg cctgccgctc cgctcgaaag tttttggtga agattttttg aagctgagaa gatggtgctg 120 aagacggaac tctgccgctt cagtggccag aagatctatc ctggggaaagg catccggttt 180 attcgtgctg attctcaggt tttccttttt gccaactcta aatgcaagcg ctacttccac 240 aaccgcctga agctctgcaa agcttacctg gacagcaatg tacaggaagc catactcgag gcgccgccc accaagaagc catactcgag gtccattgtg ggtgcttcct tggaagtgat ccagaagaag agagctgaga agcctgaggt 420 ccgtgatgct gctagagaag ctgctct

- (2) INFORMATION FOR SEQ ID NO:1720:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..67
 (D) OTHER INFORMATION: / Ceres Seq. ID 1598928
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:
 Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
 1 5 10 15
- Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu 20 25 30
- Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Leu 35 40 45
- Cys Lys Ala Tyr Leu Asp Ser Asn Val Gln Glu Ala Ala Gln Glu Gly 50 55 60

His Pro Cys 65

- (2) INFORMATION FOR SEQ ID NO:1721:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..55
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598929
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:
- Met Gln Ala Leu Leu Pro Gln Pro Pro Glu Ala Leu Gln Ser Leu Pro 1 5 10 15
- Gly Gln Gln Cys Thr Gly Ser Ser Thr Arg Arg Thr Ser Met Leu Lys 20 25 30
- Leu Ser Arg Arg Gly Ala Ala Pro Pro Arg Ser His Thr Arg Gly Pro 35 40

Leu Trp Val Leu Pro Trp Lys
50 55

- (2) INFORMATION FOR SEQ ID NO:1722:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:
- Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys

 10 15
- Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
- Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val

Arg Asp Ala Ala Arg Glu Ala Ala

- (2) INFORMATION FOR SEQ ID NO:1723:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598932
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

 thtccttcga gccgtccgcc gctcccaccc ccaccactcg ccagctcgcc acttcctccc for gtctcctccc ttccagaggc ggcgcgtaas gcccgatggc cgcctctctc ctccacgccg ccgccgcctc gctccagagt tccacccage acgcccgcgc ggssccgccg cctttcaccc ccccgcgtt gccccatccc tacgccttac gcgctctcg ttctcgacca atcgccacct cgagatttca ctccgggcga tctcggccag tcgcc
- (2) INFORMATION FOR SEQ ID NO:1724:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598933
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:
- Xaa Pro Ser Ser Arg Pro Pro Leu Pro Pro Pro Pro Leu Ala Ser Ser 1 5 10 15
- Pro Leu Pro Pro Val Ser Ser Leu Pro Glu Ala Ala Arg Xaa Ala Arg 20 25 30
- Trp Pro Pro Leu Ser Ser Thr Pro Pro Pro Pro Arg Ser Arg Val Pro 35 40 45
- Pro Ser Thr Pro Ala Arg Xaa Arg Arg Leu Ser Pro Pro Arg Val Cys 50 55
- Pro Ile Pro Thr Pro Tyr Ala Leu Leu Val Leu Asp Gln Ser Pro Pro 65 70 75 80
- Arg Asp Phe Thr Pro Gly Asp Leu Gly Gln Ser 85 90
- (2) INFORMATION FOR SEQ ID NO:1725:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598934
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:
- Xaa Leu Arg Ala Val Arg Arg Ser His Pro His His Ser Pro Ala Arg 1 5 10 15
- His Phe Leu Pro Ser Pro Pro Phe Gln Arg Arg Arg Val Xaa Pro Asp 20 25 30
- Gly Arg Leu Ser Pro Pro Arg Arg Arg Leu Ala Pro Glu Phe His 35 40 45
- Pro Ala Arg Pro Arg Xaa Xaa Ala Ala Phe His Pro Leu Ala Cys Ala 50 55 60
- Pro Ser Leu Arg Leu Thr Arg Ser Ser Phe Ser Thr Asn Arg His Leu 65 70 75 80
 Glu Ile Ser Leu Arg Ala Ile Ser Ala Ser Arg
- 85
 (2) INFORMATION FOR SEQ ID NO:1726:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..60 (D) OTHER INFORMATION: / Ceres Seq. ID 1598935 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726: Met Ala Ala Ser Leu Leu His Ala Ala Ala Ala Ser Leu Gln Ser Ser 10 Thr Gln His Ala Arg Ala Xaa Pro Pro Pro Phe Thr Pro Ser Arg Val 30 25 20 Pro His Pro Tyr Ala Leu Arg Ala Pro Arg Ser Arg Pro Ile Ala Thr 40 Ser Arg Phe His Ser Gly Arg Ser Arg Pro Val Ala 55 (2) INFORMATION FOR SEQ ID NO:1727: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..205 (D) OTHER INFORMATION: / Ceres Seq. ID 1598936 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727: aagtcagcac actgaaaccc ctgcaaaccc tagtgcttcc caccgatcca tttcagccgc 60 cgccgcgcgt assaagcagg agcagcaagg atgccggctg gccacgggct gcgctcgcgg 120 acgsscgacc tgnttcgcgc ccctttccgc aagaagggct acatcccgct caccacctac 180 ctccgcacct acaagatcgg cgact (2) INFORMATION FOR SEQ ID NO:1728: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..68 (D) OTHER INFORMATION: / Ceres Seq. ID 1598937 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728: Ser Gln His Thr Glu Thr Pro Ala Asn Pro Ser Ala Ser His Arg Ser 10 Ile Ser Ala Ala Ala Arg Xaa Lys Gln Glu Gln Gln Gly Cys Arg 20 25 Leu Ala Thr Gly Cys Ala Arg Gly Xaa Xaa Thr Xaa Phe Ala Pro Leu 40 45 Ser Ala Arg Arg Ala Thr Ser Arg Ser Pro Pro Thr Ser Ala Pro Thr 60 55 50 Arg Ser Ala Thr
 - (2) INFORMATION FOR SEQ ID NO:1729:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..67
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598938
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:
- Val Ser Thr Leu Lys Pro Leu Gln Thr Leu Val Leu Pro Thr Asp Pro 1 5 10 15
- Phe Gln Pro Pro Pro Arg Val Xaa Ser Arg Ser Ser Lys Asp Ala Gly 20 25 30
- Trp Pro Arg Ala Ala Leu Ala Asp Xaa Arg Pro Xaa Ser Arg Pro Phe 35 40 45
- Pro Gln Glu Gly Leu His Pro Ala His His Leu Pro Pro His Leu Gln 50 55 60

Asp Arg Arg

65

- (2) INFORMATION FOR SEQ ID NO:1730:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..38
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598939
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

Met Pro Ala Gly His Gly Leu Arg Ser Arg Thr Xaa Asp Leu Xaa Arg 1 5 10 15

Ala Pro Phe Arg Lys Lys Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg

Thr Tyr Lys Ile Gly Asp 35

- (2) INFORMATION FOR SEQ ID NO:1731:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..473
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598943
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

cttccgcttc caacttccgt tccgcaaatt gaaaactcgg cgttgcctgc gcccctgcct 60 cgagctcgaa ggactttgtc ctatacgtcg ttgtccagct cctcgcatat tgtggcctgg 120 tgcagattgg agatccgcc ggacttggat cgagtcctcc tgtctttgga cattcattgg 180 agtgctccat tcattgagac agcatgccta agataaagac aagccgtgtc aagtatcctg 240 aaggatggga gcttattgaa ccaacaatcc gtgagttgga tgccaaaatg agagaagctg 300 aaaatgatcc acatgatgga aagagaagt gtgaagctct ctggcctatt ttccgcattt ctcatcaaag gagccgctac atatacgatc tttattacag aaggaaggag atatcacagg 420 agctttatga gtttctgcct agaccagggt tatgcagacc gtaacctgat tgc

- (2) INFORMATION FOR SEQ ID NO:1732:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids(B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

Leu Pro Leu Pro Thr Ser Val Pro Gln Ile Glu Asn Ser Ala Leu Pro 10

Ala Pro Leu Pro Arg Ala Arg Arg Thr Leu Ser Tyr Thr Ser Leu Ser 30 25 20

Ser Ser Ser His Ile Val Ala Trp Cys Arg Leu Glu Ile Arg Pro Asp 40

Leu Asp Arg Val Leu Leu Ser Leu Asp Ile His Trp Ser Ala Pro Phe 55

Ile Glu Thr Ala Cys Leu Arg 70

- (2) INFORMATION FOR SEQ ID NO:1733:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

Phe Arg Phe Gln Leu Pro Phe Arg Lys Leu Lys Thr Arg Arg Cys Leu 1.0 5

Arg Pro Cys Leu Glu Leu Glu Gly Leu Cys Pro Ile Arg Arg Cys Pro 25 20

Ala Pro Arg Ile Leu Trp Pro Gly Ala Asp Trp Arg Ser Ala Arg Thr 45 40

Trp Ile Glu Ser Ser Cys Leu Trp Thr Phe Ile Gly Val Leu His Ser 55 50

Leu Arg Gln His Ala

- (2) INFORMATION FOR SEQ ID NO:1734:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

Met Pro Lys Ile Lys Thr Ser Arg Val Lys Tyr Pro Glu Gly Trp Glu 5 10

Leu Ile Glu Pro Thr Ile Arg Glu Leu Asp Ala Lys Met Arg Glu Ala 25 20

Glu Asn Asp Pro His Asp Gly Lys Arg Lys Cys Glu Ala Leu Trp Pro 40

Ile Phe Arg Ile Ser His Gln Arg Ser Arg Tyr Ile Tyr Asp Leu Tyr 60 55

Tyr Arg Arg Lys Glu Ile Ser Gln Glu Leu Tyr Glu Phe Leu Pro Arg 75

Pro Gly Leu Cys Arg Pro

85

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 493 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: single

 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: DNA (genomic)

 (ix) FEATURE:

 (A) NAME/KEY:
 (B) LOCATION: 1..493
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598953
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735: accataaatg cgccgcggcc gtcctcgctg cccaaccctt cgctgcgccg ccgcctccga 60 categictet tegiceceae gageaacega taateegeeg gegetgagat gitggittat 120 caagacctcc tatctggcga cgagctcctg tcggattcat tcacctacaa ggagctcgag 180 aacggcgtcc tgtgggaggt cgagggaaak tgggtcaccc aaggtcctgt tgatgtagac 240 attggtgcca atccatccgc cgagggtggt gaggatgaaa gcgttgatga cacagccgtg 300 aaggtggttg atattgttga cacattccgt ctacaggagc aacctccttt tgacaagaaa 360 tcatttgtct cttacataaa aaaatacatc aagaatctca ctgctgtgtt ggagccagak 420 aaagcggatg agttcaaaaa gggtgtcgag ggtgcaacaa gtttctcctt ggcaagctga 480
- (2) INFORMATION FOR SEQ ID NO:1736:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

aggaccttca att

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598954
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736: Met Arg Arg Gly Arg Pro Arg Cys Pro Thr Leu Arg Cys Ala Ala Ala

1 5 10 15
Ser Asp Ile Val Ser Ser Ser Pro Arg Ala Thr Asp Asn Pro Pro Ala

Ser Asp Ile Val Ser Ser Ser Pro Arg Ala Thr Asp Asn Pro Pro Ala
20 25 30

Leu Arg Cys Trp Phe Ile Lys Thr Ser Tyr Leu Ala Thr Ser Ser Cys 35 40 45

Arg Ile His Ser Pro Thr Arg Ser Ser Arg Thr Ala Ser Cys Gly Arg 50 55 60

Ser Arg Glu Xaa Gly Ser Pro Lys Val Leu Leu Met 70 75

- (2) INFORMATION FOR SEQ ID NO:1737:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598955
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

Met Leu Val Tyr Gln Asp Leu Leu Ser Gly Asp Glu Leu Leu Ser Asp 1 5 10

Ser Phe Thr Tyr Lys Glu Leu Glu Asn Gly Val Leu Trp Glu Val Glu

Gly Xaa Trp Val Thr Gln Gly Pro Val Asp Val Asp Ile Gly Ala Asn 35 40 45

Pro Ser Ala Glu Gly Gly Glu Asp Glu Ser Val Asp Asp Thr Ala Val

50 55 Lys Val Val Asp Ile Val Asp Thr Phe Arg Leu Gln Glu Gln Pro Pro 75 7.0 Phe Asp Lys Lys Ser Phe Val Ser Tyr Ile Lys Lys Tyr Ile Lys Asn 90 Leu Thr Ala Val Leu Glu Pro Xaa Lys Ala Asp Glu Phe Lys Lys Gly 105 Val Glu Gly Ala Thr Ser Phe Ser Leu Ala Ser 120 115 (2) INFORMATION FOR SEQ ID NO:1738: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 440 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..440 (D) OTHER INFORMATION: / Ceres Seq. ID 1598957 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738: atcgagacac acacagaact totootgtog gootactaat acaactagot goodtottag 60 gtatactgtg atggccacct tgtcctccac agtagtagtt gcacttggtg acctctcttc 120 ttgctccttg taacgtgtgg ctcgtgcgcg agaccggtga gctttaacgc ctccgacctc 180 . accgccgatc ccggctggga tgctgccagg gccacctgta cggtgcgccc accggcgcgg 240 tectgatgae gaeggtggtg eetgtggatt caagaaegtg aacetgeege egtteteggs 300 antgacgtcg tgcggcaacg agccctgtt caaggacggc aagggctgcg gctcctgcta 360 ccagatacga tgccaaaacc accetgeetg etceggcaac ccagagaegg tgateateac 420 tgacatgaac tactaccccg (2) INFORMATION FOR SEQ ID NO:1739: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1598958 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739: Ser Arg His Thr Gln Asn Phe Ser Cys Arg Pro Thr Asn Thr Thr Ser 10 Cys Pro Leu Arg Tyr Thr Val Met Ala Thr Leu Ser Ser Thr Val Val 25 20 Val Ala Leu Gly Asp Leu Ser Ser Cys Ser Leu 40 35 (2) INFORMATION FOR SEQ ID NO:1740: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 80 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..80 (D) OTHER INFORMATION: / Ceres Seq. ID 1598959 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

Met Leu Pro Gly Pro Pro Val Arg Cys Ala His Arg Arg Gly Pro Asp

- (2) INFORMATION FOR SEQ ID NO:1741:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..465
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598960
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741: 60 atatgattga ttagtccgta tcgtcctggc tgggatggat gccccgatcc accaattctg 120 ttgcggattt gttcgctctg tggttccggt ggtagcagat gaacatccgg ggatgtcgac 180 tcctgcgagg aagaggctga tgagggattt caagcggttg atgcaggacc ctccggccgg cataagtggc gccccgcaga taacaacata atgctgtgga atgctgtcat atttggacct 240 gatgataccc cgtgggatgg aggtacgttt aagctgactc tccagtttaa tgaagaatat 300 ccaaacaaac caccaactgt gcgatttgtt tctaggatgt tccatcctaa catttatgct 360 gatggaagca tatgcttaga tatcctgcag aatcagtgga gtccgatata tgatgtagct 420 gcgatactca cgtcaatcca gtcattgttg tgcgatccaa acccg
- (2) INFORMATION FOR SEQ ID NO:1742:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..58
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598961
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

Met Asp Ala Pro Ile His Gln Phe Cys Cys Gly Phe Val Arg Ser Val 1 5 10 15

Val Pro Val Val Ala Asp Glu His Pro Gly Met Ser Thr Pro Ala Arg

Lys Arg Leu Met Arg Asp Phe Lys Arg Leu Met Gln Asp Pro Pro Ala

- Gly Ile Ser Gly Ala Pro Gln Ile Thr Thr 50 55
- (2) INFORMATION FOR SEQ ID NO:1743:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598962

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:
Met Leu Trp Asn Ala Val Ile Phe Gly Pro Asp Asp Thr Pro Trp Asp
                                                        15
                                  10
Gly Gly Thr Phe Lys Leu Thr Leu Gln Phe Asn Glu Glu Tyr Pro Asn
                                                     30
                                25
Lys Pro Pro Thr Val Arg Phe Val Ser Arg Met Phe His Pro Asn Ile
                            40
Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Gln Trp Ser
                        55
Pro Ile Tyr Asp Val Ala Ala Ile Leu Thr Ser Ile Gln Ser Leu Leu
                                        75
                    70
Cys Asp Pro Asn Pro
                85
(2) INFORMATION FOR SEQ ID NO:1744:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 43 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..43
          (D) OTHER INFORMATION: / Ceres Seq. ID 1598963
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:
Met Phe His Pro Asn Ile Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile
                                    1.0
Leu Gln Asn Gln Trp Ser Pro Ile Tyr Asp Val Ala Ala Ile Leu Thr
                                 25
           20
Ser Ile Gln Ser Leu Leu Cys Asp Pro Asn Pro
                            40
        35
(2) INFORMATION FOR SEQ ID NO:1745:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 389 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..389
           (D) OTHER INFORMATION: / Ceres Seq. ID 1598964
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:
 ctctcgattc ggaaaacctc caaccctanc cgcgatccgr caacgcctcc atccctagsc
gactgctgca assttcagag ctcaagagtc agggcgccat kgcgacagag acggagacss
                                                                        120
 ttcgcctttc argctgagat caaccagctg ctctcactca tcatcaacac cttctattcc
                                                                        180
 aacaaggaga tetteeteeg ggageteatt tecaactett eegatgegtt ggacaaaate
                                                                       240
 aggttcgaga gcctcactga saakagcrag ctcgatgcgc mscggagctg ttcatccaca
                                                                       300
 ttgtaccara caaggetteg aacaegetet ceateategn cageggeate ggeatgacea
                                                                       360
 agtccgasct tktcwacaac ctcggtacc
 (2) INFORMATION FOR SEQ ID NO:1746:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 118 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..118
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(D) OTHER INFORMATION: / Ceres Seq. ID 1598965

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:
Leu Ser Ile Arg Lys Thr Ser Asn Pro Xaa Arg Asp Pro Xaa Thr Pro
                                    10
Pro Ser Leu Xaa Asp Cys Cys Xaa Xaa Gln Ser Ser Arg Val Arg Ala
                                25
Pro Xaa Arg Gln Arg Arg Xaa Phe Ala Phe Xaa Ala Glu Ile Asn
                            40
Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile
                        55
Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile
                    70
                                        75
Arg Phe Glu Ser Leu Thr Xaa Xaa Ser Xaa Leu Asp Ala Xaa Arg Ser
                                    90
                85
Cys Ser Ser Thr Leu Tyr Xaa Thr Arg Leu Arg Thr Arg Ser Pro Ser
                                105
            100
Ser Xaa Ala Ala Ser Ala
        115
(2) INFORMATION FOR SEQ ID NO:1747:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 505 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..505
          (D) OTHER INFORMATION: / Ceres Seq. ID 1598972
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:
                                                                        60
ataatcctgc ccacaacgcc gtctcctaaa ccttagccgc gcgkacgccc accagcagct
geceettget gtegeegeet eteteegege gaeegateta eegeegeege eaceatgteg
                                                                       120
ctgatcgccg gcgaggactt ccaacatatt ctgcgtctgc tgaacaccaa cgtggatggg
                                                                       180
aagcagaaga tcatgttcgc catgacctcc ataaagggtg ttgggcgccg cttctccaac
                                                                       240
                                                                       300
atcgtctgca agaaggccga catcgacatg aacaagaggg ccggtgagct gacgcctgaa
gagetggage geetgatgae ggtegtggee aaccetagge agtteaaggt geeggaetgg
                                                                       360
ttcctcaaca ggaagaagga ttacaaggat ggaaggttct cacaggtcgt gtccaacgcc
                                                                       420
ctcgacatga agctcaggga cgacctcgag aggctcaaga agatcaggaa ccaccgtggt
                                                                       480
ctgcgtcact actggggcct ccgtg
(2) INFORMATION FOR SEQ ID NO:1748:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 130 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..130
           (D) OTHER INFORMATION: / Ceres Seq. ID 1598973
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:
Met Ser Leu Ile Ala Gly Glu Asp Phe Gln His Ile Leu Arg Leu Leu
                                     10
Asn Thr Asn Val Asp Gly Lys Gln Lys Ile Met Phe Ala Met Thr Ser
                                                     30
                                 25
             20
 Ile Lys Gly Val Gly Arg Arg Phe Ser Asn Ile Val Cys Lys Lys Ala
 Asp Ile Asp Met Asn Lys Arg Ala Gly Glu Leu Thr Pro Glu Glu Leu
                         55
 Glu Arg Leu Met Thr Val Val Ala Asn Pro Arg Gln Phe Lys Val Pro
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Asp Trp Phe Leu Asn Arg Lys Lys Asp Tyr Lys Asp Gly Arg Phe Ser

90 85 Gln Val Val Ser Asn Ala Leu Asp Met Lys Leu Arg Asp Asp Leu Glu 100 105 110 Arg Leu Lys Lys Ile Arg Asn His Arg Gly Leu Arg His Tyr Trp Gly 120 Leu Ara 130 (2) INFORMATION FOR SEQ ID NO:1749: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..104 (D) OTHER INFORMATION: / Ceres Seq. ID 1598974 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749: Met Phe Ala Met Thr Ser Ile Lys Gly Val Gly Arg Arg Phe Ser Asn 10 Ile Val Cys Lys Lys Ala Asp Ile Asp Met Asn Lys Arg Ala Gly Glu 25 2.0 Leu Thr Pro Glu Glu Leu Glu Arg Leu Met Thr Val Val Ala Asn Pro 4.0 Arg Gln Phe Lys Val Pro Asp Trp Phe Leu Asn Arg Lys Lys Asp Tyr 55 Lys Asp Gly Arg Phe Ser Gln Val Val Ser Asn Ala Leu Asp Met Lys 75 65 70 Leu Arg Asp Asp Leu Glu Arg Leu Lys Lys Ile Arg Asn His Arg Gly 85 Leu Arg His Tyr Trp Gly Leu Arg 100 (2) INFORMATION FOR SEQ ID NO:1750: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..101 (D) OTHER INFORMATION: / Ceres Seq. ID 1598975 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750: Met Thr Ser Ile Lys Gly Val Gly Arg Arg Phe Ser Asn Ile Val Cys 10 Lys Lys Ala Asp Ile Asp Met Asn Lys Arg Ala Gly Glu Leu Thr Pro 20 25 Glu Glu Leu Glu Arg Leu Met Thr Val Val Ala Asn Pro Arg Gln Phe 40 35 Lys Val Pro Asp Trp Phe Leu Asn Arg Lys Lys Asp Tyr Lys Asp Gly 55 Arg Phe Ser Gln Val Val Ser Asn Ala Leu Asp Met Lys Leu Arg Asp 75 70 Asp Leu Glu Arg Leu Lys Lys Ile Arg Asn His Arg Gly Leu Arg His 90 85 Tyr Trp Gly Leu Arg 100

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..455
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598976
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751: aakaggaaac ccatttacgt atatgccctt gtcccggttc ctttccccat ccccaactcc 60 attatttgct tgatccttga gaagagagag gaagacgaga gctagaagcg aaggagaaaa 120 gcagttette agetaggagg gcacaggaag gaggagatgg egteaaagag gatteagaag 180 gageteaagg atetgeagaa ggaeeeteee acetegtgea gtgeaggtee tgttggtgaa 240 gacatgttcc actggcaggc aacaataatg ggtccatctg atagcccata ctctggtgga 300 360 gttttcctag tcacaatcca ttttcctcct gattatcctt tcaaaccacc aaaggtgcat 420 ttcgtactaa ggtgttccat ccaaacatca acagcaacgg gagcatttgc ctcgacatct tgaaggacca gtggagtccg gcactaacaa tctcc
- (2) INFORMATION FOR SEQ ID NO:1752:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598977
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:
- Met Ala Ser Lys Arg Ile Gln Lys Glu Leu Lys Asp Leu Gln Lys Asp 1 5 10 15

Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Gly Glu Asp Met Phe His 20 25 30

Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly 35 40 45

Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro 50 55 60

Pro Lys Val His Phe Val Leu Arg Cys Ser Ile Gln Thr Ser Thr Ala 65 70 75 80

Thr Gly Ala Phe Ala Ser Thr Ser 85

- (2) INFORMATION FOR SEQ ID NO:1753:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1598978
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr

Ser Gly Gly Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro 20 25 30

Phe Lys Pro Pro Lys Val His Phe Val Leu Arg Cys Ser Ile Gln Thr 35 40 45

Ser Thr Ala Thr Gly Ala Phe Ala Ser Thr Ser

55 50 (2) INFORMATION FOR SEQ ID NO:1754: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..51 (D) OTHER INFORMATION: / Ceres Seq. ID 1598979 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754: Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly Val Phe Leu Val Thr 10 Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val His Phe 30 2.5 Val Leu Arg Cys Ser Ile Gln Thr Ser Thr Ala Thr Gly Ala Phe Ala 40 35 Ser Thr Ser 50 (2) INFORMATION FOR SEQ ID NO:1755: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..482 (D) OTHER INFORMATION: / Ceres Seq. ID 1599016 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755: 60 ccaaacctag cgatcgcaga gagtgcgccc ggaccccgga ccgcgccggc tcgcaaactc cccacaaccc tcgtcgccgc cggctgctcc acccccgcca ccgccatggg taaattccgc 120 180 aagcttggcc gcaattactc ccaacgcctc tgcatgctca ggacgatggt gtcgcagctg qtqaagcacg agcgcatcga gaccaccgtt gccaaggcga aggaggttcg gcggaaggcg 240 gatcagatgg tgcagctagg gaaggaggt actcagcatg cagcaagacg tgctgctgcc 300 tttgttcggg gtgatgatgt cgttcataag ctatttactg agctggcctt ccgctacaga 360 gatcgagctg ggggctacac aagaatgtta agaaccagga tacgtgttgg tgatgctgct 420 ccaatggcat acatcgagtt cgtggatagg gakaatgagc ttcgagaggc caaacctgca 480 ac (2) INFORMATION FOR SEQ ID NO:1756: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1599017 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756: Pro Asn Leu Ala Ile Ala Glu Ser Ala Pro Gly Pro Arg Thr Ala Pro 10 Ala Arg Lys Leu Pro Thr Thr Leu Val Ala Ala Gly Cys Ser Thr Pro 30 25 2.0 Ala Thr Ala Met Gly Lys Phe Arg Lys Leu Gly Arg Asn Tyr Ser Gln 40 35 Arg Leu Cys Met Leu Arg Thr Met Val Ser Gln Leu Val Lys His Glu

55 50 Arg Ile Glu Thr Thr Val Ala Lys Ala Lys Glu Val Arg Arg Lys Ala 70 75 Asp Gln Met Val Gln Leu Gly Lys Glu Gly Thr Gln His Ala Ala Arg 90 85 Arg Ala Ala Ala Phe Val Arg Gly Asp Asp Val Val His Lys Leu Phe 105 100 Thr Glu Leu Ala Phe Arg Tyr Arg Asp Arg Ala Gly Gly Tyr Thr Arg 125 120 Met Leu Arg Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr 130 135 140 Ile Glu Phe Val Asp Arg Xaa Asn Glu Leu Arg Glu Ala Lys Pro Ala 150 155

- (2) INFORMATION FOR SEQ ID NO:1757:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599018
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757: Met Gly Lys Phe Arg Lys Leu Gly Arg Asn Tyr Ser Gln Arg Leu Cys 10

Met Leu Arg Thr Met Val Ser Gln Leu Val Lys His Glu Arg Ile Glu 25 20

Thr Thr Val Ala Lys Ala Lys Glu Val Arg Arg Lys Ala Asp Gln Met 40

Val Gln Leu Gly Lys Glu Gly Thr Gln His Ala Ala Arg Arg Ala Ala Ala Phe Val Arg Gly Asp Asp Val Val His Lys Leu Phe Thr Glu Leu

7.5 70 Ala Phe Arg Tyr Arg Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg

85 90 Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe

105 110 100 Val Asp Arg Xaa Asn Glu Leu Arg Glu Ala Lys Pro Ala 120

- (2) INFORMATION FOR SEQ ID NO:1758:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

115

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599019
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

Met Leu Arg Thr Met Val Ser Gln Leu Val Lys His Glu Arg Ile Glu 10 5

Thr Thr Val Ala Lys Ala Lys Glu Val Arg Arg Lys Ala Asp Gln Met 20 25

Val Gln Leu Gly Lys Glu Gly Thr Gln His Ala Ala Arg Arg Ala Ala 40 35

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Ala Phe Val Arg Gly Asp Asp Val Val His Lys Leu Phe Thr Glu Leu
                                             60
                        55
Ala Phe Arg Tyr Arg Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg
                                         75
                    70
Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe
                                    90
                85
Val Asp Arg Xaa Asn Glu Leu Arg Glu Ala Lys Pro Ala
                                105
            100
(2) INFORMATION FOR SEQ ID NO:1759:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 478 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..478
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599020
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:
acageceega etgggetata ttegttetee eggegtgete egteteteet eteagegega
                                                                        120
cgattacggt aacgeegteg eegeectaeg geteagatet tegtegteat etteteegge
aacgagcacc caaagatggt ggtccttcaa ccagatcggt tcctgagcga gctgacgagc
                                                                        180
atgtacgage ggassacgga gaagggetee gtetgggtea ccatgaageg atcaactete
                                                                        240
aagggcaagg cacagttgcg gaagatggag aataaggggc aggaggtaga gcacaggtgc
                                                                        300
ctcgtccgcg cctccaatgg caagaagaac atctccacct cggtttctct aaaggagtac
                                                                        360
acaaagtttc aagcttcata cgcaacagtt cttaaggccc atatgcatgc tctgaagaaa
                                                                        420
agggagaga aagacaagaa gaagactgca gatgctgaga aggcaattga gaccgcac
(2) INFORMATION FOR SEQ ID NO:1760:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 90 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..90
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599021
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:
 Ser Pro Asp Trp Ala Ile Phe Val Leu Pro Ala Cys Ser Val Ser Pro
                                     10
 Leu Ser Ala Thr Ile Thr Val Thr Pro Ser Pro Pro Tyr Gly Ser Asp
                                 25
             20
 Leu Arg Arg His Leu Leu Arg Gln Arg Ala Pro Lys Asp Gly Gly Pro
                             40
         35
 Ser Thr Arg Ser Val Pro Glu Arg Ala Asp Glu His Val Arg Ala Xaa
                                              60
 Xaa Gly Glu Gly Leu Arg Leu Gly His His Glu Ala Ile Asn Ser Gln
                                          75
                     70
```

85 (2) INFORMATION FOR SEQ ID NO:1761: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid

Gly Gln Gly Thr Val Ala Glu Asp Gly Glu

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

60 120

180

240

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1599022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:
Met Val Val Leu Gln Pro Asp Arg Phe Leu Ser Glu Leu Thr Ser Met

1 10 15

Tyr Glu Arg Xaa Thr Glu Lys Gly Ser Val Trp Val Thr Met Lys Arg

Ser Thr Leu Lys Gly Lys Ala Gln Leu Arg Lys Met Glu Asn Lys Gly 35 40 45

Gln Glu Val Glu His Arg Cys Leu Val Arg Ala Ser Asn Gly Lys Lys 50 55 60

Asn Ile Ser Thr Ser Val Ser Leu Lys Glu Tyr Thr Lys Phe Gln Ala 65 70 75 80

Ser Tyr Ala Thr Val Leu Lys Ala His Met His Ala Leu Lys Lys Arg 85 90 95

Glu Arg Lys Asp Lys Lys Lys Thr Ala Asp Ala Glu Lys Ala Ile Glu
100 105 110

Thr Ala

- (2) INFORMATION FOR SEQ ID NO:1762:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:
Met Tyr Glu Arg Xaa Thr Glu Lys Gly Ser Val Trp Val Thr Met Lys
1 10 15

Arg Ser Thr Leu Lys Gly Lys Ala Gln Leu Arg Lys Met Glu Asn Lys
20 25 30

Gly Gln Glu Val Glu His Arg Cys Leu Val Arg Ala Ser Asn Gly Lys 35 40 45

Lys Asn Ile Ser Thr Ser Val Ser Leu Lys Glu Tyr Thr Lys Phe Gln 50 55 60

Ala Ser Tyr Ala Thr Val Leu Lys Ala His Met His Ala Leu Lys Lys 65 70 75 80

Arg Glu Arg Lys Asp Lys Lys Lys Thr Ala Asp Ala Glu Lys Ala Ile 85 90 95

Glu Thr Ala

- (2) INFORMATION FOR SEQ ID NO:1763:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..484
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599058
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

attgcgatta atcctcccat catccatgtc cattatatac tatactccct agctagctcc tagcaggcag agcagcaagc tagctgtgta agaagaagag gaggactgga ggaggaagaa gactatcgat cgatcgatcc atccatccat cgaattaatg gcggcgacaa caccgtacaa gcccaagagg atcctgatca cgggcgccgc ggggttcatc gcgtcccacg tggcgatccg

categtgaac aggtaccetg agtacaaggt ggtggtgetg gacaagettg actactgete 300 caacetcaag aaceteetee eegteatggg eteeggegge aacaacetea agttegteaa 360 gggegacate geeagegeeg acetegteag etteateetg geeacegagg geategacae 420 egtgatgeae teegeggege agacceaegt ggacaactee teeggeaact eettggagtt 480 cace

- (2) INFORMATION FOR SEQ ID NO:1764:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599059
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

Met Ala Ala Thr Thr Pro Tyr Lys Pro Lys Arg Ile Leu Ile Thr Gly $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Ala Ala Gly Phe Ile Ala Ser His Val Ala Ile Arg Ile Val As
n Arg 20 25 30

Tyr Pro Glu Tyr Lys Val Val Leu Asp Lys Leu Asp Tyr Cys Ser 35 40 45

Asn Leu Lys Asn Leu Leu Pro Val Met Gly Ser Gly Gly Asn Asn Phe 50 55 60

Lys Phe Val Lys Gly Asp Ile Ala Ser Ala Asp Leu Val Ser Phe Ile 65 70 75 80

Leu Ala Thr Glu Gly Ile Asp Thr Val Met His Phe Ala Ala Gln Thr 85 90 95

His Val Asp Asn Ser Phe Gly Asn Ser Leu Glu Phe Thr

- (2) INFORMATION FOR SEQ ID NO:1765:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..474
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599062
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

aagttgaata ggatcgaaaa ccctaatccg tctccctct atcgcactcg cgtctctttc ctattcgcgc cgccgcct gctgcaassg ccagctcgcc gtcgtccgaa tagtacactc 120 taacgccgcc atggggcgta tgcacagccg cgggaagggt atctcgtcgt cggcgctgcc 180 gtacaagagg acgcctccta cctggctgaa gaccgccgcc tccgacgtgg aggagatgat 240 cacaaaggca gcgaagaagg gacagatgcc gtcgcagatc ggcgtcctgc tccgtgacca 300 gcacggtatc ccccttgtca agagtgtcac cggcagcaaa atcctccgca tcctcaaggc 360 ccatgggctg gcacccgaaa tcccggagac ctgtacttcc tcatcaagaa ggcggtggcg 420 ataaggaagc accttgagag gaacaggaag gacaaagact ctaaattcag gctc

- (2) INFORMATION FOR SEQ ID NO:1766:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids(B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1599063 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766: Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu 10 Pro Tyr Lys Arg Thr Pro Pro Thr Trp Leu Lys Thr Ala Ala Ser Asp 20 25 Val Glu Glu Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser 4.0 Gln Ile Gly Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys 55 Ser Val Thr Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu 70 75 Ala Pro Glu Ile Pro Glu Thr Cys Thr Ser Ser Ser Arg Arg Trp 85 90 Arg

- (2) INFORMATION FOR SEQ ID NO:1767:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599064
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu Pro Tyr Lys 1 5 10 15

Arg Thr Pro Pro Thr Trp Leu Lys Thr Ala Ala Ser Asp Val Glu Glu 20 25 30

Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser Gln Ile Gly 35 40 45

Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys Ser Val Thr 50 55 60

Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu Ala Pro Glu 65 70 75 80

- Ile Pro Glu Thr Cys Thr Ser Ser Ser Arg Arg Trp Arg 85 90
- (2) INFORMATION FOR SEQ ID NO:1768:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599065
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser Gln Ile Gly
1 5 10 15

Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys Ser Val Thr 20 25 30

Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu Ala Pro Glu 35 40 45

Ile Pro Glu Thr Cys Thr Ser Ser Ser Arg Arg Arg Trp Arg 50 55 60

(2) INFORMATION FOR SEQ ID NO:1769:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 250 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..250
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599068
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:
 ctcttttaat tecceegeeg eegeceeteg ceaegeteeg eeageegetg eeaetegeea 60
 cgttecaeca geoggegee ettettetea eteegetgge geoggegege gttatecatg 120
 gegteggaga akaageaate eaaceegatg agggagatea aggtgeagaa getggtgete 180
 aacateteeg teggagaag tggggatege eteaeeegeg eegecaaggt eetggageaa 240
 ctgagttgge
- (2) INFORMATION FOR SEQ ID NO:1770:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..49
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599069
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

Ser Phe Asn Ser Pro Ala Ala Ala Pro Arg His Ala Pro Pro Ala Ala 1 5 10 15

Gly Ala Gly Ala Arg Tyr Pro Trp Arg Arg Arg Xaa Ser Asn Pro Thr 35 40 45

Arg

- (2) INFORMATION FOR SEQ ID NO:1771:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599070
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Leu Leu Ile Pro Pro Pro Pro Pro Leu Ala Thr Leu Arg Gln Pro Leu 1 5 10 15

Pro Leu Ala Thr Phe His Gln Pro Ala Pro Leu Leu Thr Pro Leu 20 25 30

Ala Pro Ala Arg Val Ile His Gly Val Gly Glu Xaa Ala Ile Gln Pro 35 40 45

Asp Glu Gly Asp Gln Gly Ala Glu Ala Gly Ala Gln His Leu Arg Arg
50 55 60

Arg Glu Trp Gly Ser Pro His Pro Arg Arg Gln Gly Pro Gly Ala Thr 65 70 75 80 Glu Leu

(2) INFORMATION FOR SEQ ID NO:1772:

Client Docket No. 80146.003 Page 961 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..44 (D) OTHER INFORMATION: / Ceres Seq. ID 1599071 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772: Met Ala Ser Glu Xaa Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val 10 5 Gln Lys Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu 20 25 Thr Arg Ala Ala Lys Val Leu Glu Gln Leu Ser Trp 35 40 (2) INFORMATION FOR SEQ ID NO:1773: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..460 (D) OTHER INFORMATION: / Ceres Seq. ID 1599076 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773: 60 ctatgacate tgccgccgct cccttgacat tgagcgccca acctacacca acctcaacag gcttgtctcc caggtcatct catccctgac ggcttccctg aggttcgatg gtgctctgaa 120 cgttgatgtg aacgagttcc agaccaacct ggtgccctac ccgaggatcc acttcatgct 180 ttegtectae getecagtea tttetgetga gaaggeetae caegageage tgteegtgge 240 300 cqaaatcacc aacaqcqcct tcgagccatc ctccatgatg gccaagtgcg acccccgcca 360 tggcaagtac atggcatgct gcctcatgta ccgtggtgat gtggttccca aggacgtgaa cgctgctgtg gccacaatca agaccaagcg caccatccag ttcgtggact ggtgcccgac 420 tggcttcaag tgcggaatca actaccagcc tcccagcgtc (2) INFORMATION FOR SEQ ID NO:1774: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..153 (D) OTHER INFORMATION: / Ceres Seq. ID 1599077 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774: Tyr Asp Ile Cys Arg Arg Ser Leu Asp Ile Glu Arg Pro Thr Tyr Thr 10 Asn Leu Asn Arg Leu Val Ser Gln Val Ile Ser Ser Leu Thr Ala Ser 25

Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Val Asn Glu Phe Gln Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Met Leu Ser Ser Tyr Ala

Pro Val Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser Val Ala 75 70

Glu Ile Thr Asn Ser Ala Phe Glu Pro Ser Ser Met Met Ala Lys Cys 90

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Client Docket No. 80146.003
Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Leu Met Tyr Arg Gly
                                105
Asp Val Val Pro Lys Asp Val Asn Ala Ala Val Ala Thr Ile Lys Thr
        115
                            120
                                             125
Lys Arg Thr Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe Lys Cys
    130
                       135
                                           140
Gly Ile Asn Tyr Gln Pro Pro Ser Val
                   150
(2) INFORMATION FOR SEQ ID NO:1775:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 95 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..95
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599078
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:
Met Leu Ser Ser Tyr Ala Pro Val Ile Ser Ala Glu Lys Ala Tyr His
                                    10
Glu Gln Leu Ser Val Ala Glu Ile Thr Asn Ser Ala Phe Glu Pro Ser
```

 Met
 Leu
 Ser
 Tyr
 Ala
 Pro
 Val
 Ile
 Ser
 Ala
 Glu
 Lys
 Ala
 Tyr
 His

 Glu
 Glu
 Leu
 Ser
 Val
 Ala
 Glu
 Ile
 Thr
 Asn
 Ser
 Ala
 Phe
 Glu
 Pro
 Ser

 Ser
 Met
 Met
 Ala
 Lys
 Cys
 Asp
 Pro
 Arg
 His
 Gly
 Lys
 Tyr
 Met
 Ala
 Cys

 Cys
 Leu
 Met
 Tyr
 Arg
 Gly
 Asp
 Val
 Val
 Pro
 Arg
 Pro
 Lys
 Asp
 Val
 Asp
 Ala
 Frage
 Ala
 Ala

Pro Thr Gly Phe Lys Cys Gly Ile Asn Tyr Gln Pro Pro Ser Val 85 90 95

- (2) INFORMATION FOR SEQ ID NO:1776:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..446
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599084
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

aaaacctctc teccagteac egecaceaea geegeeagea gteeateaee ggtteegtte 60 gaatgggeeg caaggaegea aggetagggt ttegegegae geegaegtna eggeagegag 120 gatgagatgg eegeegetee tgeegeeget geggeagase tetaegagat ettgggagtt 180 gagaagaetg etteaeaaea agaaataaag aaggeatate acaaattgge tetgeaeete 240 eateeagata agaateetgg ggatgagkaa geeaaagaka agttteagea getgeagaag 300 gttatateea ttettggaga tgeagagaaa agagetttat atgatgagae tggeattaet 360 gatgatgatg eaetggtgg agaagetgea aatgatette aggagtaett eagaacaatg 420 tacaagaagg teaetgagge tgacat

- (2) INFORMATION FOR SEQ ID NO:1777:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1599085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

Lys Pro Leu Ser Gln Ser Pro Pro Pro Gln Pro Pro Ala Val His His 1 5 10 15

Arg Phe Arg Ser Asn Gly Pro Gln Gly Arg Lys Ala Arg Val Ser Arg 20 25 30

Asp Ala Asp Xaa Thr Ala Ala Arg Met Arg Trp Pro Pro Leu Leu Pro $35 \hspace{1cm} 40 \hspace{1cm} 45$

Pro Leu Arg Gln Xaa Ser Thr Arg Ser Trp Glu Leu Arg Arg Leu Leu 50 55 60

His Asn Lys Lys

65

- (2) INFORMATION FOR SEQ ID NO:1778:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

Met Ala Ala Ala Pro Ala Ala Ala Ala Xaa Leu Tyr Glu Ile Leu 1 5 10 15 .

Gly Val Glu Lys Thr Ala Ser Gln Gln Glu Ile Lys Lys Ala Tyr His $20 \\ \hspace{1.5cm} 25 \\ \hspace{1.5cm} 30$

Lys Leu Ala Leu His Leu His Pro Asp Lys Asn Pro Gly Asp Glu Xaa $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Ala Lys Xaa Lys Phe Gln Gln Leu Gln Lys Val Ile Ser Ile Leu Gly 50 55 60

Asp Ala Glu Lys Arg Ala Leu Tyr Asp Glu Thr Gly Ile Thr Asp Asp 65 70 75 80

Asp Ala Leu Val Gly Glu Ala Ala Asn Asp Leu Gln Glu Tyr Phe Arg 85 90 95

Thr Met Tyr Lys Lys Val Thr Glu Ala Asp 100 105

- (2) INFORMATION FOR SEQ ID NO:1779:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..61
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

Met Xaa Lys Pro Lys Xaa Ser Phe Ser Ser Cys Arg Arg Leu Tyr Pro 1 5 10 15

Phe Leu Glu Met Gln Arg Lys Glu Leu Tyr Met Met Arg Leu Ala Leu 20 25 30

Leu Met Met His Trp Trp Glu Lys Leu Gln Met Ile Phe Arg Ser 35 40 45

Thr Ser Glu Gln Cys Thr Arg Arg Ser Leu Arg Leu Thr 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1780:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..481
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599092
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

caagtgaaga agaggatteg teeccagaaa etacagagga agagacagaa gaagatgaac 60 agaaagagaa aaageetaag acgaagacaa taaaggagac taettetgaa tgggaactte 120 tgaatgatgt gaaggetgta tggettegea geecaaagga ggttaetgae gaagaataet 180 egaagtttta eeacteacta geeaaggaet teagtgatga eaageetatg ggttggagee 240 actteactge tgaaggagat gttgagttea aagetttget etteatteea eegaagetee 300 geatgatete tatgagagtt actacaacag eaacaagtea aaceteaagt tgtatgttag 360 aagagtgtte atetetgatg aatttgatga eettetteeg aagtatetea getttttgag 420 ggtatttgtt gaeteagaea caetgeeget gaatgtgtea egagaaatge teeageaaca 480

- (2) INFORMATION FOR SEQ ID NO:1781:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..138
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599093
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

Ser Glu Glu Glu Asp Ser Ser Pro Glu Thr Thr Glu Glu Glu Thr Glu

1 10 15

Glu Asp Glu Gln Lys Glu Lys Pro Lys Thr Lys Thr Ile Lys Glu
20 25 30

Thr Thr Ser Glu Trp Glu Leu Leu Asn Asp Val Lys Ala Val Trp Leu 35 40 45

Arg Ser Pro Lys Glu Val Thr Asp Glu Glu Tyr Ser Lys Phe Tyr His 50 55 60

Ser Leu Ala Lys Asp Phe Ser Asp Asp Lys Pro Met Gly Trp Ser His 65 70 75 80

Phe Thr Ala Glu Gly Asp Val Glu Phe Lys Ala Leu Leu Phe Ile Pro 85 90 95

Gln Thr Ser Ser Cys Met Leu Glu Glu Cys Ser Ser Leu Met As
n Leu 115 120 125

Met Thr Phe Phe Arg Ser Ile Ser Ala Phe 130 135

- (2) INFORMATION FOR SEQ ID NO:1782:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..265
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599094
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

accacgctgt gagtgactcg gtcgcatctt ccccattctc catcgacgca ccggcggcgg 60 cgcaagtgaa gcgaagaga aaggaagcta cgagatgtcg gcgaccactg cagcggtgcc 120 cttctggcgg gcggcggga tgacctacat cggctactcc aacatctgcg ctgcgctggt ccggaactgc ctcaaggagc ccttcaagtc tgaggccgcg tcccgssaga aggttcattt 240 ctccatttcc aagtggacgg atggc

- (2) INFORMATION FOR SEQ ID NO:1783:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..46
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599095
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

His Ala Val Ser Asp Ser Val Ala Ser Ser Pro Phe Ser Ile Asp Ala 1 5 10 15

Pro Ala Ala Gln Val Lys Arg Gly Lys Glu Ala Thr Arg Cys 20 25 30

Arg Arg Pro Leu Gln Arg Cys Pro Ser Gly Gly Arg Arg Gly
35 40 45

- (2) INFORMATION FOR SEQ ID NO:1784:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..57
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599096
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly Met
1 5 10 15

Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn Cys 20 25 30

Leu Lys Glu Pro Phe Lys Ser Glu Ala Ala Ser Xaa Xaa Lys Val His $35 \hspace{1cm} 40 \hspace{1cm} 45$

Phe Ser Ile Ser Lys Trp Thr Asp Gly 50

- (2) INFORMATION FOR SEQ ID NO:1785:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..42
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Cys Leu Lys Glu Pro Phe Lys Ser Glu Ala Ala Ser Xaa Xaa Lys Val 20 25 30

His Phe Ser Ile Ser Lys Trp Thr Asp Gly

- (2) INFORMATION FOR SEQ ID NO:1786:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..376
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599107
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

aaaccctacc cgactccgc gccgctccgc cgccnntccg cctcagcgca tcgccctccg
ccacagcgta ccgcgacctc atcgatcacc ttcaactttc aatcatggcg gacgtcgatg
tcgaaccgga gtngccgccg gcgctccaa gaagaggacg ttccgcaagt acagctaccg
cggcgtcgac ctagatgcgc ttctcgacat gtccacggac gacctcgtcc agctcttccc
cgcgcgcgcc aggagaaggt tccagagggg tctgaagagg aagcccatgg cactcatcaa
gaagctgcgc aaggcgaaaa aggatgctcc tgctggtgag aagcyagagc cagtcaagac
360
acatctccgt aacatg

- (2) INFORMATION FOR SEQ ID NO:1787:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599108
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Lys Pro Tyr Pro Thr Pro Pro Pro Leu Arg Arg Xaa Ser Ala Ser Ala 1 10 15 His Arg Pro Pro Pro Gln Arg Thr Ala Thr Ser Ser Ile Thr Phe Asn

20 25 30

Phe Gln Ser Trp Arg Thr Ser Met Ser Asn Arg Ser Xaa Arg Arg Arg

Ser Gln Glu Glu Asp Val Pro Gln Val Gln Leu Pro Arg Arg Pro 50 55 60

Arg Cys Ala Ser Arg His Val His Gly Arg Pro Arg Pro Ala Leu Pro 65 70 75 80

Arg Ala Arg Gln Glu Lys Val Pro Glu Gly Ser Glu Glu Glu Ala His 85 90 95

Gly Thr His Gln Glu Ala Ala Gln Gly Glu Lys Gly Cys Ser Cys Trp
100 105 110

- (2) INFORMATION FOR SEQ ID NO:1788:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599109
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

Asn Pro Thr Arg Leu Arg Arg Ser Ala Ala Xaa Pro Pro Gln Arg 1 5 10 15

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Client Docket No. 80146.003
Ile Ala Leu Arg His Ser Val Pro Arg Pro His Arg Ser Pro Ser Thr
                                25
Phe Asn His Gly Gly Arq Arq Cys Arq Thr Gly Xaa Ala Ala Gly Ala
                            40
Pro Lys Lys Arg Thr Phe Arg Lys Tyr Ser Tyr Arg Gly Val Asp Leu
                        55
Asp Ala Leu Leu Asp Met Ser Thr Asp Asp Leu Val Gln Leu Phe Pro
Ala Arg Ala Arg Arg Phe Gln Arg Gly Leu Lys Arg Lys Pro Met
Ala Leu Ile Lys Lys Leu Arg Lys Ala Lys Lys Asp Ala Pro Ala Gly
                               105
Glu Lys Xaa Glu Pro Val Lys Thr His Leu Arg Asn Met
        115
                          120
(2) INFORMATION FOR SEQ ID NO:1789:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 73 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
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- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..73
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

Met Ser Asn Arg Ser Xaa Arg Arg Ser Gln Glu Glu Asp Val Pro 10

Gln Val Gln Leu Pro Arg Arg Pro Arg Cys Ala Ser Arg His Val 20 25

His Gly Arg Pro Arg Pro Ala Leu Pro Arg Ala Arg Gln Glu Lys Val 40

Pro Glu Gly Ser Glu Glu Glu Ala His Gly Thr His Gln Glu Ala Ala 5.5

Gln Gly Glu Lys Gly Cys Ser Cys Trp 70

- (2) INFORMATION FOR SEQ ID NO:1790:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..182
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599111
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

categocag cocteetgge cocatteete teteteceet cecteete caeegecaee getteatece etteatetee aceteetaeg aggykgeege geeteeatge teggeegega 120 ccgcaggcct cagctctagc agcgttcaat actgtaggct agcggagagg tgggggatgg

- (2) INFORMATION FOR SEQ ID NO:1791:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599112
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

His Pro Pro Ala Leu Leu Ala Pro Phe Leu Ser Leu Pro Ser Leu Leu 1 $$ 5 $$ 10 $$ 15

Ser Thr Ala Thr Ala Ser Ser Pro Ser Ser Pro Pro Pro Thr Arg Xaa $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$

Pro Arg Leu His Ala Arg Pro Arg Pro Gln Ala Ser Ala Leu Ala Ala 35 40 45

Phe Asn Thr Val Gly 50

- (2) INFORMATION FOR SEQ ID NO:1792:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..45
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

Ile Arg Gln Pro Ser Trp Pro His Ser Ser Leu Ser Pro Pro Ser Ser 1 10 15

Pro Pro Pro Leu His Pro Leu His Leu His Leu Leu Arg Xaa Xaa 20 25 30

Arg Ala Ser Met Leu Gly Arg Asp Arg Arg Pro Gln Leu 35 40 45

- (2) INFORMATION FOR SEQ ID NO:1793:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599114
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

Ser Ala Ser Pro Pro Gly Pro Ile Pro Leu Ser Pro Leu Pro Pro Leu

5 10 15

His Arg His Arg Phe Ile Pro Phe Ile Ser Thr Ser Tyr Glu Xaa Ala 20 25 30

Ala Pro Pro Cys Ser Ala Ala Thr Ala Gly Leu Ser Ser Ser Val 35 40 45

Gln Tyr Cys Arg Leu Ala Glu Arg Trp Gly Met Ala 50 55 60

- (2) INFORMATION FOR SEQ ID NO:1794:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..427
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599134
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

ggccggccct gctcgtagct tggaggcgg ggcattctcc ggcaatgggg tgcaaggcgt 60 gcgacaagcc caagcccaac taccgcaagg cctgtggtcg ccggagagga ccagaagctc 120 cgcgactaca ttctcctcca cggccacggc tgctggagcg cgctccccgc gaaagccggg 180 ctccagcgga acggcaagag ctgcaggctg cggtggatca actaccttcg gccggggctg 240 aagcacggca tgttctccc ggagaggagg agacggtgat gagcctccac gccacgctcg 300 gcaacaagtg gtccaggatc gcacggcact tgctggcag gaccgacaac gaggtcaaga 360 actactggaa ctcgtacctc aagaagaggg tcgaggccaa ggaccagggg cccagcacgc 420

- (2) INFORMATION FOR SEQ ID NO:1795:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

ccgcgcc

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Ala Gly Pro Ala Arg Ser Leu Glu Ala Ala Ala Phe Ser Gly Asn Gly 1 5 10 15

Val Gln Gly Val Arg Gln Ala Gln Ala Gln Leu Pro Gln Gly Leu Trp \$20\$ \$25\$ 30

Ser Pro Glu Arg Thr Arg Ser Ser Ala Thr Thr Phe Ser Ser Thr Ala 35 40 45 Thr Ala Ala Gly Ala Arg Ser Pro Arg Lys Pro Gly Ser Ser Gly Thr

50 55 60
Ala Arg Ala Gly Cys Gly Gly Ser Thr Thr Phe Gly Arg Gly

- 65 70 75 (2) INFORMATION FOR SEQ ID NO:1796:
 - INFORMATION FOR SEQ ID NO.1790.
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..141
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599136
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

Pro Ala Leu Leu Val Ala Trp Arg Arg Arg His Ser Pro Ala Met Gly
1 10 15

Cys Lys Ala Cys Asp Lys Pro Lys Pro Asn Tyr Arg Lys Ala Cys Gly 20 25 30

Arg Arg Gly Pro Glu Ala Pro Arg Leu His Ser Pro Pro Arg Pro 35 40 45

Arg Leu Leu Glu Arg Ala Pro Arg Glu Ser Arg Ala Pro Ala Glu Arg 50 55 60

Gln Glu Leu Gln Ala Ala Val Asp Gln Leu Pro Ser Ala Gly Ala Glu 65 70 75 80

Ala Arg His Val Leu Pro Gly Glu Glu Glu Thr Val Met Ser Leu His $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$

Ala Thr Leu Gly Asn Lys Trp Ser Arg Ile Ala Arg His Leu Pro Gly 100 105 110

Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser Tyr Leu Lys Lys $115 \\ 120 \\ 125$

Arg Val Glu Ala Lys Asp Gln Gly Pro Ser Thr Pro Ala 130 135 140

(2) INFORMATION FOR SEQ ID NO:1797:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599137
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:

Met Gly Cys Lys Ala Cys Asp Lys Pro Lys Pro Asn Tyr Arg Lys Ala 1 5 10 15

Cys Gly Arg Arg Gly Pro Glu Ala Pro Arg Leu His Ser Pro Pro 20 25 30

Arg Pro Arg Leu Leu Glu Arg Ala Pro Arg Glu Ser Arg Ala Pro Ala 35 40 45

Glu Arg Gln Glu Leu Gln Ala Ala Val Asp Gln Leu Pro Ser Ala Gly 50 55 60

Ala Glu Ala Arg His Val Leu Pro Gly Glu Glu Glu Thr Val Met Ser 65 70 75 80

Leu His Ala Thr Leu Gly Asn Lys Trp Ser Arg Ile Ala Arg His Leu 85 90 95

Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser Tyr Leu 100 105 110

Lys Lys Arg Val Glu Ala Lys Asp Gln Gly Pro Ser Thr Pro Ala 115 120 125

- (2) INFORMATION FOR SEQ ID NO:1798:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..493
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

aagaaaaaa aaacacgcac ccgcgtccgc gtgctctctg ccccctgccc ccctcccatc tgcgccgccc tcctcatcca ccgcccgtcc cgccgccgcc agcccaaggc caggcatccg 120 ccaqcetete geaccaegeg tategsskee egecegaeeg getegtggeg atggegtaee 180 qqqcqqacqa cqactacqac tacctattca aggtggtgct catcggggac tecggcgtcg 240 gcaagtccaa cctgctctcg cgcttcacgc gcaacgagtt cagcctcgag tccaagtcca 300 ccatcggcgt cgagttcgcc acccgcagca tccacgtcga cgacaaggtc gtcaaggccc 360 420 agatetggga cacegeeggt caggaaaggt acegtgetat caegagegeg tactacegeg gasakttagg ggegetegte gtetaegagt geaegeggea egteaeette gagaaegtgg 480 agaggktggw atg

- (2) INFORMATION FOR SEQ ID NO:1799:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599139
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:
- Lys Lys Lys Lys Thr Arg Thr Arg Val Arg Val Leu Ser Ala Pro Cys

Ser Thr Thr Arg Ser Ser Arg Pro Arg Ser Gly Thr Pro Pro Val Arg 115 120 125

Lys Gly Thr Val Leu Ser Arg Ala Arg Thr Thr Ala Xaa Xaa 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1800:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..164
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599140
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:
- Arg Lys Lys Lys His Ala Pro Ala Ser Ala Cys Ser Leu Pro Pro Ala

 1 10 15

Pro Leu Pro Ser Ala Pro Pro Ser Ser Ser Thr Ala Arg Pro Ala Ala 20 25 30

Ala Ser Pro Arg Pro Gly Ile Arg Gln Pro Leu Ala Pro Arg Val Ser 35 40 45

Xaa Pro Ala Arg Pro Ala Arg Gly Asp Gly Val Pro Gly Gly Arg Arg
50 55 60

Leu Arg Leu Pro Ile Gln Gly Gly Ala His Arg Gly Leu Arg Arg 65 70 75 80

Gln Val Gln Pro Ala Leu Ala Leu His Ala Gln Arg Val Gln Pro Arg 85 90 95

Val Gln Val His His Arg Arg Arg Val Arg His Pro Gln His Pro Arg
100 105 110

Arg Arg Gln Gly Arg Gln Gly Pro Asp Leu Gly His Arg Arg Ser Gly
115 120 125

Lys Val Pro Cys Tyr His Glu Arg Val Leu Pro Arg Xaa Xaa Arg Gly 130 140

Ala Arg Arg Leu Arg Val His Ala Ala Arg His Leu Arg Glu Arg Gly 145 150 155 160

Glu Xaa Xaa Met

- (2) INFORMATION FOR SEQ ID NO:1801:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1599141															
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:															
1	Lys	Lys	Asn	Thr 5	His	Pro	Arg	Pro	Arg 10	Ala	Leu			15	
			20		Arg			25					30		
		35			Ala		40					45			
	50				Leu	55					60				
65	_				Lys 70					75					80
Lys				85	Ser				90					95	
	_		100		Gly			105					110		
		115			Lys		120					125			
Arg	Tyr 130	Arg	Ala	Ile	Thr	Ser 135	Ala	Tyr	Tyr	Arg	Gly 140	Xaa	Leu	Gly	Ala
Leu 145	Val	Val	Tyr	Glu	Cys 150	Thr	Arg	His	Val	Thr 155	Phe	Glu	Asn	Val	Glu 160
Arg	Xaa														

- (2) INFORMATION FOR SEQ ID NO:1802:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..505
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599152
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802: 60 cattcgcatc gaagactgat tggngtgtca gagccatctc tgccacaaac ttgtatctac gtgtaaatca tatttatgtc aattctgatg atataaagga aactggctac acttacatta 120 tgccaaagaa catattgaag aaattcatat gcatagcaga tctgcgtaca caaatcgctg 180 gattettata tgggetgagt ccacaggaca atectcaagt caaagagatt aggtgtatag 240 ccatccctcc gcagcatgga acacaccaga tggtgactct gccatcaaat cttcctgaac 300 360 atgagtteet taatgatett gaaceettgg gatggatgea tacacageea aatgaagete cacagetate accacaggae etgacateae atgecaagat tetggagaae aacaaacaat 420 gggatggtga gaagtgcatc attctgacat gcagcttcac cccaggatct tgctcgctga 480 ctgcttacaa gctgacacca agtgg
- (2) INFORMATION FOR SEQ ID NO:1803:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

20

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599153
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

Phe Ala Ser Lys Thr Asp Trp Xaa Val Arg Ala Ile Ser Ala Thr Asn $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ Leu Tyr Leu Arg Val Asn His Ile Tyr Val Asn Ser Asp Asp Ile Lys

25

30

Glu Thr Gly Tyr Thr Tyr Ile Met Pro Lys Asn Ile Leu Lys Lys Phe 35 40 45

Ile Cys Ile Ala Asp Leu Arg Thr Gln Ile Ala Gly Phe Leu Tyr Gly 50 55 60

Leu Ser Pro Gln Asp Asn Pro Gln Val Lys Glu Ile Arg Cys Ile Ala 65 70 75 80

Ile Pro Pro Gln His Gly Thr His Gln Met Val Thr Leu Pro Ser Asn 85 90 95

Leu Pro Glu His Glu Phe Leu Asn Asp Leu Glu Pro Leu Gly Trp Met $100 \\ 105 \\ 110$

His Thr Gln Pro Asn Glu Ala Pro Gln Leu Ser Pro Gln Asp Leu Thr 115 120 125

Ser His Ala Lys Ile Leu Glu Asn Asn Lys Gln Trp Asp Gly Glu Lys 130 135 140

Cys Ile Ile Leu Thr Cys Ser Phe Thr Pro Gly Ser Cys Ser Leu Thr 145 150 155 160

Ala Tyr Lys Leu Thr Pro Ser 165

- (2) INFORMATION FOR SEQ ID NO:1804:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599154
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

Met Pro Lys Asn Ile Leu Lys Lys Phe Ile Cys Ile Ala Asp Leu Arg 1 5 10 15

Thr Gln Ile Ala Gly Phe Leu Tyr Gly Leu Ser Pro Gln Asp Asn Pro 20 25 30

Gln Val Lys Glu Ile Arg Cys Ile Ala Ile Pro Pro Gln His Gly Thr 35 40 45 His Gln Met Val Thr Leu Pro Ser Asn Leu Pro Glu His Glu Phe Leu

50 55 60
Asn Asp Leu Glu Pro Leu Gly Trp Met His Thr Gln Pro Asn Glu Ala

65 70 75 80 Pro Gln Leu Ser Pro Gln Asp Leu Thr Ser His Ala Lys Ile Leu Glu

85 90 95
Asn Asn Lys Gln Trp Asp Gly Glu Lys Cys Ile Ile Leu Thr Cys Ser

100 105 110

Phe Thr Pro Gly Ser Cys Ser Leu Thr Ala Tyr Lys Leu Thr Pro Ser
115 120 125

- (2) INFORMATION FOR SEQ ID NO:1805:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..462
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599163
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

tgetecette teetgttete tetececaet tegagaette etecattege ggtttgeete 120 tetgeettee etaceteaga teeteeetea gattgeeatg geggaeeage teacegaega 180 eeagategee gagtteaagg aageatteag eetettegae aaggaeggeg aeggetgeat 240 eaceaceaag gaacttgaae tgtgatgege tegttgggge agaaceetae tgaggetgag 300 etteaggaea tgatgaeag gattgatget gatggeaatg gaaceatega ettecetgag tgtteeaeg tgttegaeag gaaceagaet etgaggagga geteaaggag 420 geetteegeg tgttegaeaa ggaeeagaae ggetteatet et

- (2) INFORMATION FOR SEQ ID NO:1806:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599164
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806: Ser Lys Lys Phe Thr Arg Met Val Gly Leu Arg Leu Pro Leu Thr

Ala Asp Arg Thr Ala Pro Phe Ser Cys Ser Leu Ser Pro Leu Arg Asp 20 25 30

Phe Leu His Ser Arg Phe Ala Ser Leu Pro Ser Leu Pro Gln Ile Leu 35 40 45

Pro Gln Ile Ala Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu 50 55 60

Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile 70 75 80

Thr Thr Lys Glu Leu Glu Leu 85

(2) INFORMATION FOR SEQ ID NO:1807:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599165
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Met Val Gly Leu Arg Leu Pro Leu Thr Ala Asp Arg Thr Ala Pro Phe 1 5 10 15

Ser Cys Ser Leu Ser Pro Leu Arg Asp Phe Leu His Ser Arg Phe Ala 20 25 30

Ser Leu Pro Ser Leu Pro Gln Ile Leu Pro Gln Ile Ala Met Ala Asp 35 40 45

Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu 50 55 60

Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu Leu Glu Leu 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:1808:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

Page 975 (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..66 (D) OTHER INFORMATION: / Ceres Seq. ID 1599166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808: Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met 10 5 Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu 20 25 Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu 40 45 Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe 50 55 60 Ile Ser 65 (2) INFORMATION FOR SEQ ID NO:1809: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 458 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..458 (D) OTHER INFORMATION: / Ceres Seq. ID 1599167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809: aaggaacatc cctactcgga aggctcacca aatcgtccta cgcttctgcc tcctccta cgaggtgagg aaaccctagc gactgaccat ggcgttgctc ccgcgcaccg cacggttggc cttectetet acceegeggt egtacteege egeegeeget geegetgegg gegeeteece gacctcccca gcgccatacg ggggcgcgcc cccaccggcg atgtcgaaga ggccgagttc 240 gtggtctcca aggttgatga cctgatgaac tgggcgcgta agggctcgat ttggcccatg 300 acctteggge tegectgetg egeggtegag atgatgeacg eeggegegte eegetaegae 360 ttegaceggt teggegteat etteegteee tegeegegee agteegattg catgategte 420 geoggeacge teaccaacaa aatggeteea geeteege (2) INFORMATION FOR SEQ ID NO:1810: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 152 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..152 (D) OTHER INFORMATION: / Ceres Seq. ID 1599168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810: Lys Glu His Pro Tyr Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu Leu 10 Pro Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala Thr Asp His Gly Val 20 25 Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val Val 40

Leu Arg Arg Arg Arg Cys Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser 50

Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu Ala Glu Phe 65

Val Val Ser Lys Val Asp Asp Leu Met Asn Trp Ala Arg Lys Gly Ser 85

Ile Trp Pro Met Thr Phe Gly Leu Ala Cys Cys Ala Val Glu Met Met

120

180

240

300

360

420

100 105 His Ala Gly Ala Ser Arg Tyr Asp Phe Asp Arg Phe Gly Val Ile Phe 120 125 Arg Pro Ser Pro Arg Gln Ser Asp Cys Met Ile Val Ala Gly Thr Leu 130 135 140 Thr Asn Lys Met Ala Pro Ala Ser 150 (2) INFORMATION FOR SEQ ID NO:1811: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 432 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..432 (D) OTHER INFORMATION: / Ceres Seq. ID 1599179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811: gatacgatcc gccgaattaa gttcctgcac gtacgcacgc accgggncac cagbsncccc caacagegee actgtecagt gegegegtea agettgetta getageegee atggeeteee tegeogeegt eteegtgaag eeegtggeea teaagggtet egeogghage tetateteeg qaaqqaaqct cqccqtcqcc aqqccqtcqq ccqctccatc cqcaqccccq cqcascqccq tggtggccaa gtacggcgac aagagcgtct acttcgacct cgacgacatc ggcaacacca coggacaqtq qqacetetac qqetetqacq cqcceteqce etacaacceq etacaqaqca agttettega gaegttegeg geteegttea ceaagagagg tetgetgete aagtteetge tactagacaa ca (2) INFORMATION FOR SEQ ID NO:1812: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..108 (D) OTHER INFORMATION: / Ceres Seq. ID 1599180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812: Ile Arg Ser Ala Glu Leu Ser Ser Cys Thr Tyr Ala Arg Thr Gly Xaa 10 Pro Xaa Xaa Pro Asn Ser Ala Thr Val Gln Cys Ala Arg Gln Ala Cys 25 Leu Ala Ser Arg His Gly Leu Pro Arg Arg Arg Leu Arg Glu Ala Arg 40 Gly His Gln Gly Ser Arg Arg Xaa Leu Tyr Leu Arg Lys Glu Ala Arg Arg Arg Gln Ala Val Gly Arg Ser Ile Arg Ser Pro Ala Xaa Arg Arg Gly Gly Gln Val Arg Arg Gln Glu Arg Leu Leu Arg Pro Arg Arg His 90 Arg Gln His His Arg Thr Val Gly Pro Leu Arg Leu 100 105 (2) INFORMATION FOR SEQ ID NO:1813: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

60

- (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1599181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813: Met Ala Ser Leu Ala Ala Val Ser Val Lys Pro Val Ala Ile Lys Gly 10 Leu Ala Xaa Ser Ser Ile Ser Gly Arg Lys Leu Ala Val Ala Arg Pro 30 25 20 Ser Ala Ala Pro Ser Ala Ala Pro Arg Xaa Ala Val Val Ala Lys Tyr 45 40 Gly Asp Lys Ser Val Tyr Phe Asp Leu Asp Asp Ile Gly Asn Thr Thr 55 Gly Gln Trp Asp Leu Tyr Gly Ser Asp Ala Pro Ser Pro Tyr Asn Pro 75 70 Leu Gln Ser Lys Phe Phe Glu Thr Phe Ala Ala Pro Phe Thr Lys Arg 90 85 Gly Leu Leu Leu Lys Phe Leu Leu Gly Gly 105 100 (2) INFORMATION FOR SEQ ID NO:1814: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..426 (D) OTHER INFORMATION: / Ceres Seq. ID 1599195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814: atgagetact ataaatggee aaacectage ggasseacaa aacaetetee teetteetee accgccgcca acgtcgcctg gcggccgtct gcagctccgc gcctctgctc ggaagttgtt 120 ggtgaaggtt tettgaaget gagaagatgg tgetgaagae agaactetge egetteagne 180 nakaagattt atcctgggaa aggcatccga tttatccgtg ctgattctca ggttttcctt 240 tttgccaact caaaatgcaa gcgctacttc cacaaccgcc tgaagcctgc aaagcttacc 300 tggacagcaa tgtacaggaw gcwkcacaag aaggatatcc atgctgaggc tgtcaagaag 360 aggckccgcg ccaacaagaa gccatactcg agktccattg tgggngcttc cctagaggtg 420 atccag (2) INFORMATION FOR SEQ ID NO:1815: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..51 (D) OTHER INFORMATION: / Ceres Seq. ID 1599196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815: Met Ser Tyr Tyr Lys Trp Pro Asn Pro Ser Gly Xaa Thr Lys His Ser 10 5 Pro Pro Ser Ser Thr Ala Ala Asn Val Ala Trp Arg Pro Ser Ala Ala 30 25 Pro Arg Leu Cys Ser Glu Val Val Gly Glu Gly Phe Leu Lys Leu Arg 40 Arg Trp Cys 50
 - (2) INFORMATION FOR SEQ ID NO:1816:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..39
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

Met Tyr Arg Xaa Xaa His Lys Lys Asp Ile His Ala Glu Ala Val Lys
1 10 15

Lys Arg Xaa Arg Ala Asn Lys Lys Pro Tyr Ser Xaa Ser Ile Val Xaa 20 25 30

Ala Ser Leu Glu Val Ile Gln 35

- (2) INFORMATION FOR SEQ ID NO:1817:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..442
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817: tocacttoac geoecgeege egeogeegeg teteetetge aggtaagaag gtaaggaaga 60 gggcgaaatg gtgaagcaca acaacgttat ccccaacggc acttcaagaa gcactggcag 120 aactatgtca agacatggtt caaccagecc gcccgcaage agaggegccg catcgctcgt 180 caaaagaagg ctgtgaagat attcccacgc ccaactgctg gccctcttcg ccccatcgtg 240 caatgccaga ccctcaagta caacatgaag tcgagggctg ggagaggatt tacccttgag 300 gagetgaakg etgeeggeat tecaaagaag ettgeeceaa eeattggeat ttetgtggat 360 caccgccgca agaacaaatc tctcgaggga ctgcaggcca atgtccagag gcttaagacg 420 tacaaggcca agctggttat ct
- (2) INFORMATION FOR SEQ ID NO:1818:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..42
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599223
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Val Lys His Asn Asn Val Ile Pro Asn Gly Thr Ser Arg Ser Thr 1 5 10 15

Gly Arg Thr Met Ser Arg His Gly Ser Thr Ser Pro Pro Ala Ser Arg

- Gly Ala Ala Ser Leu Val Lys Arg Arg Leu
- (2) INFORMATION FOR SEQ ID NO:1819:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

Met Val Gln Pro Ala Arg Pro Gln Ala Glu Ala Pro His Arg Ser Ser 1 10 15

Lys Glu Gly Cys Glu Asp Ile Pro Thr Pro Asn Cys Trp Pro Ser Ser 20 25 30

Pro His Arg Ala Met Pro Asp Pro Gln Val Gln His Glu Val Glu Gly 35 40 45

Trp Glu Arg Ile Tyr Pro

- (2) INFORMATION FOR SEQ ID NO:1820:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu Xaa Ala 1 5 10 15

Ala Gly Ile Pro Lys Lys Leu Ala Pro Thr Ile Gly Ile Ser Val Asp 20 25 30

His Arg Arg Lys Asn Lys Ser Leu Glu Gly Leu Gln Ala Asn Val Gln 35 40 45

Arg Leu Lys Thr Tyr Lys Ala Lys Leu Val Ile 50 55

- (2) INFORMATION FOR SEQ ID NO:1821:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..487
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599226
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

- (2) INFORMATION FOR SEQ ID NO:1822:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

Phe Tyr Lys Thr Ser Ala Arg Gly Leu Gly Phe Pro Pro Ser Arg His 1 5 5 10 10 15 Arg Phe Ala Ser Ala Ser Ala Arg Arg Lys Arg Gly Lys Phe Arg Arg Arg

20 25 30
His Leu Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys

His Leu Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys 35 40 45

Gly Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser 50 60

Gly Ala Ala Lys Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe 65 70 75 80

His Arg Pro Thr Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg 85 90 95

Ile Ser Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys
100 105 110

Tyr Pro Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn 115 120 125

Thr Leu Val Phe Ile Val Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys 130 135 140
Ala Ala Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr

145 150 155 Leu Ile

- (2) INFORMATION FOR SEQ ID NO:1823:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ala Ala Lys Lys Lys 20 25 30

Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Thr Thr Leu 35 40 45

Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg 50 55 60

Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu 65 70 75 80 Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val

Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys Ala Ala Val Lys Lys Met
100 105 110

90 95

Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile 115 120

(2) INFORMATION FOR SEQ ID NO:1824:

8.5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..463
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599235
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

gccgccgctg cttaccgcct atctcgccaa gcaccgccgc atcaccgaak tcgcaaagtg 60 cagatggcgg tgccgctgct gacgcagaag atcgtgaaga agagggtcaa gcagttcaag 120 aggcccatc ttgaccgcta caagtgcctt aatccaagct ggcgcaggcc caagggtatc 180 gactcccgcg tgaggcgtaa gttcaaggga tgcaccttga tgcccaacat tggatatggc 240 tccgacaaga agaccaggca ctaccttccc aacaagttca aaaagtttgt tgttcacaat 300 gtctccgagc tggagctgct gctgatgcac aacaggacct actgcgctga gatcgcccac 360 aacgtgtca agcttgcaag agctccgagc caaggagatt gtcgagcgtg ctgcgcaaaat ggacatcgtg 420 gtcaccaaca agcttgccag gctccgcagc caagaggacg agt

- (2) INFORMATION FOR SEQ ID NO:1825:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599236
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

Ala Ala Ala Tyr Arg Leu Ser Arg Gln Ala Pro Pro His His Arg
1 5 10 15

Xaa Arg Lys Val Gln Met Ala Val Pro Leu Leu Thr Gln Lys Ile Val 20 25 30

Lys Lys Arg Val Lys Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys 35 40 45

Cys Leu Asn Pro Ser Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val 50 55 60

Arg Arg Lys Phe Lys Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly 65 70 75 80

Ser Asp Lys Lys Thr Arg His Tyr Leu Pro Asn Lys Phe Lys Lys Phe 85 90 95

Val Val His Asn Val Ser Glu Leu Glu Leu Leu Leu Met His Asn Arg 100 105 110

Thr Tyr Cys Ala Glu Ile Ala His Asn Val Ser Thr Arg Lys Arg Lys 115 120 125

Glu Ile Val Glu Arg Ala Ala Gln Met Asp Ile Val Val Thr Asn Lys 130 140

Leu Ala Arg Leu Arg Ser Gln Glu Asp Glu 145 150

- (2) INFORMATION FOR SEQ ID NO:1826:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

Met Ala Val Pro Leu Leu Thr Gln Lys Ile Val Lys Lys Arg Val Lys

10 15

Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys Cys Leu Asn Pro Ser 20 25 30

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Client Docket No. 80146.003
Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys
                            40
Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Lys Thr
                                            60
                       55
Arg His Tyr Leu Pro Asn Lys Phe Lys Lys Phe Val Val His Asn Val
                                       75
                    70
Ser Glu Leu Glu Leu Leu Met His Asn Arg Thr Tyr Cys Ala Glu
                                   90
               85
Ile Ala His Asn Val Ser Thr Arg Lys Arg Lys Glu Ile Val Glu Arg
                                                   110
                               105
            100
Ala Ala Gln Met Asp Ile Val Val Thr Asn Lys Leu Ala Arg Leu Arg
                            120
        115
Ser Gln Glu Asp Glu
    130
(2) INFORMATION FOR SEQ ID NO:1827:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 81 amino acids
          (B) TYPE: amino acid
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- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599238
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Lys Thr Arg His Tyr Leu 1 5 10 15

Pro Asn Lys Phe Lys Lys Phe Val Val His Asn Val Ser Glu Leu Glu 20 25 30

Leu Leu Met His Asn Arg Thr Tyr Cys Ala Glu Ile Ala His Asn 35 40 45

Val Ser Thr Arg Lys Arg Lys Glu Ile Val Glu Arg Ala Ala Gln Met 50 55 60

Asp Ile Val Val Thr Asn Lys Leu Ala Arg Leu Arg Ser Gln Glu Asp 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:1828:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..497
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599243
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

agaaaaccta tagcttgcag cgccacctac accgagcagc caagcgagga agcgaagacc 60 120 catttccccg agcgcaagag taccatggcg gcggcggcag tttatggcgg cctcaagggg 180 aagettggeg tegaggatge eecegagetg cagetgaate geateegeat caceetetea tccaagaacg tcaagaacct ggagaaagtt tgtgcggatt tggtaaaggg agccaaggat 300 aagcatctga gggttaaggg gcctgtcagg atccctacta aggttctcca catcaccacc cgcaaatccc cttgcggtga aggaacaaac acatgggacc ggtttgagtt ccgcatccat 360 aagagggtga tcgacctgat cagctcccca gacgtggtga agcagatcac ctctatcacc 420 attgagccgg gtgttgaggt cgaggtgacc gttgcagacg tgtaatgacg atctatatat 480 tcgtgttgct tttgttt

- (2) INFORMATION FOR SEQ ID NO:1829:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599244
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

Arg Lys Pro Ile Ala Cys Ser Ala Thr Tyr Thr Glu Gln Pro Ser Glu
1 5 10 15

Ala Val Tyr Gly Gly Leu Lys Gly Lys Leu Gly Val Glu Asp Ala Pro $35 \hspace{1cm} 40 \hspace{1cm} 45 \hspace{1cm}$

Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Lys Gly Ala Lys Asp 65 70 75 80

Lys His Leu Arg Val Lys Gly Pro Val Arg Ile Pro Thr Lys Val Leu 85 90 95

His Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Trp

Asp Arg Phe Glu Phe Arg Ile His Lys Arg Val Ile Asp Leu Ile Ser 115 120 125

Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly 130 135 140

- (2) INFORMATION FOR SEQ ID NO:1830:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599245
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

Lys Thr Tyr Ser Leu Gln Arg His Leu His Arg Ala Ala Lys Arg Gly
1 5 10 15

Ser Glu Asp Pro Phe Pro Arg Ala Gln Glu Tyr His Gly Gly Gly 20 25 30

Ser Leu Trp Arg Pro Gln Gly Glu Ala Trp Arg Arg Gly Cys Pro Arg 35 40 45

Ala Ala Glu Ser His Pro His Pro Leu Ile Gln Glu Arg Gln 50 55 60

Glu Pro Gly Glu Ser Leu Cys Gly Phe Gly Lys Gly Ser Gln Gly 65 70 75

- (2) INFORMATION FOR SEQ ID NO:1831:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1599246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:
Met Ala Ala Ala Val Tyr Gly Gly Leu Lys Gly Lys Leu Gly Val

Glu Asp Ala Pro Glu Leu Gln Leu Asn Arg Ile Arg Ile Thr Leu Ser

Ser Lys Asn Val Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Lys
35 40 45

Gly Ala Lys Asp Lys His Leu Arg Val Lys Gly Pro Val Arg Ile Pro 50 55 60

Thr Lys Val Leu His Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly 65 70 75 80

Thr Asn Thr Trp Asp Arg Phe Glu Phe Arg Ile His Lys Arg Val Ile 85 90 95

Asp Leu Ile Ser Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr 100 105 110

Ile Glu Pro Gly Val Glu Val Glu Val Thr Val Ala Asp Val
115 120 125

- (2) INFORMATION FOR SEQ ID NO:1832:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..504
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599263
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832: 60 ggagcaggac aggttgcatt tgcatctgag ttcctgatcg ttgtattcca gtttcttccg tgagttttgt gggatcgcga ggaagaagga tgtcgtgctg cggaggcaac tgcgggtgcg 120 gegeeggetg caagtgegge aseggetgeg gagggtgeaa gatgtaceeg gacatggetg 180 agcaggtgac caccaccacc accacccaga ctctcatcat gggtgttgca ccatccaagg 240 300 geggggtega ggeggeegeg gagetgagaa eggegggtge aagtgeggeg ecaactgeae 360 ctgcgacccc tgcacctgca agtgagacta cgacggtggc ggcgatgacg ctgcagggtc tgcaggccct gatggggtcg gaaggactct ttatctctct agctaattaa taagctctag 420 ctagtatata atattctagc agtgtcgttt gctgtgtttt gttcgagtca gttagacagt 480 cagccgcgtg ccatgggcca tggg
- (2) INFORMATION FOR SEQ ID NO:1833:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599264
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:
- Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Ala Gly Cys Lys Cys

 1 5 10 15
- Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Ala Glu Gln
 20 25 30
- Val Thr Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Val Ala Pro 35 40 45
- Ser Lys Gly Gly Val Glu Ala Ala Ala Glu Leu Arg Thr Ala Gly Ala 50 55 60 60 Ser Ala Ala Pro Thr Ala Pro Ala Thr Pro Ala Pro Ala Ser Glu Thr

70 75 80
Thr Thr Val Ala Ala Met Thr Leu Gln Gly Leu Gln Ala Leu Met Gly
85 90 95

- (2) INFORMATION FOR SEQ ID NO:1834:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599265
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

Met Tyr Pro Asp Met Ala Glu Gln Val Thr Thr Thr Thr Thr Gln 1 5 10 15

Thr Leu Ile Met Gly Val Ala Pro Ser Lys Gly Gly Val Glu Ala Ala 20 25 30

Ala Glu Leu Arg Thr Ala Gly Ala Ser Ala Ala Pro Thr Ala Pro Ala 35 40 45

Thr Pro Ala Pro Ala Ser Glu Thr Thr Thr Val Ala Ala Met Thr Leu 50 60

Gln Gly Leu Gln Ala Leu Met Gly Ser Glu Gly Leu Phe Ile Ser Leu 65 70 75 80

Ala Asn

- (2) INFORMATION FOR SEQ ID NO:1835:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599266
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

Met Ala Glu Gln Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met

1 5 10 15 15

Gly Val Ala Pro Ser Lys Gly Gly Val Glu Ala Ala Ala Glu Leu Arg 20 25 30

Thr Ala Gly Ala Ser Ala Ala Pro Thr Ala Pro Ala Thr Pro Ala Pro 35 40 45

Ala Ser Glu Thr Thr Thr Val Ala Ala Met Thr Leu Gln Gly Leu Gln 50 55 60

Ala Leu Met Gly Ser Glu Gly Leu Phe Ile Ser Leu Ala Asn 65 70 75

- (2) INFORMATION FOR SEQ ID NO:1836:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1599267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:									
acattetgtt etegtttete	tteetetete	tcaactcaac	tactcaaagc	ggtagattaa	60				
ccgctctag cgtmsggtgt	tactacatet	ctcttggcca	tagagagcata	cgcgacgaag	120				
ccgggtgacc tcaaggtcaa	adacasaaca	cctctaatca	cqqaqqacgc	cgcggcgcca	180				
ctggssgctg cagacgagaa	aacaaaaacc	accaaaatcc	ccgtggccgc	cgccgccgag	240				
gtcgaccagg ccgatgtcag	ccaccaaaat	ccctcagcga	cctgctcaaa	cgggacgccg	300				
agggcagttg acggggagga	kkaggccgac	caggagggg	agaaggtcgt	gggctgggga	360				
gccancgagt gctgccgctg	ccactaccaa	ggaaacgatg	gggtcaccgc	aagcaacagt	420				
gcaggcctcg gtcgcaaccg	adcaddacda	cacqqccqaa	gaactcaagg	atggtcttcc	480				
	agoaggaoga		, , , ,						
gag									

- (2) INFORMATION FOR SEQ ID NO:1837:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599268
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:
- Met Gly Ala Cys Ala Thr Lys Pro Gly Asp Leu Lys Val Lys Gly Glu
 1 5 10 15
- Ala Pro Leu Val Ala Glu Asp Ala Ala Ala Pro Leu Xaa Ala Ala Asp 20 25 30
- Glu Lys Ala Lys Ala Ala Glu Val Pro Val Ala Ala Ala Ala Glu Val 35 40 45
- Asp Gln Ala Asp Val Ser Arg Arg Ser Pro Ser Ala Thr Cys Ser Asn 50 55 60
- Gly Thr Pro Arg Ala Val Asp Gly Glu Xaa Xaa Ala Asp Gln Glu Ala 65 70 75 80
- Glu Lys Val Val Gly Trp Gly Ala Xaa Glu Cys Cys Arg Cys Arg Cys 85 90 95
- Arg Gly Asn Asp Gly Val Thr Ala Ser Asn Ser Ala Gly Leu Gly Arg 100 105 110
- Asn Arg Ala Gly Arg His Gly Arg Arg Thr Gln Gly Trp Ser Ser Glu 115 120 125
- (2) INFORMATION FOR SEQ ID NO:1838:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..76
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599269
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:
- Met Ser Ala Ala Gly Val Pro Gln Arg Pro Ala Gln Thr Gly Arg Arg
 1 5 10 15
- Gly Gln Leu Thr Gly Arg Xaa Arg Pro Thr Arg Arg Arg Arg Arg Ser 20 25 30
- Trp Ala Gly Glu Pro Xaa Ser Ala Ala Ala Ala Ala Ala Gly Glu Thr
- Met Gly Ser Pro Gln Ala Thr Val Gln Ala Ser Val Ala Thr Glu Gln 50 55 60

Page 987 Client Docket No. 80146.003 Asp Asp Thr Ala Glu Glu Leu Lys Asp Gly Leu Pro 70 (2) INFORMATION FOR SEQ ID NO:1839: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 502 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..502 (D) OTHER INFORMATION: / Ceres Seq. ID 1599274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839: gaaaaaggaa cagaagggag aaagaaaagc agtcgagcag cggtasscgg tagssrgaga 60 gtcaggattc aggacgcggc gaggccacca tgagcactct caagttctgc cgggaatgca 120 acaacatget gtaccegegg gaggacaagg agacgegeae ceteetgtae gegtgeeaaa 180 cgtgcgagca tgaggagatt gccactgata cttgtgtgta caaaagggtt atccgcaagc 240 ctggtggtga gcccaaggat gtcctgaagg atgcagcaac tgatcctagc ctgcctcgca 300 ccagaagcgt cagatgttac aactgcaacc atccagaagc tgcctttttt caggccccga 360 420 ctaagggaga acaagccatg acgctgtact tcatctgctg caacccaagc tgcgggcaca ggtggaggga ctgagaagga tctggcttgg tcttcgctgc aaacctgccg tatttgttag 480 cctatcrcat aaatattgta gg (2) INFORMATION FOR SEQ ID NO:1840: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..63 (D) OTHER INFORMATION: / Ceres Seq. ID 1599275 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840: Lys Lys Glu Gln Lys Gly Glu Arg Lys Ala Val Glu Gln Arg Xaa Xaa 10 5 Val Xaa Xaa Glu Ser Gly Phe Arg Thr Arg Arg Gly His His Glu His 25 2.0 Ser Gln Val Leu Pro Gly Met Gln Gln His Ala Val Pro Ala Gly Gly 40 Gln Gly Asp Ala His Pro Pro Val Arg Val Pro Asn Val Arg Ala 55 50 (2) INFORMATION FOR SEQ ID NO:1841: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..114 (D) OTHER INFORMATION: / Ceres Seq. ID 1599276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

Met Ser Thr Leu Lys Phe Cys Arg Glu Cys Asn Asn Met Leu Tyr Pro

Arg Glu Asp Lys Glu Thr Arg Thr Leu Leu Tyr Ala Cys Gln Thr Cys 25 Glu His Glu Glu Ile Ala Thr Asp Thr Cys Val Tyr Lys Arg Val Ile 40

5

10

Arg Asp

- (2) INFORMATION FOR SEQ ID NO:1842:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599277
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

Met Leu Tyr Pro Arg Glu Asp Lys Glu Thr Arg Thr Leu Leu Tyr Ala 1 10 15

Cys Gln Thr Cys Glu His Glu Glu Ile Ala Thr Asp Thr Cys Val Tyr
20 25 30

Lys Arg Val Ile Arg Lys Pro Gly Gly Glu Pro Lys Asp Val Leu Lys 35 40

Asp Ala Ala Thr Asp Pro Ser Leu Pro Arg Thr Arg Ser Val Arg Cys 50 55 60

Tyr Asn Cys Asn His Pro Glu Ala Ala Phe Phe Gln Ala Pro Thr Lys
65 70 75 80

Gly Glu Gln Ala Met Thr Leu Tyr Phe Ile Cys Cys Asn Pro Ser Cys 85 90 95

Gly His Arg Trp Arg Asp 100

- (2) INFORMATION FOR SEQ ID NO:1843:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..487
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599278
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

tccaacgcgg cacagagcct cattcatctc cattcgaaac accetegcae ccacactene 60 cettegtece cageetaaat eeeegcaang atggetegea egaageakae ggegegeaag 120 tccacggkck gcaaggcccc gaggaagcag ctggcgacca aggcggcgcg caagtcggcc 180 cctgcgaccg gcggcgtgaa gaagccgcac cgcttccgcc cgggcaccgt ggcgctgcgc 240 gagateegea agtaceagaa gageaeggag etgeteatee geaagetgee etteeagege 300 ctggtccgcg agatcgcgca ggacttcaag accgacctcc gcttccagtc ctccgccgtc 360 geogegetge aggaggeege egaggettae etegteggee tgttegagga caccaacete 420 tgcgccatcc acgccaagcg cgtcaccatc atgcccaagg acatccagct cgcccgccgc 480 atccgcg

- (2) INFORMATION FOR SEQ ID NO:1844:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:
- Gln Arg Gly Thr Glu Pro His Ser Ser Pro Phe Glu Thr Pro Ser His
- Pro His Xaa Pro Phe Val Pro Ser Leu Asn Pro Arg Xaa Asp Gly Ser 20 25 30
- His Glu Ala Xaa Gly Ala Gln Val His Xaa Xaa Gln Gly Pro Glu Glu 35 40 45
- Ala Ala Gly Asp Gln Gly Gly Ala Gln Val Gly Pro Cys Asp Arg Arg 50 55 60
- Arg Glu Glu Ala Ala Pro Leu Pro Pro Gly His Arg Gly Ala Ala Arg
 70 75 80
- Asp Pro Gln Val Pro Glu Glu His Gly Ala Ala His Pro Gln Ala Ala 85 90 95
- Leu Pro Ala Pro Gly Pro Arg Asp Arg Ala Gly Leu Gln Asp Arg Pro 100 105 110
- Pro Leu Pro Val Leu Arg Arg Arg Arg Ala Ala Gly Gly Arg Arg Gly 115 120 125
- Leu Pro Arg Arg Pro Val Arg Gly His Gln Pro Leu Arg His Pro Arg 130 135 140
- Gln Ala Arg His His His Ala Gln Gly His Pro Ala Arg Pro Pro His 145 150 155 160
- (2) INFORMATION FOR SEQ ID NO:1845:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599280
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:
- Met Ala Arg Thr Lys Xaa Thr Ala Arg Lys Ser Thr Xaa Xaa Lys Ala 1 5 10 15
- Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Ala 20 25 30
- Thr Gly Gly Val Lys Lys Pro His Arg Phe Arg Pro Gly Thr Val Ala 35 40 45
- Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg 50 55 60
- Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Lys
 65 70 75 80
- Thr Asp Leu Arg Phe Gln Ser Ser Ala Val Ala Ala Leu Gln Glu Ala 85 90 95
- Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala 100 105 110
- Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Ile Gln Leu Ala 115 120 125
- Arg Arg Ile Arg
 - 130
- (2) INFORMATION FOR SEQ ID NO:1846:

120

180

240

300

360

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 373 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..373 (D) OTHER INFORMATION: / Ceres Seq. ID 1599297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846: ccagcagect ecegnatece caaagectee gaeeeeette eteteteeet eegeegeege tgcgcacgcr gggaacaagc gacatgggcg tctacacctt cgtgtgccgc aacaacggcg kckaktggac cgccaagcag cactccggcg agatcgaggc ttccgccgct accccatacg agetgeageg eegectegte geegetgeet eegeggeega etetgeetae gggteeagte gteettetee atggteacce ecageteege egtgtteeag gtgategteg gtgetgttgg tggtggtgca atgatggtga gcggaggtgg cggcggtgct gctgcatctg gtggtgctgc tgccgaggct ccc (2) INFORMATION FOR SEQ ID NO:1847: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..124 (D) OTHER INFORMATION: / Ceres Seq. ID 1599298 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847: Pro Ala Ala Ser Xaa Ile Pro Lys Ala Ser Asp Pro Leu Pro Leu Ser 10 5 Leu Arg Arg Arg Cys Ala Arg Xaa Glu Gln Ala Thr Trp Ala Ser Thr 30 25 20 Pro Ser Cys Ala Ala Thr Thr Ala Xaa Xaa Gly Pro Pro Ser Ser Thr 45 40 35 Pro Ala Arg Ser Arg Leu Pro Pro Leu Pro His Thr Ser Cys Ser Ala 60 55 Ala Ser Ser Pro Leu Pro Pro Arg Pro Thr Leu Pro Thr Gly Pro Val 75 70 Val Leu Leu His Gly His Pro Gln Leu Arg Arg Val Pro Gly Asp Arg 90 85 Arg Cys Cys Trp Trp Trp Cys Asn Asp Gly Glu Arg Arg Trp Arg Arg 105 Cys Cys Cys Ile Trp Trp Cys Cys Cys Arg Gly Ser 115 120 (2) INFORMATION FOR SEQ ID NO:1848: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..124 (D) OTHER INFORMATION: / Ceres Seq. ID 1599299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848: Gln Gln Pro Pro Xaa Ser Pro Lys Pro Pro Thr Pro Phe Leu Ser Pro

10

Ser Ala Ala Ala His Xaa Gly Asn Lys Arg His Gly Arg Leu His

5

- (2) INFORMATION FOR SEQ ID NO:1849:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Ser Ser Leu Pro Xaa Pro Gln Ser Leu Arg Pro Pro Ser Ser Leu Pro 1 5 10 15

Pro Pro Pro Leu Arg Thr Xaa Gly Thr Ser Asp Met Gly Val Tyr Thr 20 25 30

Phe Val Cys Arg Asn Asn Gly Xaa Xaa Trp Thr Ala Lys Gln His Ser 35 40 45

Gly Glu Ile Glu Ala Ser Ala Ala Thr Pro Tyr Glu Leu Gln Arg Arg 50 55 60

Leu Val Ala Ala Ala Ser Ala Ala Asp Ser Ala Tyr Gly Ser Ser Arg 65 70 75 80

Pro Ser Pro Trp Ser Pro Pro Ala Pro Pro Cys Ser Arg 85 90

- (2) INFORMATION FOR SEQ ID NO:1850:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..477
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

 aaacagccaa agaacagaaa aaaatataaa aaggtgggeg tgcaactttc ccttccttcg ccgaagccgc gcgacggaaa ccccaaaccc aacctcatct cttttctcgg cctctaccgc 120 cccctcgatc ggtcggccgg tcagctatga cgccgggaag ctcggccgc ggatccggst cgtcgttcct cggaacttca ggctcctaga agagcttgaa cgtggagaga agggcattgg 240 agatgggaca gtgagctatg gaatggatga cgcagatgac atctacatgc gatcatggac tggcactatt attggccctc ataataccgt ccatgagggt cgcatctacc agctgaagtt 360 gttctgcgac aaggactacc ctgagaagcc accatcagtt cgatttcatt caagaataaa 420
- tttaacatgc gttaatcatg aaactggagt ggttgacccg aagaagttca gcgttct (2) INFORMATION FOR SEQ ID NO:1851:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..158
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599316
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:
- Asn Ser Gln Arg Thr Glu Lys Asn Ile Lys Arg Trp Ala Cys Asn Phe 1 5 10 15
- Pro Phe Leu Arg Arg Ser Arg Ala Thr Glu Thr Pro Asn Pro Thr Ser 20 25 30
- Ser Leu Phe Ser Ala Ser Thr Ala Pro Ser Ile Gly Arg Pro Val Ser 35 40 45
- Tyr Asp Ala Gly Lys Leu Gly Arg Arg Ile Arg Xaa Val Val Pro Arg 50 60
- Asn Phe Arg Leu Leu Glu Glu Leu Glu Arg Gly Glu Lys Gly Ile Gly 65 70 75 80
- Asp Gly Thr Val Ser Tyr Gly Met Asp Asp Ala Asp Asp Ile Tyr Met 85 90 95
- Arg Ser Trp Thr Gly Thr Ile Ile Gly Pro His Asn Thr Val His Glu
 100 105 110
- Gly Arg Ile Tyr Gln Leu Lys Leu Phe Cys Asp Lys Asp Tyr Pro Glu
 115 120 125
- Lys Pro Pro Ser Val Arg Phe His Ser Arg Ile Asn Leu Thr Cys Val 130 135 140
- Asn His Glu Thr Gly Val Val Asp Pro Lys Lys Phe Ser Val 145 150 155
- (2) INFORMATION FOR SEQ ID NO:1852:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..477
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599317
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:
- acteaceact cateaceage tagtagetet ageaaageae ttgecateta eegacegeeg 60 cattecaaae ageeegaega getageagag egneaggeae etceteeagg aacatggeee 120 geaegeagea gttggeagta gtggegaean gtggtggeet tggtgetget ggeggeggeg 180 acgteggagg eegacgeea etgeeggeag gtggegtegg eeagegee etgeatetee 240 taegeggeeg eegaceae egeegaeege egegeegeet geageggegt eagagegeet eageggeet egegeegeet gtaaetgeet eagageete geekeegkyt geageggeet eaaegeeggt aaegeegeea geateeeete eaagtgegge gtersateee eetacaceat eageacetee aeegaetget eeagggtgaa etgaaee
- (2) INFORMATION FOR SEQ ID NO:1853:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..46
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599318
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

Thr His His Ser Ser Pro Ala Ser Ser Ser Ser Lys Ala Leu Ala Ile

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 5 10 Tyr Arg Pro Pro His Ser Lys Gln Pro Asp Glu Leu Ala Glu Xaa Gln 25 20 Ala Pro Pro Pro Gly Thr Trp Pro Ala Arg Ser Ser Trp Gln 40 35 (2) INFORMATION FOR SEQ ID NO:1854: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..76 (D) OTHER INFORMATION: / Ceres Seq. ID 1599319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854: Met Ala Arg Thr Gln Gln Leu Ala Val Val Ala Thr Xaa Gly Gly Leu 10 Gly Ala Ala Gly Gly Gly Asp Val Gly Gly Gly His Gln Leu Arg Ala 20 25 Gly Gly Val Gly His Arg Ala Leu His Leu Leu Arg Ala Arg Pro Gly 40 Leu Arg Ala Leu Arg Arg Leu Leu Gln Arg Arg Gln Glu Pro Gln Gln 55 60 Arg Arg Pro His His Arg Arg Pro Pro Arg Arg Leu 70 (2) INFORMATION FOR SEQ ID NO:1855: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 504 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..504 (D) OTHER INFORMATION: / Ceres Seq. ID 1599320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855: ctaatccatc gcagagcgcc gccgggngta gcgctactgc tagaggagag gaagcggaaa gggcggcggc ggcgcttgtg gtcagtcaaa gatccaacct ccggactcgc gatggggcgg cggatcctca acgatgctst gcgcacgatg gtcaacgcag accggcgggg gaacgcgtcg

- 60 120 180 gcgcttctcc gacccatctc cggcgtcatg gtctccttcc tcaacatcat gaagtaccga 240 gggtatatca aaaaatttga ggtcattgat gagaatagag ttgggaaaat tagagtggag 300 360 cttgatggac gtcttaaaga ttgcaaagct ctcacctaca ggcaagacct caaagctaag 420 qaqatagaac gatacagagt taggatgctc ccaacacgcc akggtgctat gttgtgatta ctactccgaa tggtgttttg gatcatgagg aagcaatcag gcagaacgtg ggtgggcagg 480 tccttgggtt attttccatt gact
- (2) INFORMATION FOR SEQ ID NO:1856:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..138
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599321
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

Leu Ile His Arg Arg Ala Pro Pro Xaa Val Ala Leu Leu Glu Glu

Tyr Arg Gln Asp Leu Lys Ala Lys Glu Ile Glu Arg Tyr Arg Val Arg 115 120 125

Met Leu Pro Thr Arg Xaa Gly Ala Met Leu 130 135

- (2) INFORMATION FOR SEQ ID NO:1857:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

Met Gly Arg Arg Ile Leu Asn Asp Ala Xaa Arg Thr Met Val Asn Ala 1 5 10 15

Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg Pro Ile Ser Gly Val 20 25 30

Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg Gly Tyr Ile Lys Lys 35 40 45

Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys Ile Arg Val Glu Leu
50 55 60

Asp Gly Arg Leu Lys Asp Cys Lys Ala Leu Thr Tyr Arg Gln Asp Leu 65 70 75 80

Lys Ala Lys Glu Ile Glu Arg Tyr Arg Val Arg Met Leu Pro Thr Arg 85 90 95

Xaa Gly Ala Met Leu

100

- (2) INFORMATION FOR SEQ ID NO:1858:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

Met Val Asn Ala Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg Pro 1 5 10

Ile Ser Gly Val Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg Gly $20 \\ 25 \\ 30 \\$

Tyr Ile Lys Lys Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys Ile 35 40 45

Arg Gln Asp Leu Lys Ala Lys Glu lle Glu Arg Tyr Arg Val Arg Met 65 70 75 80

Leu Pro Thr Arg Xaa Gly Ala Met Leu 85

- (2) INFORMATION FOR SEQ ID NO:1859:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..411
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599324
- (2) INFORMATION FOR SEQ ID NO:1860:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599325
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

20 25 30

Ala Leu Ser Arg Ser Ser Gln Arg Gln Asn Pro Ser Glu Xaa Pro Arg 35 40 45

Ala Arg Gln Leu Gly Val Gly Pro Gly Ile His Gly Glu Val Arg Ala 50 55 60

Ala Gln Gly His Arg Leu Arg Gln Leu Arg Arg Gly Ala Ala His Ala 65 70 75 80

Glu Gln Gly His Gln Gly Ala Arg Arg His Glu Val His Pro Glu Gly 85 90 95

Ala Gln Asp

- (2) INFORMATION FOR SEQ ID NO:1861:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136

```
(D) OTHER INFORMATION: / Ceres Seq. ID 1599326
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:
Ser Leu Gln Ser Xaa Pro Thr Xaa Pro Ser Pro Pro Leu Pro Ser Xaa
                                   10
Pro Leu Pro Cys Arg Val Arg Leu Ser Pro Arg Pro Pro Arg His Ala
                               25
           20
Leu Ser Pro Ala Pro Arg Asn Gly Lys Thr Pro Ala Asn Xaa His Ala
                           4.0
Pro Ala Ser Ser Ala Ser Ala Gln Gly Ser Met Glu Lys Tyr Glu Leu
                        55
Leu Lys Asp Ile Gly Ser Gly Asn Phe Gly Val Ala Arg Leu Met Arg
                                        75
                    70
Asn Lys Asp Thr Lys Glu Leu Val Ala Met Lys Tyr Ile Pro Arg Gly
                                   90
               85
Leu Lys Ile Asp Glu Asn Val Ala Arg Glu Ile Ile Asn His Arg Ser
            100
                              105
Leu Arg Thr Thr Ser Ser Ala Ser Arg Arg Ser Cys Ser Arg Pro
                            120
       115
Arg Thr Ser Pro Ser Ser Trp Ser
                        135
    130
(2) INFORMATION FOR SEQ ID NO:1862:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 89 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..89
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599327
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:
Val Ser Ser Leu Xaa Pro Pro Xaa Pro Pro Leu Pro Ser Pro Pro Xaa
                                    10
              5
Pro Ser Pro Val Glu Ser Gly Cys Pro His Asp Pro His Ala Thr Arg
                                                    30
           20
                                25
Ser Leu Pro Leu Leu Ala Thr Ala Lys Pro Gln Arg Xaa Pro Thr Arg
                            40
Pro Pro Ala Arg Arg Pro Arg Asp Pro Trp Arg Ser Thr Ser Cys
                        55
Ser Arg Thr Ser Ala Pro Ala Thr Ser Ala Trp Arg Gly Ser Cys Gly
                   70
                                        75
Thr Arg Thr Pro Arg Ser Ser Pro
                85
 (2) INFORMATION FOR SEQ ID NO:1863:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 514 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..514
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599360
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:
 gtaagttcta ttcgcgcaac cgcgtagaaa aaaaaaaggt ccagtcctca aactctacag
 cgggggcgag ccgaggaaga agaggtcgcc gccgccgcca ccgcttccat gtctggggga
                                                                       120
 ategecegeg geogettgee gaggagegea aggeetggeg caagaaceae eegeaeggtt
                                                                       180
 tcgtcgcaaa gccggagtcg ctgcccgacg ggacggtgaa ccttatgatt tggcactgca
                                                                       240
 ccatccccgg caagcaaggg actgattggg aaggtggata cttcccactc acccttcatt
                                                                       300
```

tcagtgagga ttaccctagc aagcctccca agtgcaagtt ccctcagggt ttcttccacc 360 caaatgtcta tccttctgga acagtctgtc tttcgatcct taatgaagat agtggttgga 420 gaccagctat tactgttaag cagattctcg tcgggatcca ggacttgcta gatcagcaaa 480 tcctgctgat cctgctcaaa cggatggcta tcac

- (2) INFORMATION FOR SEQ ID NO:1864:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..170
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599361
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

Lys Phe Tyr Ser Arg Asn Arg Val Glu Lys Lys Lys Val Gln Ser Ser 1 10 15

Asn Ser Thr Ala Gly Ala Ser Arg Gly Arg Arg Gly Arg Arg Arg Arg 20 25 30

His Arg Phe His Val Trp Gly Asn Arg Pro Arg Pro Leu Ala Glu Glu 35 40 45

Arg Lys Ala Trp Arg Lys Asn His Pro His Gly Phe Val Ala Lys Pro 50 55 60

Glu Ser Leu Pro Asp Gly Thr Val Asn Leu Met Ile Trp His Cys Thr 65 70 75 80

Ile Pro Gly Lys Gln Gly Thr Asp Trp Glu Gly Gly Tyr Phe Pro Leu 85 90 95

Thr Leu His Phe Ser Glu Asp Tyr Pro Ser Lys Pro Pro Lys Cys Lys 100 105 110

Phe Pro Gln Gly Phe Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val 115 120 125

Cys Leu Ser Ile Leu Asn Glu Asp Ser Gly Trp Arg Pro Ala Ile Thr 130 135 140

Val Lys Gln Ile Leu Val Gly Ile Gln Asp Leu Leu Asp Gln Gln Ile 145 150 155 160

Leu Leu Ile Leu Leu Lys Arg Met Ala Ile 165 170

- (2) INFORMATION FOR SEQ ID NO:1865:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

Met Ile Trp His Cys Thr Ile Pro Gly Lys Gln Gly Thr Asp Trp Glu 1 5 10

Gly Gly Tyr Phe Pro Leu Thr Leu His Phe Ser Glu Asp Tyr Pro Ser 20 25 30

Lys Pro Pro Lys Cys Lys Phe Pro Gln Gly Phe Phe His Pro Asn Val

Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu Asn Glu Asp Ser Gly
50 55 60

Trp Arg Pro Ala Ile Thr Val Lys Gln Ile Leu Val Gly Ile Gln Asp 65 70 75 80
Leu Leu Asp Gln Gln Ile Leu Leu Ile Leu Leu Lys Arg Met Ala Ile

85 90 95

- (2) INFORMATION FOR SEQ ID NO:1866:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..519
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866: acaatctttc ttgtatcact aagctagtgg ccacaactcg ttggcaacga ggaagcagca 60 ataagccgag aagctatgcc gccgccatat atggcacagg ctgccggcac cgccgatgcc 120 actgatgagg ctccactgct gctggcctcg tcggcggcgg ggtcgacgcc gtcgccgcca 180 getgeageae egegeeggaa eaggttegee ttegtetgeg ceaegetege eteegteaee 240 300 accatgctac atggctacaa cetgacgctg atgageggeg eggagetgtt catgegggag gacgtggggc tcaccgacgg cgaggtcgag gtgctggcgg ggtccatgaa cgtgttcatg 360 ctcgcgtcca tcctcgccgc cggctgagtg gccgaccacc tgggacgccg ccgcaccctc 420 gtgctcgcca acgccttcct catggccggc gcgctcgcca tgtcgctcgg caccagcttc 480 gccgcgctca tggcggcgcg cttcgtcaca gcgtcggct
- (2) INFORMATION FOR SEQ ID NO:1867:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599364
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

Met Pro Pro Pro Tyr Met Ala Gln Ala Gly Thr Ala Asp Ala Thr 1 5 5 10 10 15 Asp Glu Ala Pro Leu Leu Leu Ala Ser Ser Ala Ala Gly Ser Thr Pro

20 25 30 Ser Pro Pro Ala Ala Ala Pro Arg Arg Asn Arg Phe Ala Phe Val Cys

Ser Pro Pro Ala Ala Ala Pro Arg Arg Ash Arg Phe Ala Phe Val Cys
35
40
45

Ala Thr Leu Ala Ser Val Thr Thr Met Leu His Gly Tyr Asn Leu Thr 50 55 60

Leu Met Ser Gly Ala Glu Leu Phe Met Arg Glu Asp Val Gly Leu Thr 65 70 75 80

Asp Gly Glu Val Glu Val Leu Ala Gly Ser Met Asn Val Phe Met Leu 85 90 95

Ala Ser Ile Leu Ala Ala Gly 100

- (2) INFORMATION FOR SEQ ID NO:1868:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:															
Met 1	Ala	Gln	Ala	Ala 5	Gly	Thr	Ala	Asp	Ala 10	Thr	Asp	Glu	Ala	Pro 15	Leu
Leu	Leu	Ala	Ser 20	Ser	Ala	Ala	Gly	Ser 25	Thr	Pro	Ser	Pro	Pro 30	Ala	Ala
Ala	Pro	Arg 35	Arg	Asn	Arg	Phe	Ala 40	Phe	Val	Cys	Ala	Thr 45	Leu	Ala	Ser
Val	Thr 50	Thr	Met	Leu		Gly 55	Tyr	Asn	Leu	Thr	Leu 60	Met	Ser	Gly	Ala
Glu 65	Leu	Phe	Met	Arg	Glu 70	Asp	Val	Gly	Leu	Thr 75	Asp	Gly	Glu	Val	Glu 80
Val	Leu	Ala	Gly	Ser 85	Met	Asn	Val	Phe	Met 90	Leu	Ala	Ser	Ile	Leu 95	Ala
Ala	Gly														

- (2) INFORMATION FOR SEQ ID NO:1869:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..455
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599373
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869: actgetecet eteaeggacg ettegeteta gteggaaggt ttegaggaae teeegggete 60 120 gaggagatcg ggacgatgat gggagggcgc gctctgctgc tgctcctggt ctcggcgctg 180 ctcgttcaga tccgcgcctc tgacccgctg ctgtacgagc cgttcgatga ggacttcgag ggaagatgga tcgtctccaa gaaggatgaa taccaaggtg tatggaagca tgccaagagt 240 gatgggcatg aggactatgg tctccttgtt agtgacaaag caaggaaata cgccataatc 300 aaggagettg atgageeagt taeettaaat gatgggaeag tggteetgea gtttgaagtg 360 agacttcaga atggcyttga atgtggaggt gcctacatta agtacatccg ccctcaggat 420 gctggatggg atgccaagga gtttgayaat gagac
- (2) INFORMATION FOR SEQ ID NO:1870:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..151
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599374
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:
- Thr Ala Pro Ser His Gly Arg Phe Ala Leu Val Gly Arg Phe Arg Gly 1 5 10 15 Thr Pro Gly Leu Glu Glu Ile Gly Thr Met Met Gly Gly Arg Ala Leu
- 20 25 30
- Leu Leu Leu Val Ser Ala Leu Leu Val Gln Ile Arg Ala Ser Asp 35 40 45
- Pro Leu Leu Tyr Glu Pro Phe Asp Glu Asp Phe Glu Gly Arg Trp Ile 50 55 60 60 Val Ser Lys Lys Asp Glu Tyr Gln Gly Val Trp Lys His Ala Lys Ser
- 65 70 75 80
 Asp Gly His Glu Asp Tyr Gly Leu Leu Val Ser Asp Lys Ala Arg Lys
- 85 90 95

 Tyr Ala Ile Ile Lys Glu Leu Asp Glu Pro Val Thr Leu Asn Asp Gly
 100 105 110

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Thr Val Val Leu Gln Phe Glu Val Arg Leu Gln Asn Gly Xaa Glu Cys
                         120
       115
Gly Gly Ala Tyr Ile Lys Tyr Ile Arg Pro Gln Asp Ala Gly Trp Asp
                135
Ala Lys Glu Phe Xaa Asn Glu
                150
(2) INFORMATION FOR SEQ ID NO:1871:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 126 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..126
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599375
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:
Met Met Gly Gly Arg Ala Leu Leu Leu Leu Val Ser Ala Leu Leu
                                   10
Val Gln Ile Arg Ala Ser Asp Pro Leu Leu Tyr Glu Pro Phe Asp Glu
           20
                                25
Asp Phe Glu Gly Arg Trp Ile Val Ser Lys Lys Asp Glu Tyr Gln Gly
                            40
Val Trp Lys His Ala Lys Ser Asp Gly His Glu Asp Tyr Gly Leu Leu
                       55
Val Ser Asp Lys Ala Arg Lys Tyr Ala Ile Ile Lys Glu Leu Asp Glu
Pro Val Thr Leu Asn Asp Gly Thr Val Val Leu Gln Phe Glu Val Arg
                                   90
Leu Gln Asn Gly Kaa Glu Cys Gly Gly Ala Tyr Ile Lys Tyr Ile Arg
           100
                               105
Pro Gln Asp Ala Gly Trp Asp Ala Lys Glu Phe Xaa Asn Glu
       115
                           120
(2) INFORMATION FOR SEQ ID NO:1872:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 125 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..125
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599376
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:
Met Gly Gly Arg Ala Leu Leu Leu Leu Val Ser Ala Leu Leu Val
                                   10
Gln Ile Arg Ala Ser Asp Pro Leu Leu Tyr Glu Pro Phe Asp Glu Asp
                               25
Phe Glu Gly Arg Trp Ile Val Ser Lys Lys Asp Glu Tyr Gln Gly Val
                            40
Trp Lys His Ala Lys Ser Asp Gly His Glu Asp Tyr Gly Leu Leu Val
Ser Asp Lys Ala Arg Lys Tyr Ala Ile Ile Lys Glu Leu Asp Glu Pro
                    70
Val Thr Leu Asn Asp Gly Thr Val Val Leu Gln Phe Glu Val Arg Leu
                                    90
```

Gln Asn Gly Xaa Glu Cys Gly Gly Ala Tyr Ile Lys Tyr Ile Arg Pro 100 105 110

Gln Asp Ala Gly Trp Asp Ala Lys Glu Phe Xaa Asn Glu

115 120 125

- (2) INFORMATION FOR SEQ ID NO:1873:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..487
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599385
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

ctcqaqcctq accettacge cttcqctcqc qccgccgcqc qccqccqcta cgccccqcac 60 ctcgcttcat ttcgtgtcgc caagatgacg aagcgcacta agaaggcagg aattgttggc 120 aaatatggaa ccaggtatgg tgctagcttg cgtaagcaaa tcaagaagat ggaggtatct 180 cagcattcca agtacttttg cgagttctgt gggaagtttg ctgtgaagag gaaagcagtt 240 300 ggaatttggg ggtgcaagga ctgtgggaag gtgaaggctg gtggtgcggc caaccgccgg 360 caqqcccqqc qqcqqcqaqc tggtgcgtgg cgaacgcggc cgtcggggac gacaggctgc 420 agcaggeget ggactaegeg tgeggeeaeg gggeggaetg cagegeeate cageceageg ggtcgtgctt cgagccggac accaagctcg cgcacgcctc gtatgcgttc gacagctact 480 accageg

- (2) INFORMATION FOR SEQ ID NO:1874:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599386
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

Leu Glu Pro Asp Pro Tyr Ala Phe Ala Arg Ala Ala Ala Arg Arg 1 5 10 15

Tyr Ala Pro His Leu Ala Ser Phe Arg Val Ala Lys Met Thr Lys Arg
20 25 30

Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr Gly Ala 35 40 45

Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser Gln His Ser Lys 50 55 60

Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Arg Lys Ala Val 65 70 75 80 Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys Ala Gly Gly Ala

85 90 95
Ala Asn Arg Arg Gln Ala Arg Arg Arg Arg Ala Gly Ala Trp Arg Thr

Arg Pro Ser Gly Thr Thr Gly Cys Ser Arg Arg Trp Thr Thr Arg Ala
115 120 125

Ala Thr Gly Arg Thr Ala Ala Pro Ser Ser Pro Ala Gly Arg Ala Ser 130 135

Ser Arg Thr Pro Ser Ser Arg Thr Pro Arg Met Arg Ser Thr Ala Thr 145 150 155 160
Thr Ser

- (2) INFORMATION FOR SEQ ID NO:1875:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599387
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 1 5 10 15

Arg Tyr Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser 20 25 30

Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys 35 40 45

Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys 50 55 60

Ala Gly Gly Ala Ala Asn Arg Arg Gln Ala Arg Arg Arg Arg Ala Gly 65 70 75 80

Ala Trp Arg Thr Arg Pro Ser Gly Thr Thr Gly Cys Ser Arg Arg Trp 85 90 95

Thr Thr Arg Ala Ala Thr Gly Arg Thr Ala Ala Pro Ser Ser Pro Ala 100 105 110

Gly Arg Ala Ser Ser Arg Thr Pro Ser Ser Arg Thr Pro Arg Met Arg 115 120 125

Ser Thr Ala Thr Thr Ser 130

- (2) INFORMATION FOR SEQ ID NO:1876:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys 20 25 30

Gly Lys Val Lys Ala Gly Gly Ala Ala As
n Arg Arg Gl
n Ala Arg Arg 35 40 45

Arg Arg Ala Gly Ala Trp Arg Thr Arg Pro Ser Gly Thr Thr Gly Cys 50 55 60

Ser Arg Arg Trp Thr Thr Arg Ala Ala Thr Gly Arg Thr Ala Ala Pro 65 70 75 80

Ser Ser Pro Ala Gly Arg Ala Ser Ser Arg Thr Pro Ser Ser Arg Thr 85 90 95

Pro Arg Met Arg Ser Thr Ala Thr Thr Ser 100 105

- (2) INFORMATION FOR SEQ ID NO:1877:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1599393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:										
	accactccca	gtcccagtct	cccaccgtcc	cacgaaacac	actcaactct	gccccgaagc	60			
					gcagcccaag		120			
					caaacagccg		180			
	agtcaggcgc	caaagcgaag	cccgcggcgg	gcccgcgcgt	cgcggcggcc	acgaccctcg	240			
	ccgccgccgc	cgccgcagca	gcagcagcag	caaatgccgc	ctcggccgcg	tegtegeeeg	300			
	ggccggaaac	ggctccgacc	gtgccggacg	tgtgcgtcgg	cggggacaag	gacggggacg	360			
	cggacgcgga	cgcgagcgcg	tggactggga	cctcgacgcc	gggctgagcg	cggcggc				

- (2) INFORMATION FOR SEQ ID NO:1878:
 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..138
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878: Pro Leu Pro Val Pro Val Ser His Arg Pro Thr Lys His Thr Gln Leu

1 5 10 15 Cys Pro Glu Ala Glu Asn Arg Gln Pro Asp Met Lys Glu Asn Gln Ser 20 25 30

Ala Ala Gln Gly Arg Gly Ala Ala Gly Pro Arg Arg Gln Pro Lys 35 40

Ala Ala Pro Gly Gln Thr Ala Glu Ala Ala Gln Val Arg Arg Gln 50 55 60

Ser Glu Ala Arg Gly Gly Pro Ala Arg Arg Gly Gly His Asp Pro Arg 65 70 75 80

Arg Arg Arg Arg Ser Ser Ser Ser Lys Cys Arg Leu Gly Arg 85 90 95

Val Val Ala Arg Ala Gly Asn Gly Ser Asp Arg Ala Gly Arg Val Arg 100 105 110

Arg Arg Gly Gln Gly Arg Gly Arg Gly Arg Glu Arg Val Asp 115 120 125

Trp Asp Leu Asp Ala Gly Leu Ser Ala Ala 130 135

- (2) INFORMATION FOR SEQ ID NO:1879:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

Met Lys Glu Asn Gln Ser Ala Ala Ala Gln Gly Arg Gly Ala Ala Gly

10
15
10
15

Pro Arg Arg Gln Pro Lys Ala Ala Ala Pro Gly Gln Thr Ala Glu Ala 20 25 30

Ala Gln Val Arg Arg Gln Ser Glu Ala Arg Gly Gly Pro Ala Arg Arg 35 40 45

Gly Gly His Asp Pro Arg Arg Arg Arg Arg Ser Ser Ser Ser Ser 50 55 60

Lys Cys Arg Leu Gly Arg Val Val Ala Arg Ala Gly Asn Gly Ser Asp 65 70 75 80

Arg Ala Gly Arg Val Arg Arg Arg Gly Gln Gly Arg Gly Arg Gly Arg 85 90 95
Gly Arg Glu Arg Val Asp Trp Asp Leu Asp Ala Gly Leu Ser Ala Ala

- (2) INFORMATION FOR SEQ ID NO:1880:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..453
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599396
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880: aagctgattt ctgcttgtta gctactcacg tcaacagaaa atctcgcgtt cacctcctct 60 120 coagtetete egecteege ttacttetet gaetetgtee tetttggttt ettteetgte ggcgacggct ggggtgctgc gccgctcktc accttcaccg ccgacgagca ttcacaagta 180 gtggtctctt actggtggcg gcgtagaggt gacgaaaaaa ccttgacaat gagcagcata 240 ggcacaggtt atgatetgte tgteaceaen tteteteeeg atggeegegt etteeaggte 300 gagtatgcca cgaaggctgt cgacaacagc gggaccgttg ttgggatcaa gtgcaaagat 360 420 ggcattgttc tgggtgtcga gaagctggta acctcaaaga tgatgctgga rggatcaaac cgtaggatcc attcagtgca caggcactcg ggc
- (2) INFORMATION FOR SEQ ID NO:1881:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..75
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599397
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Val Thr Xaa Phe Ser

1 10 15

Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Thr Lys Ala Val Asp 20 25 30

Asn Ser Gly Thr Val Val Gly Ile Lys Cys Lys Asp Gly Ile Val Leu 35 40 45

Gly Val Glu Lys Leu Val Thr Ser Lys Met Met Leu Xaa Gly Ser Asn 50 55 60

Arg Arg Ile His Ser Val His Arg His Ser Gly 65 70 75

- (2) INFORMATION FOR SEQ ID NO:1882:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..46
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599398
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

Met Ile Cys Leu Ser Pro Xaa Ser Leu Pro Met Ala Ala Ser Ser Arg

120

180

240

300

360

40

- (2) INFORMATION FOR SEQ ID NO:1883:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

35

- (A) NAME/KEY: -
- (B) LOCATION: 1..369
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599403
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883: accategeaa tteacaagea aageaateag ageeaageae ceacegteet cetteette ettegaetea teaaageatg tettgetgeg geggeaactg egegtgeaee teeggetgea

actgcggcag cggatgcggc gactgcaaca cctgcaactg cggcaccagc tgcggctgct cctgctgcag ctgcaactga gccacccgcg atgacgagac aaccacccgg cctcccccc atcgtactac aactatgtag cggcgtctaa ataagatccc tccaccggcc accgccattg ttccttcctg tcgctgcatg gttgcctgcc tcgtgcccgg gctaatatac atatacgggg

gtgtttggg

- (2) INFORMATION FOR SEQ ID NO:1884:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599404
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

Thr Ile Ala Ile His Lys Gln Ser Asn Gln Ser Gln Ala Pro Thr Val 1 5 10 15

Leu Leu Ser Phe Leu Arg Leu Ile Lys Ala Cys Leu Ala Ala Ala Ala 20 25 30

Thr Ala Arg Ala Pro Pro Ala Ala Thr Ala Ala Ala Asp Ala Ala Thr 35 40 45

Ala Thr Pro Ala Thr Ala Ala Pro Ala Ala Ala Ala Pro Ala Ala Ala 50 55 60

Ala Thr Glu Pro Pro Ala Met Thr Arg Gln Pro Pro Gly Leu Pro Pro 65 70 75 80

Ile Val Leu Gln Leu Cys Ser Gly Val

85

- (2) INFORMATION FOR SEQ ID NO:1885:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599405
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

Pro Ser Gln Phe Thr Ser Lys Ala Ile Arg Ala Lys His Pro Pro Ser

```
10
                5
Ser Phe Leu Ser Phe Asp Ser Ser Lys His Val Leu Leu Arg Arg Gln
                                25
            20
Leu Arg Val His Leu Arg Leu Gln Leu Arg Gln Arg Met Arg Arg Leu
                            40
Gln His Leu Gln Leu Arg His Gln Leu Arg Leu Leu Leu Gln Leu
                        55
Gln Leu Ser His Pro Arg
(2) INFORMATION FOR SEQ ID NO:1886:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 65 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..65
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599406
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:
His Arg Asn Ser Gln Ala Lys Gln Ser Glu Pro Ser Thr His Arg Pro
Pro Phe Phe Pro Ser Thr His Gln Ser Met Ser Cys Cys Gly Gly Asn
           2.0
Cys Ala Cys Thr Ser Gly Cys Asn Cys Gly Ser Gly Cys Gly Asp Cys
                            40
Asn Thr Cys Asn Cys Gly Thr Ser Cys Gly Cys Ser Cys Ser Cys
Asn
65
(2) INFORMATION FOR SEQ ID NO:1887:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 508 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..508
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599416
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:
aagcccactt tocccagtac totactcacc cacccactca cggactcatc tactgagcag
cgcggtgggc atccgagcga gagggcgagc gcggaaggat cggaattccg aaggttgggc
                                                                       120
                                                                       180
atggaggcga gcggcgagaa ggctgcggtg gtgcgacggc tgatggaggc gaaggaggtg
                                                                       240
tccgggaaga ccttctcggg aatcgccgcc gagacgggtc tcaccaacgt ctacgtggcg
cagetgetge ggegeeagge geageteaag geegaeaegg tgeeegeget gagggeggee
ctgcccacgc tcacggacga cctcatcgaa ctcatgatgc agccgccctt ccggtcctac
caccccaaca tcgtccacga gcccgccatt tacagattga atgaagctgt tatgcatttt
                                                                       420
ggagagagca tcaaggaaat catcaatgag gagtttggtg atggaatcat gtcagccata
                                                                       480
gacttctatt gttcagttga caaggttg
(2) INFORMATION FOR SEQ ID NO:1888:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 169 amino acids
           (B) TYPE: amino acid
          (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
```

(ix) FEATURE:

(A) NAME/KEY: peptide

(ii) MOLECULE TYPE: peptide

- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599417
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Lys Pro Thr Phe Pro Ser Thr Leu Leu Thr His Pro Leu Thr Asp Ser 1 5 10 15

Ser Thr Glu Gln Arg Gly Gly His Pro Ser Glu Arg Ala Ser Ala Glu 20 25 30

Gly Ser Glu Phe Arg Arg Leu Gly Met Glu Ala Ser Gly Glu Lys Ala 35 40 45

Ala Val Val Arg Arg Leu Met Glu Ala Lys Glu Val Ser Gly Lys Thr 50 55 60

Phe Ser Gly Ile Ala Ala Glu Thr Gly Leu Thr Asn Val Tyr Val Ala 65 70 75 80

Gln Leu Leu Arg Arg Gln Ala Gln Leu Lys Ala Asp Thr Val Pro Ala 85 90 95

Leu Arg Ala Ala Leu Pro Thr Leu Thr Asp Asp Leu Ile Glu Leu Met 100 105 110

Met Gln Pro Pro Phe Arg Ser Tyr His Pro Asn Ile Val His Glu Pro $115 \\ 120 \\ 125$

Ala Ile Tyr Arg Leu Asn Glu Ala Val Met His Phe Gly Glu Ser Ile 130 135 140

Lys Glu Ile Ile Asn Glu Glu Phe Gly Asp Gly Ile Met Ser Ala Ile 145 150 155 160

Asp Phe Tyr Cys Ser Val Asp Lys Val 165

- (2) INFORMATION FOR SEQ ID NO:1889:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

Met Glu Ala Ser Gly Glu Lys Ala Ala Val Val Arg Arg Leu Met Glu 1 5 10 15 Ala Lys Glu Val Ser Gly Lys Thr Phe Ser Gly Ile Ala Ala Glu Thr

Ala Lys Glu Val Ser Gly Lys Thr Phe Ser Gly 11e Ala Ala Glu Inr 20 25 30

Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg Gln Ala Gln
35 40 45

Leu Lys Ala Asp Thr Val Pro Ala Leu Arg Ala Ala Leu Pro Thr Leu
50 55 60

Thr Asp Asp Leu Ile Glu Leu Met Met Gln Pro Pro Phe Arg Ser Tyr 65 70 75 80

Val Met His Phe Gly Glu Ser Ile Lys Glu Ile Ile Asn Glu Glu Phe 100 105 110

Gly Asp Gly Ile Met Ser Ala Ile Asp Phe Tyr Cys Ser Val Asp Lys 115 120 125

Val

- (2) INFORMATION FOR SEQ ID NO:1890:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599419
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:
- Glu Thr Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg Gln 20 25 30
- Ala Gln Leu Lys Ala Asp Thr Val Pro Ala Leu Arg Ala Ala Leu Pro 35 40 45
- Thr Leu Thr Asp Asp Leu Ile Glu Leu Met Met Gln Pro Pro Phe Arg 50 55 60
- Ser Tyr His Pro Asn Ile Val His Glu Pro Ala Ile Tyr Arg Leu Asn 65 70 75 80
- Glu Ala Val Met His Phe Gly Glu Ser Ile Lys Glu Ile Ile Asn Glu 85 90 95

Asp Lys Val

115

- (2) INFORMATION FOR SEQ ID NO:1891:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599424
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891: ggcagtagaa gccgagaagg taggcccgct cgttccaaca tcacaaactc cacacggctc tectqtetee getgeeeget ecaceteect ecatgeegte ggetteeete egeetegeeg 120 180 tcqtcqqcqc gggcgcggcg ggcctggttg ccgcccgcga gctacgccgc gagggccatg cgcccgtcgt cttcgagcgc gccgccgccg ttgggggcac ttggctctac acgcctcccg 240 ccacgtcctc cgacccgctc ggcgccgcgg cgacgcattc cagcctctac gcatcgctcc 300 gcaccaacct gccacgcgag accatgggct tectegaett eccettegee getggegeeg 360 cgggctcccg agacccccgc cggtttcccg ggcacgagga ggtgctccgc tacctggagg 420 cgttcgcgcg ccggttcgac ctgctccggc tcgtccgctt cgagacggag gtgctcagtg 480
- (2) INFORMATION FOR SEQ ID NO:1892:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599425
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:
- Gly Ser Arg Ser Arg Glu Gly Arg Pro Ala Arg Ser Asn Ile Thr Asn 1 5 10 15
- Ser Thr Arg Leu Ser Cys Leu Arg Cys Pro Leu His Leu Pro Pro Cys 20 25 30
- Arg Arg Leu Pro Ser Ala Ser Pro Ser Ser Ala Arg Ala Arg Ala 35 40 45

Trp Leu Pro Pro Ala Ser Tyr Ala Ala Arg Ala Met Arg Pro Ser Ser 55 Ser Ser Ala Pro Pro Pro Leu Gly Ala Leu Gly Ser Thr Arg Leu Pro 7.5 70 Pro Arg Pro Pro Thr Arg Ser Ala Pro Arg Arg Ile Pro Ala Ser 85 90 Thr His Arg Ser Ala Pro Thr Cys His Ala Arg Pro Trp Ala Ser Ser 100 105 110 Thr Ser Pro Ser Pro Leu Ala Pro Arg Ala Pro Glu Thr Pro Ala Gly 115 120 125 Phe Pro Gly Thr Arg Arg Cys Ser Ala Thr Trp Arg Arg Ser Arg Ala 135 140 Gly Ser Thr Cys Ser Gly Ser Ser Ala Ser Arg Arg Cys Ser Val 155 150

- (2) INFORMATION FOR SEQ ID NO:1893:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599426
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893: Ala Val Glu Ala Glu Lys Val Gly Pro Leu Val Pro Thr Ser Gln Thr

1 5 10 15
Pro His Gly Ser Pro Val Ser Ala Ala Arg Ser Thr Ser Leu His Ala

Pro His Gly Ser Pro Val Ser Ala Ala Arg Ser Thr Ser Leu His Ala
20 25 30

Val Gly Phe Pro Pro Pro Arg Arg Arg Arg Gly Arg Gly Gly Pro
35 40 45

Gly Cys Arg Pro Arg Ala Thr Pro Arg Gly Pro Cys Ala Arg Arg Leu 50 55 60

Arg Ala Arg Arg Arg Trp Gly His Leu Ala Leu His Ala Ser Arg 65 70 75 80
His Val Leu Arg Pro Ala Arg Arg Arg Gly Asp Ala Phe Gln Pro Leu

His Val Leu Arg Pro Ala Arg Arg Gly Asp Ala Phe Gln Plo Leu 85 90 95

Arg Ile Ala Pro His Gln Pro Ala Thr Arg Asp His Gly Leu Pro Arg

100 105 110

Leu Pro Leu Arg Arg Trp Arg Arg Gly Leu Pro Arg Pro Pro Pro Val
115 120 125

Ser Arg Ala Arg Gly Gly Ala Pro Leu Pro Gly Gly Val Arg Ala Pro

130 135 140
Val Arg Pro Ala Pro Ala Arg Pro Leu Arg Asp Gly Gly Ala Gln Cys

155

Glu

- (2) INFORMATION FOR SEQ ID NO:1894:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599427

Client Docket No. 80146.003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894: Met Pro Ser Ala Ser Leu Arg Leu Ala Val Val Gly Ala Gly Ala Ala 10 Gly Leu Val Ala Ala Arg Glu Leu Arg Arg Glu Gly His Ala Pro Val Val Phe Glu Arg Ala Ala Ala Val Gly Gly Thr Trp Leu Tyr Thr Pro 40 Pro Ala Thr Ser Ser Asp Pro Leu Gly Ala Ala Ala Thr His Ser Ser 55 Leu Tyr Ala Ser Leu Arg Thr Asn Leu Pro Arg Glu Thr Met Gly Phe 70 75 Leu Asp Phe Pro Phe Ala Ala Gly Ala Ala Gly Ser Arg Asp Pro Arg 90 85 Arg Phe Pro Gly His Glu Glu Val Leu Arg Tyr Leu Glu Ala Phe Ala 100 105 Arg Arg Phe Asp Leu Leu Arg Leu Val Arg Phe Glu Thr Glu Val Leu 125 115 120 Ser Val Arg 130 (2) INFORMATION FOR SEQ ID NO:1895: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 500 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599434
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895: atcacccct accagtttca attttcaaaa gggcgtggag gcgccgcacc accgccgccg ccaccactga cgagggagga aacgccacct ccccgagcca gtccgatgtt gtccgaccag 120 gagetggeec agtacgtgga gteectegte cageacaceg etgegeaggg tggcaceggg 180 atateggegg atgeegtggt gegeeagete ggggegeage teggegttga ceteteeeee 240 aaggegeage teateegeag egteetegte gegeteeteg geeeegegge egegeeggeg 300 ccggaccccg cgggttcgcg taaggatccc ttcgaccccg caaccgctgc cgccgccggc 360 420 gggcccgcg ccgagactcc tccacagcag atgcacttct ctaccgccgc cgcgtcgtcg geecegeee ettetecage egtteeceae ttetteeege ageageacea geaceagatg 480 cagtacttcc tgtccgcccc
- (2) INFORMATION FOR SEQ ID NO:1896:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599435
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:
- Ile Thr Pro Tyr Gln Phe Gln Phe Ser Lys Gly Arg Gly Gly Ala Ala 10 5
- Pro Pro Pro Pro Pro Leu Thr Arg Glu Glu Thr Pro Pro Pro Arg 25
- Ala Ser Pro Met Leu Ser Asp Gln Glu Leu Ala Gln Tyr Val Glu Ser 4.5 40
- Leu Val Gln His Thr Ala Ala Gln Gly Gly Thr Gly Ile Ser Ala Asp 60 55 Ala Val Val Arg Gln Leu Gly Ala Gln Leu Gly Val Asp Leu Ser Pro

Pro Ala Thr Ala Ala Ala Ala Gly Gly Pro Arg Ala Glu Thr Pro Pro 115 120 125

Gln Gln Met His Phe Ser Thr Ala Ala Ala Ser Ser Ala Pro Ala Pro 130 135 140

Ser Pro Ala Val Pro His Phe Phe Pro Gln Gln His Gln His Gln Met 145 150 155 160

Gln Tyr Phe Leu Ser Ala 165

(2) INFORMATION FOR SEQ ID NO:1897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..131
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

Met Leu Ser Asp Gln Glu Leu Ala Gln Tyr Val Glu Ser Leu Val Gln 1 5 10 15

His Thr Ala Ala Gln Gly Gly Thr Gly Ile Ser Ala Asp Ala Val Val 20 25 30

Arg Gln Leu Gly Ala Gln Leu Gly Val Asp Leu Ser Pro Lys Ala Gln 35 40 45

Leu Ile Arg Ser Val Leu Val Ala Leu Leu Gly Pro Ala Ala Ala Pro 50 55 60

Ala Pro Asp Pro Ala Gly Ser Arg Lys Asp Pro Phe Asp Pro Ala Thr 65 70 75 80

Ala Ala Ala Gly Gly Pro Arg Ala Glu Thr Pro Pro Gln Gln Met 85 90 95

His Phe Ser Thr Ala Ala Ala Ser Ser Ala Pro Ala Pro Ser Pro Ala 100 105 110

Val Pro His Phe Phe Pro Gln Gln His Gln His Gln Met Gln Tyr Phe 115 120 125

Leu Ser Ala

130

- (2) INFORMATION FOR SEQ ID NO:1898:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

Met Pro Trp Cys Ala Ser Ser Gly Arg Ser Ser Ala Leu Thr Ser Pro 1 5 10 15

Pro Arg Arg Ser Ser Ser Ala Ala Ser Ser Ser Arg Ser Ser Ala Pro 20 25 30

Arg Pro Arg Arg Arg Thr Pro Arg Val Arg Val Arg Ile Pro Ser 35 40 45

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..414
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599438
- (2) INFORMATION FOR SEQ ID NO:1900:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599439
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:
- Ala Pro Thr Pro Pro His His Leu His Ser Lys Gln Gly Glu Gly Glu 1 5 10 15
- Arg Gln Thr Asn Pro Pro His Arg Pro Ser Ser Val Ser Ser Leu Ala 20 25 30
- His Ala Arg Pro Asn Val Ala Ala Pro Arg Ala Pro Arg Leu His Arg 35 40 45
- Pro Leu Arg Arg Gly Arg Gly Arg Ala Ala Asp Pro Asp Leu Leu Leu 50 60
- Leu Phe Leu Leu Leu Ala Gly Pro Pro Pro His Pro Ser Pro Arg Pro 65 70 75 80
- Ala Gly Leu Arg Val Pro Arg Pro Arg Pro Gly Leu Leu Arg Gly Leu 85 90 95
- Arg Arg His Ala Leu Pro Arg Pro Ala Ala Gly Gly Ser Arg Arg Leu 100 105 110

 Arg Gln Ala Arg Leu Pro Gly Pro Arg Pro Ala Pro Arg Arg Phe Gln
- Arg Gln Ala Arg Leu Pro Gly Pro Arg Pro Ala Pro Arg Arg Pne Gln
 115 120 125
 Glv
- (2) INFORMATION FOR SEQ ID NO:1901:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599440
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

Leu Pro Pro His Leu Thr Ile Ser Thr Pro Asn Lys Gly Lys Ala Ser 1 5 10 15

Asp Arg Gln Thr His Pro Ile Ala Pro Pro Leu Ser Pro Leu Leu Pro 20 25 30

Thr Pro Ala Pro Met Ser Pro Pro Leu Glu Pro His Asp Tyr Ile Gly 35 40 45

Leu Ser Ala Ala Ala Ala Ala Ala Pro Pro Thr Pro Thr Ser Ser Ser 50 55 60

Ser Ser Ser Ser Pro Ala Pro Arg Leu Thr Leu Arg Leu Gly Leu 65 70 75 80

Pro Gly Ser Glu Ser Pro Asp Arg Asp Arg Asp Cys Cys Glu Asp Phe 85 90 95

Ala Ala Thr Leu Ser Leu Gly Pro Leu Pro Ala Ala Ala Ala Val Ser 100 105 110

Ala Lys Arg Ala Phe Pro Asp Pro Ala Gln Arg Pro Gly Ala Ser Lys 115 120 125

Ala Ser Asp Ala Lys Gln Gln Ala Ser 130 135

- (2) INFORMATION FOR SEQ ID NO:1902:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599441
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

Ser His Pro Thr Ser Pro Ser Pro Leu Gln Thr Arg Gly Arg Arg Ala 1 5 10 15

Thr Asp Lys Pro Thr Pro Ser Pro Leu Leu Cys Leu Leu Ser Cys Pro 20 25 30

Arg Pro Pro Gln Cys Arg Arg Pro Ser Ser Pro Thr Thr Thr Ser Ala 35 40 45

Ser Pro Pro Arg Pro Arg Pro Arg Arg Arg Pro Arg Pro Pro Pro 50 55 60

Leu Pro Pro Pro Arg Arg Pro Pro Ala Ser Pro Phe Ala Ser Ala Cys 65 70 75 80
Arg Ala Pro Ser Pro Pro Thr Ala Thr Gly Thr Ala Ala Arg Thr Ser

85 90 95
Pro Pro Arg Ser Pro Ser Ala Arg Cys Arg Arg Gln Pro Pro Ser Pro

100 105 110
Pro Ser Ala Pro Ser Arg Thr Pro Pro Ser Ala Pro Ala Leu Pro Arg

125

115 120 Leu Ala Thr Pro Ser Ser Arg Leu Pro 130 135

- (2) INFORMATION FOR SEQ ID NO:1903:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..486
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599443
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

 aacatgettt acacgetete ceteceaett egtgegageg teeegaacta agttgetegt 60
 ggtggaggtg gtttgtggeg atggeettea agetggteae caageeegeg geggegtege 120
 cegetgetge teaetgggga gatetegeee gggggeegea gggtaegage egegttgeet 180
 teggaeeage geeeaggaae aaggggetee geaeggeeaa caacteegea aegeeeatgg

teggaceage geceaggaae aaggggetee geaeggeeaa caacteegea aegeeeatgg 240 ctaaggaaga gagggttgat egaagtgaaa tattgacatt ggatageate agacaagttt 300 tgattagact agaagacage atcatatttg gacttttgga gagageacag ttttgttaca 360 aegetgacae atatgatage aatgetttee acatggatgg ttttggaggg tetttggttg 420 aatatatggt tagagaaact gaaaagetee atgegeaggt tgggaggtae aagageeeag 480

atgagc

- (2) INFORMATION FOR SEQ ID NO:1904:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599444
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:
- His Ala Leu His Ala Leu Pro Pro Thr Ser Cys Glu Arg Pro Glu Leu 1 5 10 15 Ser Cys Ser Trp Trp Arg Trp Phe Val Ala Met Ala Phe Lys Leu Val
- Ser Cys Ser Trp Trp Arg Trp Phe Val Ala Met Ala Phe Lys Leu Val
 20 25 30
- Thr Lys Pro Ala Ala Ala Ser Pro Ala Ala Ala His Trp Gly Asp Leu 35 40 45
- Ala Arg Gly Pro Gln Gly Thr Ser Arg Val Ala Phe Gly Pro Ala Pro 50 55 60
- Arg Asn Lys Gly Leu Arg Thr Ala Asn Asn Ser Ala Thr Pro Met Ala 65 70 75 80
- Lys Glu Glu Arg Val Asp Arg Ser Glu Ile Leu Thr Leu Asp Ser Ile 85 90 95 Arg Gln Val Leu Ile Arg Leu Glu Asp Ser Ile Ile Phe Gly Leu Leu
- 100 105 110 Glu Arg Ala Gln Phe Cys Tyr Asn Ala Asp Thr Tyr Asp Ser Asn Ala
- 115 120 125

 Phe His Met Asp Gly Phe Gly Gly Ser Leu Val Glu Tyr Met Val Arg
- 130 135 140 Glu Thr Glu Lys Leu His Ala Gln Val Gly Arg Tyr Lys Ser Pro Asp
- Glu Thr Glu Lys Leu His Ala Gln Val Gly Arg Tyr Lys Ser Pro Asp 145 150 155 160 Glu
- (2) INFORMATION FOR SEQ ID NO:1905:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905: Met Ala Phe Lys Leu Val Thr Lys Pro Ala Ala Ala Ser Pro Ala Ala 10 Ala His Trp Gly Asp Leu Ala Arg Gly Pro Gln Gly Thr Ser Arg Val 25 Ala Phe Gly Pro Ala Pro Arg Asn Lys Gly Leu Arg Thr Ala Asn Asn 40 Ser Ala Thr Pro Met Ala Lys Glu Glu Arg Val Asp Arg Ser Glu Ile 55 Leu Thr Leu Asp Ser Ile Arg Gln Val Leu Ile Arg Leu Glu Asp Ser 70 75 Ile Ile Phe Gly Leu Leu Glu Arg Ala Gln Phe Cys Tyr Asn Ala Asp 90 Thr Tyr Asp Ser Asn Ala Phe His Met Asp Gly Phe Gly Ser Leu 105 100 Val Glu Tyr Met Val Arg Glu Thr Glu Lys Leu His Ala Gln Val Gly 125 120 115 Arg Tyr Lys Ser Pro Asp Glu 135 130 (2) INFORMATION FOR SEQ ID NO:1906: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..83 (D) OTHER INFORMATION: / Ceres Seq. ID 1599446 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906: Met Ala Lys Glu Glu Arg Val Asp Arg Ser Glu Ile Leu Thr Leu Asp 10 5 Ser Ile Arg Gln Val Leu Ile Arg Leu Glu Asp Ser Ile Ile Phe Gly 25 20 Leu Leu Glu Arg Ala Gln Phe Cys Tyr Asn Ala Asp Thr Tyr Asp Ser 40 Asn Ala Phe His Met Asp Gly Phe Gly Gly Ser Leu Val Glu Tyr Met 60 55 Val Arg Glu Thr Glu Lys Leu His Ala Gln Val Gly Arg Tyr Lys Ser 70 Pro Asp Glu (2) INFORMATION FOR SEQ ID NO:1907: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 343 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..343 (D) OTHER INFORMATION: / Ceres Seq. ID 1599450 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907: gaaaaaataa gaagagagag aaaaagaaaa aggagaggcc cgcgactgta gtgggattgt 60 gggaagatgc ctcgggatgg cgcgcaggcg gcgcgcaccg gagcgcggcg agatggacga 120 ggtggtagag gcggacccgg atacggaggc ggaggatcag gaggagaggt gggcgaggct 180 240 gctgcggagc tgctctccga cgtggtgcgg cgcgtcgagg cgtccggcgg cgagcggtgg

ceggegegga aggaegtegt etectgegee tgegtgtgee geeggtggeg ggaegeegee

gtctccgtcg tgcgtccgcc ggcggagtcc ggcaagatca cct

- (2) INFORMATION FOR SEQ ID NO:1908:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599451
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Met Pro Arg Asp Gly Ala Gln Ala Ala Arg Thr Gly Ala Arg Asp 1 10 15

Gly Glu Val Gly Glu Ala Ala Ala Glu Leu Leu Ser Asp Val Val Arg 35 40 45

Arg Val Glu Ala Ser Gly Gly Glu Arg Trp Pro Ala Arg Lys Asp Val 50 60

Val Ser Cys Ala Cys Val Cys Arg Arg Trp Arg Asp Ala Ala Val Ser 65 70 75 80

Val Val Arg Pro Pro Ala Glu Ser Gly Lys Ile Thr 85 90

- (2) INFORMATION FOR SEQ ID NO:1909:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599452
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

Met Ala Arg Arg Arg Ala Pro Glu Arg Gly Glu Met Asp Glu Val 1 5 10

Val Glu Ala Asp Pro Asp Thr Glu Ala Glu Asp Gln Glu Glu Arg Trp
20 25 30

Ala Arg Leu Leu Arg Ser Cys Ser Pro Thr Trp Cys Gly Ala Ser Arg

Arg Pro Ala Ala Ser Gly Gly Arg Arg Gly Arg Thr Ser Ser Pro Ala 50 60

Pro Ala Cys Ala Ala Gly Gly Gly Thr Pro Pro Ser Pro Ser Cys Val 65 70 75 80

Arg Arg Ser Pro Ala Arg Ser Pro 85

- (2) INFORMATION FOR SEQ ID NO:1910:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599453
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:
- Met Asp Glu Val Val Glu Ala Asp Pro Asp Thr Glu Ala Glu Asp Gln

- (2) INFORMATION FOR SEQ ID NO:1911:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..450
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911: 60 acceptgcage ggcaagggtg tecaggteec gtaaaatetg gettttetee etececatae cccgcacaca cactcgcttt cttcggttct tcctcctcga gcagccactt ccgtctctaa 120 180 ccctacagcg acgacgagag cgaggctatg aaggggaaga agccggtcaa ggagctcaag ctcaccgtgc cggcgcagga gaccccggta gacaagttcc tgacggcaag tggcacgttc 240 aaggatggtg agctgaggct caatcagagc ggcttgcggc ttatctctga ggaaaacggg 300 360 gatgaagatg aatctacaaa gctgaaggtg gaagatgtgc agttatcaat ggatgatctt gagatgattc aagtcattgg caaaggaagc ggtggtgttg tccagctagt gaggcacaaa 420 tgggtgggca cattgtttgc cttaaagggt
- (2) INFORMATION FOR SEQ ID NO:1912:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599455
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

Arg Ala Ala Ala Arg Val Ser Arg Ser Arg Lys Ile Trp Leu Phe Ser 1 10 15

Leu Pro Ile Pro Arg Thr His Thr Arg Phe Leu Arg Phe Phe Leu Leu 20 25 30

Glu Gln Pro Leu Pro Ser Leu Thr Leu Gln Arg Arg Arg Glu Arg Gly 35 40 45

Tyr Glu Gly Glu Glu Ala Gly Gln Gly Ala Gln Ala His Arg Ala Gly
50 55 60

Ala Gly Asp Pro Gly Arg Gln Val Pro Asp Gly Lys Trp His Val Gln 65 70 75 80 Gly Trp

- (2) INFORMATION FOR SEQ ID NO:1913:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599456

Gln Glu Thr Pro Val Asp Lys Phe Leu Thr Ala Ser Gly Thr Phe Lys 20 25 30

Asp Gly Glu Leu Arg Leu Asn Gln Ser Gly Leu Arg Leu Ile Ser Glu 35 40 45

Glu Asn Gly Asp Glu Asp Glu Ser Thr Lys Leu Lys Val Glu Asp Val 50 55 60

Gln Leu Ser Met Asp Asp Leu Glu Met Ile Gln Val Ile Gly Lys Gly 65 70 75 80

Ser Gly Gly Val Val Gln Leu Val Arg His Lys Trp Val Gly Thr Leu 85 90 95

Phe Ala Leu Lys Gly 100

- (2) INFORMATION FOR SEQ ID NO:1914:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599461
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914: aaacaaatcc ccccgcacgc ctccgcagcc gacgatgacc accgccgcag acgactacca 60 120 ccactccgac ggattcgtca tgcccgacgt cctcgccaag ggccgggagg cctgctacaa ggcacgggat gccttctacg cgtgcataga gaagcacgcg gacaaaaagc ccaccgagat 180 240 cgccaccatg ggtctcctct accccgccga ctgcaaaaag tcccgcgccg acttcgtcag 300 caactgccgc cccacctggg tcaagcactt cgaccggcag tactccgcca agaagcgggt gcagaggctg ctcgacggcg atggggaccg ccggggcccc atgtcgctgc cccagcccta 360 caccttcaag caataggtag tcttcctgtg gttcagatct tggtattgag ctcaattgga 420 tcagtgctac gctggtgtct agatgctata gtattggttt caggctttgt gtcatttagc 480 tggatgcata tgtgatgtgt
- (2) INFORMATION FOR SEQ ID NO:1915:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..164
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

Lys Gln Ile Pro Pro His Ala Ser Ala Ala Asp Asp Asp His Arg Arg 1 5 10 15
Arg Arg Leu Pro Pro Leu Arg Arg Ile Arg His Ala Arg Arg Pro Arg

20 25 30 30 Arg Val

Gln Gly Pro Gly Gly Leu Leu Gln Gly Thr Gly Cys Leu Leu Arg Val 35 40 45

His Arg Glu Ala Arg Gly Gln Lys Ala His Arg Asp Arg His His Gly 50 55 60

Ser Pro Leu Pro Arg Arg Leu Gln Lys Val Pro Arg Arg Leu Arg Gln 65 70 75 80

Gln Leu Pro Pro His Leu Gly Gln Ala Leu Arg Pro Ala Val Leu Arg 85 90 95 Gln Glu Ala Gly Ala Glu Ala Ala Arg Arg Arg Trp Gly Pro Pro Gly 100 100 110

Pro His Val Ala Ala Pro Ala Leu His Leu Gln Ala Ile Gly Ser Leu 115 120 125

Pro Val Val Gln Ile Leu Val Leu Ser Ser Ile Gly Ser Val Leu Arg 130 135 140

Trp Cys Leu Asp Ala Ile Val Leu Val Ser Gly Phe Val Ser Phe Ser 145 150 155 160

Trp Met His Met

- (2) INFORMATION FOR SEQ ID NO:1916:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599463
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

Asn Lys Ser Pro Arg Thr Pro Pro Gln Pro Thr Met Thr Thr Ala Ala 1 5 10 15

Asp Asp Tyr His His Ser Asp Gly Phe Val Met Pro Asp Val Leu Ala

Lys Gly Arg Glu Ala Cys Tyr Lys Ala Arg Asp Ala Phe Tyr Ala Cys 35 40 45

Ile Glu Lys His Ala Asp Lys Lys Pro Thr Glu Ile Ala Thr Met Gly 50 55 60

Leu Leu Tyr Pro Ala Asp Cys Lys Lys Ser Arg Ala Asp Phe Val Ser 65 70 75 80 Asn Cys Arg Pro Thr Trp Val Lys His Phe Asp Arg Gln Tyr Ser Ala

85 90 95
Lys Lys Arg Val Gln Arg Leu Leu Asp Gly Asp Gly Asp Arg Gly

Pro Met Ser Leu Pro Gln Pro Tyr Thr Phe Lys Gln
115

- (2) INFORMATION FOR SEQ ID NO:1917:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

Met Thr Thr Ala Ala Asp Asp Tyr His His Ser Asp Gly Phe Val Met

1 5 10 15

Pro Asp Val Leu Ala Lys Gly Arg Glu Ala Cys Tyr Lys Ala Arg Asp

Ala Phe Tyr Ala Cys Ile Glu Lys His Ala Asp Lys Lys Pro Thr Glu 35 40 45

Ile Ala Thr Met Gly Leu Leu Tyr Pro Ala Asp Cys Lys Lys Ser Arg 50 55 60
Ala Asp Phe Val Ser Asn Cys Arg Pro Thr Trp Val Lys His Phe Asp

65 70 75 80

Arg Gln Tyr Ser Ala Lys Lys Arg Val Gln Arg Leu Leu Asp Gly Asp 85 90 95

Gly Asp Arg Arg Gly Pro Met Ser Leu Pro Gln Pro Tyr Thr Phe Lys 100 105 110

- (2) INFORMATION FOR SEQ ID NO:1918:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..465
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918: 60 gcgcaagcgg aagaaagggg gagcgcaaca ttcgcggccg cggggaggga gagagacaag 120 gggggcggtc acacacacgc ggaccgcgcg agctagcgag cgagcgagat ccccctctcg cgctgctgga tccgatctga cctgacctta cctcgtcgcc gccagccgtg agagagagaa 180 gaggaagagg aggaggaggc ggagatggca ccggtgtcgg cgctcgccaa gtacaagctc 240 gtcttcctgg gggaccagtc cgtcggcaag accagcatca tcacccgctt catgtacgat 300 aagttcgaca acacttacca ggctacaatt ggtattgatt tcctgtcaaa gacaatgtac 360 cttgaagata gaactgtgag actccaactc tgggatacag ctggtcagga aaggttcagg 420 agtttaattc caagctatat cagagactct tcagttgctg tcatt
- (2) INFORMATION FOR SEQ ID NO:1919:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..47
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599475
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

Arg Lys Arg Lys Lys Gly Gly Ala Gln His Ser Arg Pro Arg Gly Gly 1 5 10 15 Arg Glu Thr Arg Gly Ala Val Thr His Thr Arg Thr Ala Arg Ala Ser

20 25 30

Glu Arg Ala Arg Ser Pro Ser Arg Ala Ala Gly Ser Asp Leu Thr
35 40 45

- (2) INFORMATION FOR SEQ ID NO:1920:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599476

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

Met Ala Pro Val Ser Ala Leu Ala Lys Tyr Lys Leu Val Phe Leu Gly

1 5 10 15

Asp Gln Ser Val Gly Lys Thr Ser Ile Ile Thr Arg Phe Met Tyr Asp

Lys Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile Asp Phe Leu Ser 40 Lys Thr Met Tyr Leu Glu Asp Arg Thr Val Arg Leu Gln Leu Trp Asp 60 55 Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro Ser Tyr Ile Arg 75 Asp Ser Ser Val Ala Val Ile 85 (2) INFORMATION FOR SEQ ID NO:1921: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..58 (D) OTHER INFORMATION: / Ceres Seq. ID 1599477 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921: Met Tyr Asp Lys Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile Asp 5 Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Arg Thr Val Arg Leu Gln 30 25 20 Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro Ser 40 Tyr Ile Arg Asp Ser Ser Val Ala Val Ile 5.5 (2) INFORMATION FOR SEQ ID NO:1922: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 498 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..498 (D) OTHER INFORMATION: / Ceres Seq. ID 1599487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922: 60 aataaatccc ccgcctccct gctctcctcc gtaaatcaca aaacttygcc caattcccca ctagcaaccg tccccacaat cctccgacga tgcctgccgc gccgacgctg ttgcccccct 120 gcgacgcgga ggagccgctg ctggcggagt cctccgaccg cttctccatg ttcccgatcc 180 240 gtttcccgca gatctgggag ttctacaaga aggcggtggc ctccttctgg acggcggagg aggttggcct ctctgccgac gcccggcact gggacgaggc tctgtccccc gacgagcgc 300 360 actttatctc ccacgtgctc gccttcttcg ctgcctccga cggcatcgtg ctcgagaacc 420 tegetteceg etteatgace gaegtgeagg tegeegagge gegggeette taeggettee 480 agategecat egagaacate cacteggaga tgtatteget getgetegag aettacatee gcgaccacgt cgagaagg (2) INFORMATION FOR SEQ ID NO:1923: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide

(B) LOCATION: 1..125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

(D) OTHER INFORMATION: / Ceres Seq. ID 1599488

```
Asn Lys Ser Pro Ala Ser Leu Leu Ser Ser Val Asn His Lys Thr Xaa
                                10
Pro Asn Ser Pro Leu Ala Thr Val Pro Thr Ile Leu Arg Arg Cys Leu
                             25
          20
Pro Arg Arg Cys Cys Pro Pro Ala Thr Arg Arg Ser Arg Cys Trp
                         40
Arg Ser Pro Pro Thr Ala Ser Pro Cys Ser Arg Ser Val Ser Arg Arg
                     55
                                        60
Ser Gly Ser Ser Thr Arg Arg Arg Trp Pro Pro Ser Gly Arg Arg Arg
                                    75
                  70
Arg Leu Ala Ser Leu Pro Thr Pro Gly Thr Gly Thr Arg Leu Cys Pro
                                 90
            85
Pro Thr Ser Gly Thr Leu Ser Pro Thr Cys Ser Pro Ser Ser Leu Pro
           100 105
Pro Thr Ala Ser Cys Ser Arg Thr Ser Leu Pro Ala Ser
                120
       115
```

- (2) INFORMATION FOR SEQ ID NO:1924:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924: Met Pro Ala Ala Pro Thr Leu Leu Pro Pro Cys Asp Ala Glu Glu Pro 10 5 Leu Leu Ala Glu Ser Ser Asp Arg Phe Ser Met Phe Pro Ile Arg Phe 25 2.0 Pro Gln Ile Trp Glu Phe Tyr Lys Lys Ala Val Ala Ser Phe Trp Thr 45 4.0 Ala Glu Glu Val Gly Leu Ser Ala Asp Ala Arg His Trp Asp Glu Ala 55 60 Leu Ser Pro Asp Glu Arg His Phe Ile Ser His Val Leu Ala Phe Phe 75 70 Ala Ala Ser Asp Gly Ile Val Leu Glu Asn Leu Ala Ser Arg Phe Met 85 90 Thr Asp Val Gln Val Ala Glu Ala Arg Ala Phe Tyr Gly Phe Gln Ile 100 105 11.0 Ala Ile Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Leu Glu Thr 120 125
- Tyr Ile Arg Asp His Val Glu Lys 130 135
- (2) INFORMATION FOR SEQ ID NO:1925:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..110
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599490
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:
- Met Phe Pro Ile Arg Phe Pro Gln Ile Trp Glu Phe Tyr Lys Lys Ala 1 5 10 15 Val Ala Ser Phe Trp Thr Ala Glu Glu Val Gly Leu Ser Ala Asp Ala

120 180

240

300

360

420

480

540

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
                                25
            20
Arg His Trp Asp Glu Ala Leu Ser Pro Asp Glu Arg His Phe Ile Ser
                           40
His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Leu Glu Asn
                        55
Leu Ala Ser Arg Phe Met Thr Asp Val Gln Val Ala Glu Ala Arg Ala
                                        75
                    70
Phe Tyr Gly Phe Gln Ile Ala Ile Glu Asn Ile His Ser Glu Met Tyr
                                    90
                85
Ser Leu Leu Glu Thr Tyr Ile Arg Asp His Val Glu Lys
                                105
            100
(2) INFORMATION FOR SEQ ID NO:1926:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 542 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..542
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599491
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:
gcccacgctg cataaacaac tctatctcaa cggcgacgac gctcccatct taacagccag
gaagetggeg tettgettgt cettgttett tteccaceeg getaeeceeg tegtegeege
cgctttcccc gtggtttcag agctcaagtc ggctagctag gccgcctggc taatctccct
gccttctata agtacagaga tcagggaagc ggcactccat ccactgactg accgctcatg
gegaaggtee acctetacgt egeegeggee tgegeegteg teetegeget egeeacceeg
gccctcgccg gtgaccccga catgctgcag gacgtctgcc cggctgacta cgcctccccg
gtgaagctga acgggttcgc gtgcaaggcg aacttttcgg cggacgactt cttcttcgac
gggctgagga acccgggcaa caccaacaac ccggcgggct ccgtggtgac ggcggccaac
gtggagaagt teetggggeg tgaacaeget gggegtetee atggeegege ategaetaeg
(2) INFORMATION FOR SEQ ID NO:1927:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 52 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
```

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..52
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599492
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

Pro Thr Leu His Lys Gln Leu Tyr Leu Asn Gly Asp Asp Ala Pro Ile
1 5 10 15

Leu Thr Ala Arg Lys Leu Ala Ser Cys Leu Ser Leu Phe Phe Ser His 20 25 30

Pro Ala Thr Pro Val Val Ala Ala Ala Phe Pro Val Val Ser Glu Leu 35 40 45

Lys Ser Ala Ser

- (2) INFORMATION FOR SEQ ID NO:1928:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

Met Ala Lys Val His Leu Tyr Val Ala Ala Cys Ala Val Val Leu 5 10

Ala Leu Ala Thr Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp 30 25 20

Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala 40 45

Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Asp Gly Leu Arg 55 60 50

Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val Val Thr Ala Ala 75 70

Asn Val Glu Lys Phe Leu Gly Arg Glu His Ala Gly Arg Leu His Gly 90 85

Arg Ala Ser Thr Thr

100

- (2) INFORMATION FOR SEQ ID NO:1929:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..73
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu 10 5

Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe 25

Asp Gly Leu Arg Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val 4.5 4.0

Val Thr Ala Ala Asn Val Glu Lys Phe Leu Gly Arg Glu His Ala Gly 60 55

Arg Leu His Gly Arg Ala Ser Thr Thr 7.0

- (2) INFORMATION FOR SEQ ID NO:1930:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..512
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

60 tecagetece caaateacae teegecatgg ceggeacgtg egeteacgte gagtteetee 120 gegegeagee ggegtgggeg etggegetgg cegeggtggg cetgetegtg geegtgegeg 180 cegecgeceg ettegegete tgggtetaeg cegegtteet cegeceggge aageecetge 240 geogeogeta eggegeetgg geogtegtga egggegeeae egaeggeate ggeogegeeg 300 tegectteeg ectegeegeg teegggeteg ggetegteet egteggeege aaccaggaga 360 agetggeege egtegeegee gagateaagg ceaggeacee caaggteeee gaggtgegga 420 ctttcgtgct cgacttcgcc ggcgaggggc tggccgccgc cgtcgaggcg ctcaaggact 480 ccatccgggg cctcgacgtc ggcgtgctcg tc

- Attorney Docket No. 2750-1237P Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:1931: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..170 (D) OTHER INFORMATION: / Ceres Seq. ID 1599496 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931: Gln His Arg Thr Ala Leu His Arg Ser Pro Ala Glu Pro Ser Arg Ala 5 10 Leu Leu Ser Pro Pro Ala Pro Gln Ile Thr Leu Arg His Gly Arg His 20 25 Val Arg Ser Arg Arg Val Pro Pro Arg Ala Ala Gly Val Gly Ala Gly 40 Ala Gly Arg Gly Gly Pro Ala Arg Gly Arg Ala Arg Arg Arg Pro Leu 60 55 Arg Ala Leu Gly Leu Arg Arg Val Pro Pro Pro Gly Gln Ala Pro Ala 70 75 Pro Pro Leu Arg Arg Leu Gly Arg Arg Asp Gly Arg His Arg Arg His 8.5 90 Arg Pro Arg Arg Arg Leu Pro Pro Arg Arg Val Arg Ala Arg Ala Arg 100 105 Pro Arg Arg Pro Gln Pro Gly Glu Ala Gly Arg Arg Arg Arg Asp 120 125 Gin Gly Gln Ala Pro Gln Gly Pro Arg Gly Ala Asp Phe Arg Ala Arg 135 140 Leu Arg Arg Arg Gly Ala Gly Arg Arg Arg Gly Ala Gln Gly Leu 150 155 His Pro Gly Pro Arg Arg Arg Arg Ala Arg 165 (2) INFORMATION FOR SEQ ID NO:1932: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..170 (D) OTHER INFORMATION: / Ceres Seq. ID 1599497 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932: Ser Thr Ala Pro His Cys Ile Gly Arg Gln Pro Ser Arg Ala Glu Pro 10 Cys Ser Leu Leu Gln Leu Pro Lys Ser His Ser Ala Met Ala Gly Thr

125 120 115 Lys Ala Arg His Pro Lys Val Pro Glu Val Arg Thr Phe Val Leu Asp 140 135 Phe Ala Gly Glu Gly Leu Ala Ala Ala Val Glu Ala Leu Lys Asp Ser 150 155 Ile Arg Gly Leu Asp Val Gly Val Leu Val 165 (2) INFORMATION FOR SEQ ID NO:1933: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..142 (D) OTHER INFORMATION: / Ceres Seq. ID 1599498 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933: Met Ala Gly Thr Cys Ala His Val Glu Phe Leu Arg Ala Gln Pro Ala 10 5 Trp Ala Leu Ala Leu Ala Ala Val Gly Leu Leu Val Ala Val Arg Ala 25 30 20 Ala Ala Arg Phe Ala Leu Trp Val Tyr Ala Ala Phe Leu Arg Pro Gly 40 Lys Pro Leu Arg Arg Arg Tyr Gly Ala Trp Ala Val Val Thr Gly Ala 60 55 Thr Asp Gly Ile Gly Arg Ala Val Ala Phe Arg Leu Ala Ala Ser Gly 75 70 Leu Gly Leu Val Leu Val Gly Arg Asn Gln Glu Lys Leu Ala Ala Val 90 85 Ala Ala Glu Ile Lys Ala Arg His Pro Lys Val Pro Glu Val Arg Thr 105 Phe Val Leu Asp Phe Ala Gly Glu Gly Leu Ala Ala Ala Val Glu Ala 120 125 Leu Lys Asp Ser Ile Arg Gly Leu Asp Val Gly Val Leu Val 130 135 (2) INFORMATION FOR SEQ ID NO:1934: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..514 (D) OTHER INFORMATION: / Ceres Seq. ID 1599507 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934: ctggagaact tgactgtctg ccctgtctgc aggcactcgt cttcttccwg gagagaaaaa gcagaagaca atacaaagat gtccaagatg gcggaggaga aggcggcggc agtgggcgga 120 ctcggaggag ccgggggggc ggacgcggcg cagcagcagc cgcaccccca agacttccgt 180 ccgagtctga gctcatctcc gcgcgctgcc gccgccgccg ccgccgctcg acgcccaccg 240 cgcagccatg gcggaacaga ccgagaaggc ttttctcaag cagcctaagg tgttcctcag ctcaaagaaa tctggcaagg gtaagaagcc aggcaagggt ggcaatcgat tttggaagag 360 420 cattggcctt ggtttcaaga ctcccaggga agcaattgaa gggacctaca ttgacaagaa atgtccattc actggaaccg tttctatcag aggcagaatt attgctggaa catgccacag tgctaaaatg aacagaacca tcattgttcg cagg (2) INFORMATION FOR SEQ ID NO:1935: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599508
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:
- Leu Glu Asn Leu Thr Val Cys Pro Val Cys Arg His Ser Ser Ser Ser 5 10
- Xaa Arg Glu Lys Ala Glu Asp Asn Thr Lys Met Ser Lys Met Ala Glu 20 25
- Glu Lys Ala Ala Ala Val Gly Gly Leu Gly Gly Ala Gly Ala Ala Asp 40
- Ala Ala Gln Gln Gln Pro His Pro Gln Asp Phe Arg Pro Ser Leu Ser 55
- Ser Ser Pro Arg Ala Ala Ala Ala Ala Ala Ala Arg Arg Pro Pro 75 70
- Arg Ser His Gly Gly Thr Asp Arg Glu Gly Phe Ser Gln Ala Ala 90 85
- (2) INFORMATION FOR SEQ ID NO:1936:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599509
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:
- Gly Glu Leu Asp Cys Leu Pro Cys Leu Gln Ala Leu Val Phe Phe Xaa 10
- Glu Arg Lys Ser Arg Arg Gln Tyr Lys Asp Val Gln Asp Gly Gly 25
- Glu Gly Gly Gly Ser Gly Arg Thr Arg Arg Ser Arg Gly Gly Gly Arg 4.0
- Gly Ala Ala Ala Ala Pro Pro Arg Leu Pro Ser Glu Ser Glu Leu 60 55
- Ile Ser Ala Arg Cys Arg Arg Arg Arg Arg Ser Thr Pro Thr Ala 75 70
- Gln Pro Trp Arg Asn Arg Pro Arg Arg Leu Phe Ser Ser Leu Arg 90
- Cys Ser Ser Ala Gln Arg Asn Leu Ala Arg Val Arg Ser Gln Ala Arg 100 105 110
- Val Ala Ile Asp Phe Gly Arg Ala Leu Ala Leu Val Ser Arg Leu Pro 120 125 Gly Lys Gln Leu Lys Gly Pro Thr Leu Thr Arg Asn Val His Ser Leu
- 140 135 Glu Pro Phe Leu Ser Glu Ala Glu Leu Leu Leu Glu His Ala Thr Val 155
- Leu Lys

- (2) INFORMATION FOR SEQ ID NO:1937:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..89 (D) OTHER INFORMATION: / Ceres Seq. ID 1599510 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937: Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe 10 Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Pro Gly Lys Gly Gly 30 25 20 Asn Arg Phe Trp Lys Ser Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu 45 40 Ala Ile Glu Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe Thr Gly Thr 60 55 Val Ser Ile Arg Gly Arg Ile Ile Ala Gly Thr Cys His Ser Ala Lys 75 70 Met Asn Arg Thr Ile Ile Val Arg Arg 85 (2) INFORMATION FOR SEQ ID NO:1938: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..401 (D) OTHER INFORMATION: / Ceres Seq. ID 1599520 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938: caaggatcag gactctgtgt ctaaagccct tgagctcagt ggctctgaca ttggtggtgg 60 ctatgagctt tatgttgatg aagccaaacc aagaggcgat ggccagcgtg gtggtggtag 120 atctggtggc cgttctggtg ggagatttgg tgaccgttct ggtggccggc gtggtggtgg 180 tagatttggt gaaagatctg ggggcaggga tggtggcggc agattcggtg gccgacgtgg 240 300 tggtagggat ggcggccgag gacgtggtgg ccgtggcttt ggtaacaagc acagcgctgg cactcccagt gcaggaaaga agactacttt tggtgatgat tgatgatgaa cgcggaggat 360 qcqgcaaaag gatccaatga aattgtgttt ttttggtctt g (2) INFORMATION FOR SEQ ID NO:1939: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..113 (D) OTHER INFORMATION: / Ceres Seq. ID 1599521 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939: Lys Asp Gln Asp Ser Val Ser Lys Ala Leu Glu Leu Ser Gly Ser Asp 10 Ile Gly Gly Gly Tyr Glu Leu Tyr Val Asp Glu Ala Lys Pro Arg Gly 25 20 Asp Gly Gln Arg Gly Gly Gly Arg Ser Gly Gly Arg Ser Gly Gly Arg Phe Gly Asp Arg Ser Gly Gly Arg Arg Gly Gly Gly Arg Phe Gly Glu 55 Arg Ser Gly Gly Arg Asp Gly Gly Gly Arg Phe Gly Gly Arg Arg Gly

75

90

Gly Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Phe Gly Asn Lys

His Ser Ala Gly Thr Pro Ser Ala Gly Lys Lys Thr Thr Phe Gly Asp 105 100

Asp

- (2) INFORMATION FOR SEQ ID NO:1940:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599522
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

Arg Ile Arg Thr Leu Cys Leu Lys Pro Leu Ser Ser Val Ala Leu Thr 10 5

Leu Val Val Ala Met Ser Phe Met Leu Met Lys Pro Asn Gln Glu Ala 30 25 2.0

Met Ala Ser Val Val Val Asp Leu Val Ala Val Leu Val Gly Asp 40

Leu Val Thr Val Leu Val Ala Gly Val Val Val Asp Leu Val Lys 55

Asp Leu Gly Ala Gly Met Val Ala Ala Asp Ser Val Ala Asp Val Val 75 70

Val Gly Met Ala Ala Glu Asp Val Val Ala Val Ala Leu Val Thr Ser 90 85

Thr Ala Leu Ala Leu Pro Val Gln Glu Arg Arg Leu Leu Val Met 105 100

- Ile Asp Asp Glu Arg Gly Gly Cys Gly Lys Arg Ile Gln 120 115
- (2) INFORMATION FOR SEQ ID NO:1941:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599523
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

Met Ser Phe Met Leu Met Lys Pro Asn Gln Glu Ala Met Ala Ser Val 5 10

Val Val Val Asp Leu Val Ala Val Leu Val Gly Asp Leu Val Thr Val 25

Leu Val Ala Gly Val Val Val Val Asp Leu Val Lys Asp Leu Gly Ala 45 40

Gly Met Val Ala Ala Asp Ser Val Ala Asp Val Val Gly Met Ala

Ala Glu Asp Val Val Ala Val Ala Leu Val Thr Ser Thr Ala Leu Ala 75 70

Leu Pro Val Gln Glu Arg Arg Leu Leu Leu Val Met Ile Asp Asp Glu 90

Arg Gly Gly Cys Gly Lys Arg Ile Gln 100

- (2) INFORMATION FOR SEQ ID NO:1942:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..459
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599524
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942: 60 acagettgeg tggtetgtgg teteatetea eteacaetet etetetet eggegaegte 120 tacgccgagt gcccaggcat tettcaggcg caggtcgctg gctcgctgcc gccctacacc aggtgccccg gtcttcttcc gtcccttcgc cggcgacgag cactgccagc gtgatccttt 180 240 ccgacaggac agtatagcgg atggcttcgt cggtgcgggc gccatcgggg tcggtgatcg 300 ccgtggcatc gtcctcttcc tcagcagccg cggccggggt gtgcggcacg ggctcgccgt gegeegegtg caagtteetg egtegeaagt geeageegga etgegtgtte gegeeetaet 360 420 teccacegga caaceegcag aagttegtge gegtgeaegg egtettegge gegageaaeg tgaccaagct gatgaacgaa atccacccgt tgcagcgcg
- (2) INFORMATION FOR SEQ ID NO:1943:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:
- Gln Leu Ala Trp Ser Val Val Ser Ser His Ser His Ser Leu Ser Leu 1 5 5 10 15 Ser Ala Thr Ser Thr Pro Ser Ala Gln Ala Phe Phe Arg Arg Arg Ser

Leu Ala Arg Cys Arg Pro Thr Pro Gly Ala Pro Val Phe Arg Pro 35 40 45

Phe Ala Gly Asp Glu His Cys Gln Arg Asp Pro Phe Arg Gln Asp Ser
50 55 60

Ile Ala Asp Gly Phe Val Gly Ala Gly Ala Ile Gly Val Gly Asp Arg 65 70 75 80

Arg Gly Ile Val Leu Phe Leu Ser Ser Arg Gly Arg Gly Val Arg His 85 90 95

Gly Leu Ala Val Arg Arg Val Gln Val Pro Ala Ser Gln Val Pro Ala 100 105 110

Gly Leu Arg Val Arg Ala Leu Leu Pro Thr Gly Gln Pro Ala Glu Val 115 120 125

Arg Ala Arg Ala Arg Arg Leu Arg Arg Glu Gln Arg Asp Gln Ala Asp 130 135 140

- Glu Arg Asn Pro Pro Val Ala Ala
 - 150
- (2) INFORMATION FOR SEQ ID NO:1944:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599526
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

 Met
 Ala
 Ser
 Ser
 Val
 Arg
 Ala
 Pro
 Ser
 Gly
 Ser
 Val
 Ile
 Ala
 Val
 Ala

 Ser
 Ser
 Ser
 Ser
 Ala
 Ala
 Ala
 Ala
 Gly
 Val
 Cys
 Gly
 Thr
 Gly
 Ser

 Pro
 Cys
 Ala
 Ala
 Cys
 Lys
 Phe
 Leu
 Arg
 Arg
 Lys
 Cys
 Gln
 Pro
 Asp
 Cys

 Val
 Phe
 Ala
 Pro
 Pro
 Pro
 Asp
 Asp
 Asp
 Phe
 Inc
 Inc
 Inc
 Inc
 Apr
 Apr
 Inc
 Inc

- (2) INFORMATION FOR SEQ ID NO:1945:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..452
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945: 60 acgcacgccc agacagacga gaccagatcg gggaccctcg cggcgcccag ttcccgagcg 120 aacccaaccc actacccaca kyccagaagc aaaagcccct cgccttttcc gcgccttggt 180 tetecteceg tecateegeg gegagaaega eegaegaeka eaggeegaga tgtgetgetg 240 cccgagcaag gcgtgctgca tctgcacgct catcgtgctg gtgctggtgg ccgtcggcct 300 cgtcttcggc ttcggcgtct acacccgcgg cttccacaag ctcaccagca acatgcacct gcaggacgat gcatacggcc gcggtggcgc cggcggctcc ttccgcgcct acggccactt 360 tgccccgccg ccgtactaga aggaccgccg ccccttctcc gagatctagg gcctggatgc 420 tgggcgattc gagccccgct ccgctctcgg tg
- (2) INFORMATION FOR SEQ ID NO:1946:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..150
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599531
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

Thr His Ala Gln Thr Asp Glu Thr Arg Ser Gly Thr Leu Ala Ala Pro 1 5 5 10 10 15 Ser Ser Arg Ala Asn Pro Thr His Tyr Pro Xaa Xaa Arg Ser Lys Ser

20 25 30
Pro Ser Pro Phe Pro Arg Leu Gly Ser Pro Pro Val His Pro Arg Arg
35 40 45

Glu Arg Pro Thr Xaa Thr Gly Arg Asp Val Leu Leu Pro Glu Gln Gly
50 55 60

Val Leu His Leu His Ala His Arg Ala Gly Ala Gly Gly Arg Arg Pro
65 70 75 80

Arg Leu Arg Leu Arg Arg Leu His Pro Arg Leu Pro Gln Ala His Gln
85 90 95

Gln His Ala Pro Ala Gly Arg Cys Ile Arg Pro Arg Trp Arg Arg 100 105 110

Leu Leu Pro Arg Leu Arg Pro Leu Cys Pro Ala Ala Val Leu Glu Gly 115 120 125

Pro Pro Pro Leu Leu Arg Asp Leu Gly Pro Gly Cys Trp Ala Ile Arg

135 140 130 Ala Pro Leu Arg Ser Arg 145 150 (2) INFORMATION FOR SEQ ID NO:1947: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..125 (D) OTHER INFORMATION: / Ceres Seq. ID 1599532 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947: Arg Thr Pro Arg Gln Thr Arg Pro Asp Arg Gly Pro Ser Arg Arg Pro 10 Val Pro Glu Arg Thr Gln Pro Thr Thr His Xaa Pro Glu Ala Lys Ala 25 20 Pro Arg Leu Phe Arg Ala Leu Val Leu Leu Pro Ser Ile Arg Gly Glu 40 Asn Asp Arg Arg Xaa Gln Ala Glu Met Cys Cys Cys Pro Ser Lys Ala 55 Cys Cys Ile Cys Thr Leu Ile Val Leu Val Leu Val Ala Val Gly Leu 7.5 70 Val Phe Gly Phe Gly Val Tyr Thr Arg Gly Phe His Lys Leu Thr Ser Asn Met His Leu Gln Asp Asp Ala Tyr Gly Arg Gly Gly Ala Gly Gly 105 Ser Phe Arg Ala Tyr Gly His Phe Ala Pro Pro Pro Tyr 120 115 (2) INFORMATION FOR SEQ ID NO:1948: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..150 (D) OTHER INFORMATION: / Ceres Seq. ID 1599533 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948: Ala Arg Pro Asp Arg Arg Asp Gln Ile Gly Asp Pro Arg Gly Ala Gln 5 10 Phe Pro Ser Glu Pro Asn Pro Leu Pro Thr Xaa Gln Lys Gln Lys Pro 25 Leu Ala Phe Ser Ala Pro Trp Phe Ser Ser Arg Pro Ser Ala Ala Arg 40 Thr Thr Asp Asp Xaa Arg Pro Arg Cys Ala Ala Ala Arg Ala Arg Arg 5.5 Ala Ala Ser Ala Arg Ser Ser Cys Trp Cys Trp Trp Pro Ser Ala Ser 75 70 Ser Ser Ala Ser Ala Ser Thr Pro Ala Ala Ser Thr Ser Ser Pro Ala 90 85 Thr Cys Thr Cys Arg Thr Met His Thr Ala Ala Val Ala Pro Ala Ala 105 Pro Ser Ala Pro Thr Ala Thr Leu Pro Arg Arg Thr Arg Arg Thr 115 120 125 Ala Ala Pro Ser Pro Arg Ser Arg Ala Trp Met Leu Gly Asp Ser Ser

Pro Ala Pro Leu Ser Val 145 150

- (2) INFORMATION FOR SEQ ID NO:1949:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..480
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949: aaaagccgaa ccactgctcc gcccactcca tcccggctcc gtcgtcgcgt gccatcctag 60 ggtttctttc cccgtcggcg cctccccaga tttggccgcc gccgcgctga cccaggttgt 120 cttgatggcg cccgctgtag aagccgtgaa ggagacaggc accttccaga aggttcctgc 180 cttgaacgaa aggatactgt catccatgtc caggaggtct gttgctgcac acccttggca 240 tgatctggag ataggtcctg gtgctccaac catattcaac tgcgtcattg agataccaag 300 gggcagcaag gttaaatatg aacttgacaa gaaaactgga ctgatcaagg tggaccgtgt 360 gctgtattca tcagttgttt accctcacaa ctatggattc attcctcgca cgctttgtga 420 agacagtgat cctttggatg tactggttat aatgcaggag cctgttatcc caggctgttt 480
- (2) INFORMATION FOR SEQ ID NO:1950:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599545
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950: Lys Ala Glu Pro Leu Leu Arg Pro Leu His Pro Gly Ser Val Val Ala

1 5 10 15

Cys His Pro Arg Val Ser Phe Pro Val Gly Ala Ser Pro Asp Leu Ala
20 25 30

Ala Ala Leu Thr Gln Val Val Leu Met Ala Pro Ala Val Glu Ala

Val Lys Glu Thr Gly Thr Phe Gln Lys Val Pro Ala Leu Asn Glu Arg

Ile Leu Ser Ser Met Ser Arg Arg Ser Val Ala Ala His Pro Trp His 65 70 75 80

Asp Leu Glu Ile Gly Pro Gly Ala Pro Thr Ile Phe Asn Cys Val Ile 85 90 95

Glu Ile Pro Arg Gly Ser Lys Val Lys Tyr Glu Leu Asp Lys Lys Thr
100 105 110

His Asn Tyr Gly Phe Ile Pro Arg Thr Leu Cys Glu Asp Ser Asp Pro
130
140
Leu Asp Val Leu Val Ile Met Glu Pro Val Ile Pro Gly Cys

Leu Asp Val Leu Val Ile Met Gln Glu Pro Val Ile Pro Gly Cys 145 150 155

- (2) INFORMATION FOR SEQ ID NO:1951:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599546
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:

Met Ala Pro Ala Val Glu Ala Val Lys Glu Thr Gly Thr Phe Gln Lys
1 5 10 15

Val Pro Ala Leu Asn Glu Arg Ile Leu Ser Ser Met Ser Arg Arg Ser 20 25 30

Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Gly Ala Pro
35 40 45

Thr Ile Phe Asn Cys Val Ile Glu Ile Pro Arg Gly Ser Lys Val Lys 50 55

Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys Val Asp Arg Val Leu 65 70 75 80

Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly Phe Ile Pro Arg Thr 85 90 95

Leu Cys Glu Asp Ser Asp Pro Leu Asp Val Leu Val Ile Met Gln Glu
100 105 110

Pro Val Ile Pro Gly Cys

115

- (2) INFORMATION FOR SEQ ID NO:1952:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599547
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

Met Ser Arg Arg Ser Val Ala Ala His Pro Trp His Asp Leu Glu Ile 1 5 5 10 10 15 Gly Pro Gly Ala Pro Thr Ile Phe Asn Cys Val Ile Glu Ile Pro Arg

20 25 30 Gly Ser Lys Val Lys Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys

35
40
45
45
40
45
40
45
40
45

Val Asp Arg Val Leu Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly 50 55 60

Phe Ile Pro Arg Thr Leu Cys Glu Asp Ser Asp Pro Leu Asp Val Leu 65 70 75 80

Val Ile Met Gln Glu Pro Val Ile Pro Gly Cys 85 90

- (2) INFORMATION FOR SEQ ID NO:1953:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..512
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599548
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:

gcagaagaag ccggcggcga agaaggtggc ggaggaggag ccctcggaga aggcggctcc ggcggagaag gccccgcgg ggaagaaggc caaggcggag aagcggctac ctgcgggcaa gtccgccggc aaggagggcg gcgacaagaa ggggaggaag aaggcgaaga agagcgtgga

60

120

gacctacaag atctacatct tcaaggtcct gaagcaggtg caccccgaca tcggcatctc 240 ctccaaggcc atgtccatca tgaactcctt catcaacgac atcttcgaga agctcgccg gagggccgcc aagctcgccc ggtacaacaa gaagcccacc atcacctccc gcgaggtcca 360 gacctccgtc cgcctcgtcc tccccggcga gctcgccaag cacgccgtct cggagggtac 420 gagggcgtc accaagttca cctcgtctta gccgccttgt agtagtggt gttggctggt 480 gtgtgtaagt ggtgcagtgg cttttgcctg tg

- (2) INFORMATION FOR SEQ ID NO:1954:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

20 25 30
Gly Glu Ala Ala Thr Cys Gly Gln Val Arg Arg Gln Gly Gly Arg Arg

35 40 45
Glu Glu Glu Glu Glu Glu Glu Glu Glu Arg Gly Asp Leu Gln Asp

50 55 60
Leu His Leu Gln Gly Pro Glu Ala Gly Ala Pro Arg His Arg His Leu

65 70 75 80

Leu Gln Gly His Val His His Glu Leu Leu His Gln Arg His Leu Arg
85 90 95

65 90 95
Glu Ala Arg Arg Gly Gly Arg Gln Ala Arg Pro Val Gln Gln Glu Ala
100 105 110

His His Leu Pro Arg Asp Pro Asp Leu Arg Pro Pro Arg Pro Pro 115 120 125

Arg Arg Ala Arg Gln Ala Arg Arg Leu Gly Gly Tyr Gln Gly Arg His 130 135 140

Gln Val His Leu Val Leu Ala Ala Leu 145 150

- (2) INFORMATION FOR SEQ ID NO:1955:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..149
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Gln Lys Lys Pro Ala Ala Lys Lys Val Ala Glu Glu Glu Pro Ser Glu 1 5 15

Lys Ala Ala Pro Ala Glu Lys Ala Pro Ala Gly Lys Lys Ala Lys Ala 20 25 30

Glu Lys Arg Leu Pro Ala Gly Lys Ser Ala Gly Lys Glu Gly Gly Asp 35 40 45

Lys Lys Gly Arg Lys Lys Ala Lys Lys Ser Val Glu Thr Tyr Lys Ile 50 55 60

Tyr Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser 65 70 75 80
Ser Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu

180

240

300

360

420

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 85 90 Lys Leu Ala Ala Glu Ala Ala Lys Leu Ala Arg Tyr Asn Lys Lys Pro 110 105 100 Thr Ile Thr Ser Arg Glu Ile Gln Thr Ser Val Arg Leu Val Leu Pro 120 125 115 Gly Glu Leu Ala Lys His Ala Val Ser Glu Gly Thr Lys Ala Val Thr 140 135 130 Lys Phe Thr Ser Ser 145 (2) INFORMATION FOR SEQ ID NO:1956: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..436 (D) OTHER INFORMATION: / Ceres Seq. ID 1599551 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956: ctcccgaagg ttctaggctc gattgaacaa attggagcgg cactacactc ctccacgcct ccacctccag cctcccactg atctggcctc tctcgagtta atcctagatc aatatgagaa ggggctacag ttacagtcct tcaccaccaa ggggctacag gagaagggcg cgcagtccaa gtcctcatga tcattatggt ggtcgtggta gggatctccc aaccagtctt ctggtcagga atctccgtcg ggactgcagg ccagaagacc tccgtcgccc atttggacag tttggtcgag ttaaagatat atatcttcca agagattatt acactgggga tccccgaggg tttgggtttg tccagtatta tgatcctgct gatgctgctg atgcgaagta ctatatggat gggcaggtag ttcttggtag gcaaat (2) INFORMATION FOR SEQ ID NO:1957: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1599552 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957: Met Arg Arg Gly Tyr Ser Tyr Ser Pro Ser Pro Pro Arg Gly Tyr Arg 10 Arg Arg Ala Arg Ser Pro Ser Pro His Asp His Tyr Gly Gly Arg Gly 30 25 Arg Asp Leu Pro Thr Ser Leu Leu Val Arg Asn Leu Arg Arg Asp Cys 40 4.5 Arg Pro Glu Asp Leu Arg Arg Pro Phe Gly Gln Phe Gly Arg Val Lys 55 60

Asp Ile Tyr Leu Pro Arg Asp Tyr Tyr Thr Gly Asp Pro Arg Gly Phe

Gly Phe Val Gln Tyr Tyr Asp Pro Ala Asp Ala Asp Ala Lys Tyr

75

90

Tyr Met Asp Gly Gln Val Val Leu Gly Arg Gln 105 100 (2) INFORMATION FOR SEQ ID NO:1958:

70

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..77 (D) OTHER INFORMATION: / Ceres Seq. ID 1599553 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958: Met Ile Ile Met Val Val Val Gly Ile Ser Gln Pro Val Phe Trp 10 Ser Gly Ile Ser Val Gly Thr Ala Gly Gln Lys Thr Ser Val Ala His 25 Leu Asp Ser Leu Val Glu Leu Lys Ile Tyr Ile Phe Gln Glu Ile Ile 45 35 40 Thr Leu Gly Ile Pro Glu Gly Leu Gly Leu Ser Ser Ile Met Ile Leu 60 55 Leu Met Leu Leu Met Arg Ser Thr Ile Trp Met Gly Arg 70 (2) INFORMATION FOR SEQ ID NO:1959: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..74 (D) OTHER INFORMATION: / Ceres Seq. ID 1599554 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959: Met Val Val Val Gly Ile Ser Gln Pro Val Phe Trp Ser Gly Ile 10 Ser Val Gly Thr Ala Gly Gln Lys Thr Ser Val Ala His Leu Asp Ser 30 25 2.0 Leu Val Glu Leu Lys Ile Tyr Ile Phe Gln Glu Ile Ile Thr Leu Gly 45 40 Ile Pro Glu Gly Leu Gly Leu Ser Ser Ile Met Ile Leu Leu Met Leu 55 60 Leu Met Arg Ser Thr Ile Trp Met Gly Arg 70 (2) INFORMATION FOR SEQ ID NO:1960: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 455 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..455 (D) OTHER INFORMATION: / Ceres Seq. ID 1599555 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960: gttatccggt tcaaagccga gcggcgtctc ctctctccag cggctccagc caatccggca atcccgctcc cccagctcgc tgctcgcccg ctctcctccg ccctccgcca tggcggcctt ceceteegee teecegtege eggegatete egectegace tggageatgg etteecteeg
 - gttatceggt tcaaagccga geggegtete eteteteeag eggeteeage caatceggea 60 atceegete eccagetege tgetegeeg eteteeteeg eceteegeea tggeggeett 120 ecceteegee teecegtege eggegatete eggeggeage tggageatgg etteeeteeg 180 taegteeete eccegeactee egegggeagg etgeteggg etgetegge etgeteggg etgetegge etgeteggg etgeteggge geeteggee etgeteggg etgeteggg teeteteeggg etgeteggee 300 egtetegaat eteeteteee teggegetga gaactcaage tttgageate ggttgtytgg 360 tattgatgee eggateagg atagteggat eggateagg agaeggett ectaaaytta 420 acaggeetee eggateagg atageactge tgegt
 - (2) INFORMATION FOR SEQ ID NO:1961:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:
- Val Ile Arg Phe Lys Ala Glu Arg Arg Leu Leu Ser Pro Ala Ala Pro 1 5 10 15
- Ala As
n Pro Ala Ile Pro Leu Pro Gl
n Leu Ala Ala Arg Pro Leu Ser 20 25 30
- Ser Ala Leu Arg His Gly Gly Leu Pro Leu Arg Leu Pro Val Ala Gly 35 40 45
- Asp Leu Arg Leu Asp Leu Glu His Gly Phe Pro Pro Tyr Val Pro Pro 50 55 60
- Arg Thr Pro Pro Leu Pro Arg Gly Gln Ala Pro Phe Val Val Leu Ala 65 70 75 80
- Arg Gly Gly His Gly Cys Ile Gly Arg Leu Pro Arg Val Leu Leu 85 90 95
- Arg Pro Arg Ala Arg Leu Glu Ser Pro Leu Pro Arg Arg
 100 105
- (2) INFORMATION FOR SEQ ID NO:1962:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599557
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:
- Leu Ser Gly Ser Lys Pro Ser Gly Val Ser Ser Leu Gl
n Arg Leu Gl
n 1 5 10 15
- Pro Ile Arg Gln Ser Arg Ser Pro Ser Ser Leu Leu Ala Arg Ser Pro 20 25 30
- Pro Pro Ser Ala Met Ala Ala Phe Pro Ser Ala Ser Pro Ser Pro Ala 35 40 45
- Ala Leu Arg Pro Ser Pro Ala Gly Arg Leu Arg Ser Ser Phe Ser Pro 65 70 75 80
- Ala Ala Ala Thr Ala Ala Ser Val Gly Cys Leu Gly Ser Phe Ser 85 90 95
- Gly Leu Ala Pro Val Ser Asn Leu Leu Ser Leu Gly Ala Glu Asn Ser $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$
- Ser Phe Glu His Arg Leu Xaa Gly Ile Asp Ala Arg Gly Xaa Ile Val 115 120 125
- Ala Met Arg His Gly Arg Arg Val Ser 130 135
- (2) INFORMATION FOR SEQ ID NO:1963:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963: Tyr Pro Val Gln Ser Arg Ala Ala Ser Pro Leu Ser Ser Gly Ser Ser

Gln Ser Gly Asn Pro Ala Pro Pro Ala Arg Cys Ser Pro Ala Leu Leu 20 25 30

Arg Pro Pro Pro Trp Arg Pro Ser Pro Pro Pro Pro Arg Arg Arg Arg 35 40 45

Ser Pro Pro Arg Pro Gly Ala Trp Leu Pro Ser Val Arg Pro Ser Pro 50 55 60

His Ser Ala Pro Pro Pro Arg Ala Gly Ser Val Arg Arg Ser Arg Pro 65 70 75 80

Arg Arg Pro Arg Leu His Arg Ser Ala Ala Ser Gly Pro Ser Pro 85 90 95

Ala Ser Arg Pro Ser Arg Ile Ser Ser Pro Ser Ala Leu Arg Thr Gln
100 105 110

Ala Leu Ser Ile Gly Cys Xaa Val Leu Met Pro Val Glu Xaa 115 120 125

- (2) INFORMATION FOR SEQ ID NO:1964:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..515
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964: 60 agtattacca ggatgtcttt cagccgcaga ttagcaggcc gcctgcgctc cttgccccta agcctcgttt ccggtgtacg actccaacga cgacgagatg gcctccccgc tccgtcggag 120 cttcccctcc ctcggccgcg cgcttctcac gccggcgccg gcgcggatgc tctccgcgga 180 ggcctccgat gccctcgttg agatcaagcc cagggagatt gggatggtct ccggcatccc 240 cgaggagcac ctccgccgta aggttgtaat ttattcacca gctaggactg catctcagca 300 aggttcaggc aaagttggga ggtggaaaat taactttttg tcaacccaaa agtgggagaa 360 cccattgatg ggatggacat ctactgggga tccatatgct aatgtcggtg aagcaggact 420 tacattcaac agtgcggagt cagcaaaagc atttgctgaa aaacatggat ggaatttatg 480 tggtacggaa acggcataca cctcttctga agcct
- (2) INFORMATION FOR SEQ ID NO:1965:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..139
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

Met Ala Ser Pro Leu Arg Arg Ser Phe Pro Ser Leu Gly Arg Ala Leu
1 5 10 15

Leu Thr Pro Ala Pro Ala Arg Met Leu Ser Ala Glu Ala Ser Asp Ala 20 25 30

Leu Val Glu Ile Lys Pro Arg Glu Ile Gly Met Val Ser Gly Ile Pro 35 40 45

Glu Glu His Leu Arg Arg Lys Val Val Ile Tyr Ser Pro Ala Arg Thr 50 55 60

Ala Glu Ser Ala Lys Ala Phe Ala Glu Lys His Gly Trp Asn Leu Cys
115 120 125

Gly Thr Glu Thr Ala Tyr Thr Ser Ser Glu Ala 130 135

- (2) INFORMATION FOR SEQ ID NO:1966:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:
 Met Leu Ser Ala Glu Ala Ser Asp Ala Leu Val Glu Ile Lys Pro Arg
 1 10 15

Glu Ile Gly Met Val Ser Gly Ile Pro Glu Glu His Leu Arg Arg Lys
20 25 30

Val Val Ile Tyr Ser Pro Ala Arg Thr Ala Ser Gln Gln Gly Ser Gly 35 40 45

Lys Val Gly Arg Trp Lys Ile Asn Phe Leu Ser Thr Gln Lys Trp Glu 50 55 60

Asn Pro Leu Met Gly Trp Thr Ser Thr Gly Asp Pro Tyr Ala Asn Val 65 70 75 80

Gly Glu Ala Gly Leu Thr Phe Asn Ser Ala Glu Ser Ala Lys Ala Phe 85 90 95

Ala Glu Lys His Gly Trp Asn Leu Cys Gly Thr Glu Thr Ala Tyr Thr 100 105 110

Ser Ser Glu Ala

115

- (2) INFORMATION FOR SEQ ID NO:1967:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599566
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

Met Val Ser Gly Ile Pro Glu Glu His Leu Arg Arg Lys Val Val Ile
1 5 10 15

Tyr Ser Pro Ala Arg Thr Ala Ser Gln Gln Gly Ser Gly Lys Val Gly
20 25 30

Arg Trp Lys Ile Asn Phe Leu Ser Thr Gln Lys Trp Glu Asn Pro Leu 35 40 45

Met Gly Trp Thr Ser Thr Gly Asp Pro Tyr Ala Asn Val Gly Glu Ala 50 55 60

Gly Leu Thr Phe Asn Ser Ala Glu Ser Ala Lys Ala Phe Ala Glu Lys 65 70 75 80
His Gly Trp Asn Leu Cys Gly Thr Glu Thr Ala Tyr Thr Ser Ser Glu

90 95 85 Ala (2) INFORMATION FOR SEQ ID NO:1968: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..327

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (D) OTHER INFORMATION: / Ceres Seq. ID 1599574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968: 60 atcagccatc ccctcccgcg gcaagtctct ctgaattgtg ggtctccggc gnatggcgc tctagctcca tccaagnatt ctgggcacca agctcaactt cgccggctcc tcccgctacg ccacggcage geccaeegeg ggggeteaga agategtete cetetteage aagaageetg 180 cccagaagcc caagccctct gcggtgtcgt cctcttctcc ggacatcagc gacgagctcg 240 ccaagtggta cggtcctgac aggaggatct acctgccgga tgggctcttg gaccgctcgg 300 aggtaccgga gtacctcacc ggagagg
- (2) INFORMATION FOR SEQ ID NO:1969:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599575
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

Ile Ser His Pro Leu Pro Arg Gln Val Ser Leu Asn Cys Gly Ser Pro 10 5 Ala Xaa Gly Gly Ser Ser Ser Ile Gln Xaa Phe Trp Ala Pro Ser Ser 25 2.0

Thr Ser Pro Ala Pro Pro Ala Thr Pro Arg Gln Arg Pro Pro Arg Gly 40

Leu Arg Arg Ser Ser Pro Ser Ser Ala Arg Ser Leu Pro Arg Ser Pro 55

Ser Pro Leu Arg Cys Arg Pro Leu Leu Arg Thr Ser Ala Thr Ser Ser 75 70

Pro Ser Gly Thr Val Leu Thr Gly Gly Ser Thr Cys Arg Met Gly Ser 90

Trp Thr Ala Arg Arg Tyr Arg Ser Thr Ser Pro Glu Arg 105

- (2) INFORMATION FOR SEQ ID NO:1970:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..68
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599576
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

Met Ala Ala Leu Ala Pro Ser Lys Xaa Ser Gly His Gln Ala Gln Leu

Client Docket No. 80146.003 Arg Arg Leu Leu Pro Leu Arg His Gly Ser Ala His Arg Gly Gly Ser 25 Glu Asp Arg Leu Pro Leu Gln Gln Glu Ala Cys Pro Glu Ala Gln Ala 40 4.5 Leu Cys Gly Val Val Leu Phe Ser Gly His Gln Arg Arg Ala Arg Gln 55 Val Val Arg Ser (2) INFORMATION FOR SEQ ID NO:1971: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..325 (D) OTHER INFORMATION: / Ceres Seq. ID 1599588 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971: agaaactcac tegecatege egggeatege gggeategsa cacaaaegea acetgeagee atggcacaga agetegege acegaeggeg geggtegteg tegteetget ggegetegee 120 ttgtcggccg ccgcgcagaa ctgcgggtgc gcgtcgggcc tgtgctgcag ccggttcggg 180 tactgcggga cgggcgagga ctactgcggc gccgggtgcc agtcgggccc ctgcgacgtg 240 ceggagacca acaacgegte egtggccage ategtgacge eggeettett egaegegete 300 ctcgcgcagg ccgccgcctc gtgcg (2) INFORMATION FOR SEQ ID NO:1972: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..108 (D) OTHER INFORMATION: / Ceres Seq. ID 1599589 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972: Arg Asn Ser Leu Ala Ile Ala Gly His Arg Gly His Xaa Thr Gln Thr 10 5 Gln Pro Ala Ala Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Ala Val 30 25 20 Val Val Val Leu Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys 4.0 Gly Cys Ala Ser Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr 5.5 Gly Glu Asp Tyr Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val 75 70 Pro Glu Thr Asn Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe 90 8.5 Phe Asp Ala Leu Leu Ala Gln Ala Ala Ala Ser Cys 100 105 (2) INFORMATION FOR SEQ ID NO:1973: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599590
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

Glu Thr His Ser Pro Ser Pro Gly Ile Ala Gly Ile Xaa His Lys Arg 1 5 10

Asn Leu Gln Pro Trp His Arg Ser Ser Arg His Arg Arg Arg Ser

Ser Ser Cys Trp Arg Ser Pro Cys Arg Pro Pro Arg Arg Thr Ala 35 40 45

Gly Ala Arg Arg Ala Cys Ala Ala Ala Gly Ser Gly Thr Ala Gly Arg 50 55 60

Ala Arg Thr Thr Ala Ala Pro Gly Ala Ser Arg Ala Pro Ala Thr Cys
65 70 75 80

Arg Arg Pro Thr Thr Arg Pro Trp Pro Ala Ser 85 90

- (2) INFORMATION FOR SEQ ID NO:1974:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599591
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Lys Leu Thr Arg His Arg Arg Ala Ser Arg Ala Ser Xaa Thr Asn Ala 1 5 10 15

Thr Cys Ser His Gly Thr Glu Ala Arg Ala Thr Asp Gly Gly Gly Arg 20 25 30

Arg Arg Pro Ala Gly Ala Arg Leu Val Gly Arg Arg Ala Glu Leu Arg 35 40 45

Val Arg Val Gly Pro Val Leu Gln Pro Val Arg Val Leu Arg Asp Gly 50 55 60

Arg Gly Leu Leu Arg Arg Arg Val Pro Val Gly Pro Leu Arg Arg Ala 65 70 75 80

Gly Asp Gln Gln Arg Val Arg Gly Gln His Arg Asp Ala Gly Leu Leu 85 90 95

Arg Arg Ala Pro Arg Ala Gly Arg Arg Leu Val

- (2) INFORMATION FOR SEQ ID NO:1975:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..350
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599617
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

acaattccac ataacctcgc ccgcgccgcc tcnnccacga gacgccttct tgctctcgss 60 ttccggtgac gcccgccact tcctccccga cgagatgacg aaacgcacca agaaggcagg 120 aatcgttggc aaatatggta ccaggtatgg tgccagttta cgtaaacaga tcaagaagat gagaggtctcg cagcactcca aatacttctg tgagttctgt ggcaagtttg ccgtgaagag 240 gaaagcagt ngtatctggg gatgcaagga ctgtgggaan gttaacgccg gtngcgccta 300 cacaatgaac actgctagtg cggtcactss tgagaagcac aatccggcgc

- (2) INFORMATION FOR SEQ ID NO:1976:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Gln Phe His Ile Thr Ser Pro Ala Pro Pro Xaa Pro Arg Asp Ala Phe 1 5 10 15

Leu Leu Ser Xaa Ser Gly Asp Ala Arg His Phe Leu Pro Asp Glu Met 20 25 30

Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg 35 40 45

Tyr Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser Gln 50 60

His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Arg
70 75 80

Lys Ala Val Xaa Ile Trp Gly Cys Lys Asp Cys Gly Xaa Val Asn Ala 85 90 95

Gly Xaa Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Xaa Glu Lys 100 105 110

His Asn Pro Ala 115

- (2) INFORMATION FOR SEQ ID NO:1977:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599619
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr 1 5 10 15

Arg Tyr Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser 20 25 30

Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys 35 40 45

Arg Lys Ala Val Xaa Ile Trp Gly Cys Lys Asp Cys Gly Xaa Val Asn 50 55 60

Ala Gly Xaa Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Xaa Glu 65 70 75 80

Lys His Asn Pro Ala

- (2) INFORMATION FOR SEQ ID NO:1978:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..276
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599628

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

 gagtttcgat ctctcccatc cgagtgtctc ctcctccgcc gccgccgccg ccgcttccgt 60
 cgtctccgcc cgccgaggcc atgccgtccc acaagacctt ccggatcaag aagaagctgg 120
 ccaagaagat gcgccagaac cgccccatcc cctactggat ccgcatgcgc accgacaaca 180
 ccatcaggta caacgccaag cgcaggcact ggcgtcgcac caaactcgga ttctgagcgg 240
 tggaagarat gctggctaat gacgcttngg gggtat
- (2) INFORMATION FOR SEQ ID NO:1979:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599629
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:
 Glu Phe Arg Ser Leu Pro Ser Glu Cys Leu Leu Arg Arg Arg Arg
 1 10 15
- Arg Arg Phe Arg Arg Leu Arg Pro Pro Arg Pro Cys Arg Pro Thr Arg
- Pro Ser Gly Ser Arg Arg Ser Trp Pro Arg Arg Cys Ala Arg Thr Ala
- Pro Ser Pro Thr Gly Ser Ala Cys Ala Pro Thr Thr Pro Ser Gly Thr 50 60
- Thr Pro Ser Ala Gly Thr Gly Val Ala Pro Asn Ser Asp Ser Glu Arg 65 70 75 80
- Trp Lys Xaa Cys Trp Leu Met Thr Leu Xaa Gly Tyr 85 90
- (2) INFORMATION FOR SEQ ID NO:1980:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599630
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:
- Ser Phe Asp Leu Ser His Pro Ser Val Ser Ser Ser Ala Ala Ala Ala 1 5 10 15
- Ala Ala Ser Val Val Ser Ala Arg Arg Gly His Ala Val Pro Gln Asp
 20 25 30
- Leu Pro Asp Gln Glu Glu Ala Gly Gln Glu Asp Ala Pro Glu Pro Pro 35 40 45
- His Pro Leu Leu Asp Pro His Ala His Arg Gln His His Gln Val Gln
 50 55 60
- Arg Gln Ala Gln Ala Leu Ala Ser His Gln Thr Arg Ile Leu Ser Gly 65 70 75 80
- Gly Arg Xaa Ala Gly

- (2) INFORMATION FOR SEQ ID NO:1981:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..77
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

Val Ser Ile Ser Pro Ile Arg Val Ser Pro Pro Pro Pro Pro Pro Pro 1 5 10 15

Pro Leu Pro Ser Ser Pro Pro Ala Glu Ala Met Pro Ser His Lys Thr 20 25 30

Phe Arg Ile Lys Lys Leu Ala Lys Lys Met Arg Gln Asn Arg Pro 35 40 45

Ile Pro Tyr Trp Ile Arg Met Arg Thr Asp Asn Thr Ile Arg Tyr Asn 50 55 60

Ala Lys Arg Arg His Trp Arg Arg Thr Lys Leu Gly Phe 65 70 75

- (2) INFORMATION FOR SEQ ID NO:1982:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..371
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

 accaaggaaa ttcacaaaga gatactagte cetaccaaag catacttect gaaacactet
 tgcaatccac tgagtcctgt ttgttgagac ttgagacgca tagagctage gtcgacaatg
 tegetegtga ggegemsaac gtgttegace cettetegat ggacetetgg gacecetteg
 acaccatgtt eegetecate gtecegtegg eggeetecac caacteegag acegeegtet
 tegecagege eegeategac tggaaggaga egeeegagge geacgtgtte aaggeegace
 teeeggegt caagaaggag gagatcaagg tegaggtega ggaeggcaac gtgetggtea
 teageggeca g
- (2) INFORMATION FOR SEQ ID NO:1983:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599639
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:
- Gln Gly Asn Ser Gln Arg Asp Thr Ser Pro Tyr Gln Ser Ile Leu Pro 1 5 5 10 15 Glu Thr Leu Leu Gln Ser Thr Glu Ser Cys Leu Leu Arg Leu Glu Thr
- 20 25 30
 His Arg Ala Ser Val Asp Asn Val Ala Arg Glu Ala Xaa Asn Val Phe
- His Arg Ala Ser val Asp Ash val Ala Alg Glu Mid Add Mon val The
 35 40 45
 Asp Dro Pho Sor Met Asp Leu Tro Asp Pro Phe Asp Thr Met Phe Arg
- Asp Pro Phe Ser Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg 50 55 60
 Ser Ile Val Pro Ser Ala Ala Ser Thr Asn Ser Glu Thr Ala Val Phe
- 65 70 75 80
 Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro Glu Ala His Val Phe
- 85 90 95

 Lys Ala Asp Leu Pro Gly Val Lys Lys Glu Glu Ile Lys Val Glu Val
 100 105 110
- Glu Asp Gly Asn Val Leu Val Ile Ser Gly Gln

120 115 (2) INFORMATION FOR SEQ ID NO:1984: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..84 (D) OTHER INFORMATION: / Ceres Seq. ID 1599640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984: Met Ser Leu Val Arg Arg Xaa Thr Cys Ser Thr Pro Ser Arg Trp Thr 10 Ser Gly Thr Pro Ser Thr Pro Cys Ser Ala Pro Ser Ser Arg Arg 20 25 Pro Pro Pro Thr Pro Arg Pro Pro Ser Ser Pro Ala Pro Ala Ser Thr 40 Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala 55 60 Ser Arg Arg Arg Ser Arg Ser Arg Ser Arg Thr Ala Thr Cys Trp 75 Ser Ser Ala Ala (2) INFORMATION FOR SEQ ID NO:1985: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1599641 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985: Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro 10 5 Ser Ala Ala Ser Thr Asn Ser Glu Thr Ala Val Phe Ala Ser Ala Arg 25 2.0 Ile Asp Trp Lys Glu Thr Pro Glu Ala His Val Phe Lys Ala Asp Leu 40 Pro Gly Val Lys Lys Glu Glu Ile Lys Val Glu Val Glu Asp Gly Asn 55 Val Leu Val Ile Ser Gly Gln 70 (2) INFORMATION FOR SEQ ID NO:1986: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..200 (D) OTHER INFORMATION: / Ceres Seq. ID 1599657 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986: aacqatttca ccggaqtcac gtcgtggttt gcggccaagt gcgacctcat ccttctnctg

tttgatccgc ataagcttga catcagcgat gagttcaagc gtgtgatcgg gtctctccgc

360

420

Client Docket No. 80146.003 gggcatgatg acaagatacg catagttctc aacaaggccg accaagttga tgcacagcag ctgatgagag tgtacggagc (2) INFORMATION FOR SEQ ID NO:1987: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..66 (D) OTHER INFORMATION: / Ceres Seq. ID 1599658 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987: Asn Asp Phe Thr Gly Val Thr Ser Trp Phe Ala Ala Lys Cys Asp Leu 10 Ile Leu Xaa Leu Phe Asp Pro His Lys Leu Asp Ile Ser Asp Glu Phe 30 25 Lys Arg Val Ile Gly Ser Leu Arg Gly His Asp Asp Lys Ile Arg Ile 40 Val Leu Asn Lys Ala Asp Gln Val Asp Ala Gln Gln Leu Met Arg Val 50 55 Tyr Gly 65 (2) INFORMATION FOR SEQ ID NO:1988: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..34 (D) OTHER INFORMATION: / Ceres Seq. ID 1599659 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988: Thr Ile Ser Pro Glu Ser Arg Arg Gly Leu Arg Pro Ser Ala Thr Ser 10 5 Ser Phe Xaa Cys Leu Ile Arg Ile Ser Leu Thr Ser Ala Met Ser Ser 25 20 Ser Val (2) INFORMATION FOR SEQ ID NO:1989: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 423 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..423 (D) OTHER INFORMATION: / Ceres Seq. ID 1599663 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989: cacaatttgt tcaggttttc aataacagtc cagatgagac agcttatttc aggatgttac 60 120 tcaatcgtga gagtatcact aactcggttg ccatgatcca gccttccttg atatcatttt cttttgattc acctccatct ccggtatttc tagatgtggc atcaatagca gcagatcgta tactgctact tgatgcgtac tttagtgttg tcatttttss atggaatgac aattgctcag 240

tggagaaaca tgggttatca gaaccaacct gagcatgagc aatttgcaca actattacaa

gcaccacatg aggaggcaca gatgataata aagggtcgat ttccagttcc aagactagtg

gtctgcgaca acatggctcg caggcratgt ttttgttngc taagctgaat ccatcggcca

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cat
(2) INFORMATION FOR SEQ ID NO:1990:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 89 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..89
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599664
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:
Gln Phe Val Gln Val Phe Asn Asn Ser Pro Asp Glu Thr Ala Tyr Phe
                                    10
               5
Arg Met Leu Leu Asn Arg Glu Ser Ile Thr Asn Ser Val Ala Met Ile
          20
                                25
Gln Pro Ser Leu Ile Ser Phe Ser Phe Asp Ser Pro Pro Ser Pro Val
                            40
Phe Leu Asp Val Ala Ser Ile Ala Ala Asp Arg Ile Leu Leu Leu Asp
                                            60
                        55
Ala Tyr Phe Ser Val Val Ile Phe Xaa Trp Asn Asp Asn Cys Ser Val
                    70
                                        75
Glu Lys His Gly Leu Ser Glu Pro Thr
                85
(2) INFORMATION FOR SEQ ID NO:1991:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 72 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1...72
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599665
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:
Met Leu Leu Asn Arg Glu Ser Ile Thr Asn Ser Val Ala Met Ile Gln
                                     10
                5
Pro Ser Leu Ile Ser Phe Ser Phe Asp Ser Pro Pro Ser Pro Val Phe
                                                     30
                                25
Leu Asp Val Ala Ser Ile Ala Ala Asp Arg Ile Leu Leu Asp Ala
                                                 4.5
                            40
Tyr Phe Ser Val Val Ile Phe Xaa Trp Asn Asp Asn Cys Ser Val Glu
                        55
Lys His Gly Leu Ser Glu Pro Thr
                    70
 (2) INFORMATION FOR SEQ ID NO:1992:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 71 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..71
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599666
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:
 Met Arg Thr Leu Val Leu Ser Phe Xaa Xaa Gly Met Thr Ile Ala Gln
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Trp Arg Asn Met Gly Tyr Gln Asn Gln Pro Glu His Glu Gln Phe Ala
                                25
Gln Leu Leu Gln Ala Pro His Glu Glu Ala Gln Met Ile Ile Lys Gly
                            40
Arg Phe Pro Val Pro Arg Leu Val Val Cys Asp Asn Met Ala Arg Arg
                        55
Xaa Cys Phe Cys Xaa Leu Ser
                    70
(2) INFORMATION FOR SEQ ID NO:1993:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 415 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..415
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599678
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:
                                                                        60
cttcaggsst tctagggttt tngcgccgcc gccgccgccg cttcgtcgtc tccgccgcag
cgatgccgtc gcacaagacc ttccggatca agaagaagct ggcgaagaag atgcgccaga
                                                                       120
                                                                       180
mccgccccat cccctactgg atccgcatgc gcacggacaa caccatcagg tacaacgcca
agegeaggea etggegeege accaageteg gettetgage gegeggateg geeggeteet
                                                                       240
gcgtcggaat tctagggtct ctacctttcc tttggtttta tcgatgtctc ttgtgtttct
                                                                       300
                                                                       360
gtaagctagc aaacagttcc agaaagcttt tgttaagatt ttgatgacgc taagaggatt
gatgctacta tgctgtactc aggattccat gctgcattgc gatctaaatt aagag
(2) INFORMATION FOR SEQ ID NO:1994:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 100 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..100
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599679
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:
Phe Arg Xaa Ser Arg Val Xaa Ala Pro Pro Pro Pro Leu Arg Arg
                                     10
                5
Leu Arg Arg Ser Asp Ala Val Ala Gln Asp Leu Pro Asp Gln Glu Glu
                                 25
Ala Gly Glu Glu Asp Ala Pro Xaa Pro Pro His Pro Leu Leu Asp Pro
                            40
His Ala His Gly Gln His His Gln Val Gln Arg Gln Ala Gln Ala Leu
                                             60
                         55
Ala Pro His Gln Ala Arg Leu Leu Ser Ala Arg Ile Gly Arg Leu Leu
```

Arg Arg Asn Ser Arg Val Ser Thr Phe Pro Leu Val Leu Ser Met Ser

Leu Val Phe Leu 100

(2) INFORMATION FOR SEQ ID NO:1995:

8.5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid

7.0

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

Ser Xaa Xaa Leu Gly Phe Xaa Arg Arg Arg Arg Arg Phe Val Val 10 5

Ser Ala Ala Ala Met Pro Ser His Lys Thr Phe Arg Ile Lys Lys 30 25 20

Leu Ala Lys Lys Met Arg Gln Xaa Arg Pro Ile Pro Tyr Trp Ile Arg 40 35

Met Arg Thr Asp Asn Thr Ile Arg Tyr Asn Ala Lys Arg Arg His Trp 55

Arg Arg Thr Lys Leu Gly Phe 70

- (2) INFORMATION FOR SEQ ID NO:1996:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..51
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599681
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:

Met Pro Ser His Lys Thr Phe Arg Ile Lys Lys Leu Ala Lys Lys 10 5

Met Arg Gln Xaa Arg Pro Ile Pro Tyr Trp Ile Arg Met Arg Thr Asp 25

Asn Thr Ile Arg Tyr Asn Ala Lys Arg Arg His Trp Arg Arg Thr Lys 40

Leu Gly Phe

50

- (2) INFORMATION FOR SEQ ID NO:1997:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..336
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599686
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

aatctgaccc actctcgtcg cacgcaacgc aagtagcaaa gcaggaccca tcctctccca teteteggte tecceatece aaccegeege egeegeegee getteteeeg tetecagege ccacagogca ttgtatccgc ggggcgagct gagtcaccaa gctggtctag ggcccatcca tttggaaccc tcgcgagaag caaagcgnac ggagcgccab sntcttagat cgattgctcg 240 ccaggctgtt ggcgaggagt cgtcaaccct cacggcrgcc atgtctgtgg agckcatcct 300 gtggcttttc tccttcgtct ccgtcatggt cctcat

- (2) INFORMATION FOR SEQ ID NO:1998:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998: Ser Asp Pro Leu Ser Ser His Ala Thr Gln Val Ala Lys Gln Asp Pro 10
- Ser Ser Pro Ile Ser Arg Ser Pro His Pro Asn Pro Pro Pro Pro 25
- Pro Leu Leu Pro Ser Pro Ala Pro Thr Ala His Cys Ile Arg Gly Ala 40

Ser

- (2) INFORMATION FOR SEQ ID NO:1999:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..396
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599692
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999: ctccgatctc cctctctct gttctgctca catcgacgcg gttcggttcc agtttcactc ccactgccgt ctcgssaacc tcccctgttc cacgcttcgt cctcgcgttc ccaaccaagc 120 180 tetecegect genatkgeeg egaceteece ettegaetge gteeteetag acetegaega 240 caccetgtae eegggegaca egggeategg egeggeeetg aggegeaaca tegaegagtt 300 cctccaggcc aagctcggcg tgtcggccga cgaggcccgc cacgcgcgcc gagctcttcc gegegeacgg cageteete geegggetea tegegetegg etaegaegtg caeeeggaeg 360 agtaccacag ctacgtgcac ggcaggctac cgtacg
- (2) INFORMATION FOR SEQ ID NO:2000:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599693
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:
- Leu Arg Ser Pro Ser Leu Ser Phe Cys Ser His Arg Arg Gly Ser Val 10 -5
- Pro Val Ser Leu Pro Leu Pro Ser Xaa Xaa Pro Pro Leu Phe His Ala 25 20
- Ser Ser Ser Arg Ser Gln Pro Ser Ser Pro Ala Cys Xaa Xaa Arg Asp 4.0
- Leu Pro Leu Arg Leu Arg Pro Pro Arg Pro Arg Arg His Pro Val Pro 55
- Gly Arg His Gly His Arg Arg Gly Pro Glu Ala Gln His Arg Arg Val 70 75
- Pro Pro Gly Gln Ala Arg Arg Val Gly Arg Arg Gly Pro Pro Arg Ala 90
- Pro Ser Ser Ser Ala Arg Thr Ala Ala Pro Ser Pro Gly Ser Ser Arg 105 110
- Ser Ala Thr Thr Cys Thr Arg Thr Ser Thr Thr Ala Thr Cys Thr Ala 120 115
- Gly Tyr Arg Thr
 - 130
- (2) INFORMATION FOR SEQ ID NO: 2001:

Page 1053 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..131 (D) OTHER INFORMATION: / Ceres Seq. ID 1599694 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001: Ser Asp Leu Pro Leu Ser Arg Ser Ala His Ile Asp Ala Val Arg Phe 10 5 Gln Phe His Ser His Cys Arg Leu Xaa Asn Leu Pro Cys Ser Thr Leu 30 25 20 Arg Pro Arg Val Pro Asn Gln Ala Leu Pro Pro Xaa Xaa Ala Ala Thr 40 Ser Pro Phe Asp Cys Val Leu Leu Asp Leu Asp Asp Thr Leu Tyr Pro 55 Gly Asp Thr Gly Ile Gly Ala Ala Leu Arg Arg Asn Ile Asp Glu Phe 75 70 Leu Gln Ala Lys Leu Gly Val Ser Ala Asp Glu Ala Arg His Ala Arg 90 85 Arg Ala Leu Pro Arg Ala Arg Gln Leu Pro Arg Ala His Arg Ala 105 Arg Leu Arg Arg Ala Pro Gly Arg Val Pro Gln Leu Arg Ala Arg Gln 120 115 Ala Thr Val 130 (2) INFORMATION FOR SEQ ID NO:2002: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..433 (D) OTHER INFORMATION: / Ceres Seq. ID 1599697 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002: tcagagtcaa ccggcccaac cctctcagtc tcggcctctc gggtcgccag tcctcgccta 60 ggtttaggct tccaccggcc gcagcctcca caccaagagc ggnncgagat cgccggaaga 120 ggggggaggc gcggagatga gcgggasssn gttcaacgct tcaagtcgcg tgtgccggtg 180 gcgtggagtc cccggctgta catcacgctg gtgcggggcc taccgggcac gcgccgcctc 240 cacegeegea egetegagge catgegeete egeegetgee acegeacegt egageacege 300 accacgccgt cgctgctcgg gatgctcacc caggtgaagc gcctcgtcgc cgtcgagacc 360 gaggagatcg tacaacgcgc gcaasagggc cgaggcggag aggegegege cagaccceeg 420 ctcqtcqtct ccc (2) INFORMATION FOR SEQ ID NO:2003: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE:

> (A) NAME/KEY: peptide (B) LOCATION: 1..144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

(D) OTHER INFORMATION: / Ceres Seq. ID 1599698

Ser Glu Ser Thr Gly Pro Thr Leu Ser Val Ser Ala Ser Arg Val Ala 10 Ser Pro Arg Leu Gly Leu Gly Phe His Arg Pro Gln Pro Pro His Gln 25 Glu Arg Xaa Glu Ile Ala Gly Arg Gly Gly Arg Arg Gly Asp Glu Arg 40 Xaa Xaa Val Gln Arg Phe Lys Ser Arg Val Pro Val Ala Trp Ser Pro Arg Leu Tyr Ile Thr Leu Val Arg Gly Leu Pro Gly Thr Arg Arg Leu 75 His Arg Arg Thr Leu Glu Ala Met Arg Leu Arg Arg Cys His Arg Thr 8.5 90 Val Glu His Arg Thr Thr Pro Ser Leu Leu Gly Met Leu Thr Gln Val 110 105 100 Lys Arg Leu Val Ala Val Glu Thr Glu Glu Ile Val Gln Arg Ala Gln 120 125 115 Xaa Gly Arg Gly Glu Ala Arg Ala Arg Pro Pro Leu Val Val Ser 140 130 135

(2) INFORMATION FOR SEQ ID NO:2004:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..418
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599712
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

 aagcgaagag cgcctccct ccccctcgag atcttctct cctcccgcg ccgctatgga
 cgctgttgac tcggtggtcg acccgctccg gagttcgcca aggacagcat ccgcctcgtc
 aagcgctgcc acaagcccga ccgcaagwag ttcaccaagg tcgccgcgcg cactgcgatc
 ggcttcatcg tcatgggatt cgtcggcttc tttgtcaagc tcatcttcat ccccatcaac
 aacatcatcg tcggctccgg ctgatccatg cccctcagga gtggacaatg gcgtctccgc
 ttggaggcgc asstctggca tccggaaagc agttnttta ggtgaaggac gagtcccgt
 gtagacctgt aactcttcgt tnggtctts tcgattgctk ttctagtgcg gcatggac
 (2) INFORMATION FOR SEQ ID NO:2005:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599713
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:
- Ser Glu Glu Arg Leu Pro Ser Pro Ser Arg Ser Ser Leu Pro Pro Arg 1 5 10 15
- Ala Ala Met Asp Ala Val Asp Ser Val Val Asp Pro Leu Arg Ser Ser 20 25 30
- Pro Arg Thr Ala Ser Ala Ser Ser Ser Ala Ala Thr Ser Pro Thr Ala
- Xaa Ser Ser Pro Arg Ser Pro Arg Ala Leu Arg Ser Ala Ser Ser Ser 50 55 60
- Trp Asp Ser Ser Ala Ser Leu Ser Ser Ser Ser Ser Ser Pro Ser Thr 65 70 75 80

Thr Ser Ser Ser Ala Pro Ala Asp Pro Cys Pro Ser Gly Val Asp Asn 85 90 95

Gly Val Ser Ala Trp Arg Arg Xaa Ser Gly Ile Arg Lys Ala Val Xaa 100 105 110

Leu Gly Glu Gly Arg Val Pro Trp 115 120

- (2) INFORMATION FOR SEQ ID NO:2006:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599714
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

Ala Lys Ser Ala Ser Pro Pro Pro Arg Asp Leu Leu Ser Leu Pro Ala

Pro Leu Trp Thr Leu Leu Thr Arg Trp Ser Thr Arg Ser Gly Val Arg 20 25 30

Gln Gly Gln His Pro Pro Arg Gln Ala Leu Pro Gln Ala Arg Pro Gln 35 40 45

Xaa Val His Gln Gly Arg Arg Ala His Cys Asp Arg Leu His Arg His 50 55 60

Gly Ile Arg Arg Leu Leu Cys Gln Ala His Leu His Pro His Gln Gln 65 70 75 80

His His Arg Arg Leu Arg Leu Ile His Ala Pro Gln Glu Trp Thr Met 85 90 95

Ala Ser Pro Leu Gly Gly Ala Xaa Leu Ala Ser Gly Lys Gln Phe Xaa 100 105 110

- (2) INFORMATION FOR SEQ ID NO: 2007:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599715
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Met Asp Ala Val Asp Ser Val Val Asp Pro Leu Arg Ser Ser Pro Arg

1 5 10 15

Thr Ala Ser Ala Ser Ser Ser Ala Ala Thr Ser Pro Thr Ala Xaa Ser
20 25 30

Ser Pro Arg Ser Pro Arg Ala Leu Arg Ser Ala Ser Ser Ser Trp Asp 35 40 45

Ser Ser Ala Ser Leu Ser Ser Ser Ser Ser Pro Ser Thr Thr Ser 50 55 60

Ser Ser Ala Pro Ala Asp Pro Cys Pro Ser Gly Val Asp Asn Gly Val 65 70 75 80

Ser Ala Trp Arg Xaa Ser Gly Ile Arg Lys Ala Val Xaa Leu Gly 85 90 95

Glu Gly Arg Val Pro Trp

100

(2) INFORMATION FOR SEQ ID NO:2008:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..440
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599724
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

 tctatttgaa agttcaggta aaagatacag gctgtggaat tggtccacag gatctacctc
 atgtatttac aaagtttgct catcctcaaa gcggaggaaa ccgagggttt aatggtagtg
 gtcttggcct tgccatatgc aagaggtttg ttagtctcat gggagggcac atctggattg
 acaacgaagg aaccggaaga ggttgcaccg caacattcgt cgtcaagctc ggcgtgtgt
 acaacacaaa cacctaccag cagcagctga tccctctagt atggccaagc agcgcagact
 ccgatttgcg tgctccgaaa cctcttccgg acgggagagg atctactccc ttganatctc
 ggtaccaaag gagcgtatga gcctagtgta aatgattgag ggcatagtgc caagtagggg
 420
- (2) INFORMATION FOR SEQ ID NO:2009:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

accgattagt gccaccgtct

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599725
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:
- Tyr Leu Lys Val Gln Val Lys Asp Thr Gly Cys Gly Ile Gly Pro Gln 1 5 10 15
- Asp Leu Pro His Val Phe Thr Lys Phe Ala His Pro Gln Ser Gly Gly 20 25 30
- Asn Arg Gly Phe Asn Gly Ser Gly Leu Gly Leu Ala Ile Cys Lys Arg
- Phe Val Ser Leu Met Gly Gly His Ile Trp Ile Asp Ser Glu Gly Thr
 50 55 60
- Gly Arg Gly Cys Thr Ala Thr Phe Val Val Lys Leu Gly Val Cys Asp 65 70 75 80
- Asn Thr Asn Thr Tyr Gln Gln Gln Leu Ile Pro Leu Val Trp Pro Ser 85 90 95
- Ser Ala Asp Ser Asp Leu Arg Ala Pro Lys Pro Leu Pro Asp Gly Arg 100 105 110
- Gly Ser Thr Pro Leu Xaa Ser Arg Tyr Gln Arg Ser Val 115 120 125
- (2) INFORMATION FOR SEQ ID NO:2010:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599726
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:
- Met Tyr Leu Gln Ser Leu Leu Ile Leu Lys Ala Glu Glu Thr Glu Gly
 1 5 10 15

```
Leu Met Val Val Val Leu Ala Leu Pro Tyr Ala Arg Gly Leu Leu Val
                                25
Ser Trp Glu Gly Thr Ser Gly Leu Thr Ala Lys Glu Pro Glu Glu Val
                                                 45
                            40
Ala Pro Gln His Ser Ser Ser Ser Ser Ala Cys Val Thr Thr Gln Thr
                                             60
                        55
Pro Thr Ser Ser Ser
(2) INFORMATION FOR SEQ ID NO:2011:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 73 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..73
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599727
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:
Met Gly Gly His Ile Trp Ile Asp Ser Glu Gly Thr Gly Arg Gly Cys
                                     10
Thr Ala Thr Phe Val Val Lys Leu Gly Val Cys Asp Asn Thr Asn Thr
                                 25
            20
Tyr Gln Gln Gln Leu Ile Pro Leu Val Trp Pro Ser Ser Ala Asp Ser
                                                 45
                             40
Asp Leu Arg Ala Pro Lys Pro Leu Pro Asp Gly Arg Gly Ser Thr Pro
                         55
                                             60
Leu Xaa Ser Arg Tyr Gln Arg Ser Val
                    70
(2) INFORMATION FOR SEQ ID NO:2012:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 212 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..212
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599732
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:
acaccettet actagageag etgagetgag agtgaeagea geggrssgea atggegeaga
                                                                         60
tgctcctcct cctcctcctc cttgccgcac ccacagtgcc agcgnaggca gcagccaccg
                                                                        120
cctccactcc gacgctcgtg ttcctcctgg ccgggcagtc caacatgggc ggccgcggcg
                                                                        180
gcgcgaccaa cggcacctgg gacggcgtgg tg
 (2) INFORMATION FOR SEQ ID NO:2013:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 70 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..70
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599733
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:
 His Pro Ser Thr Arg Ala Ala Glu Leu Arg Val Thr Ala Ala Xaa Xaa
                                     10
                 5
```

Asn Gly Ala Asp Ala Pro Pro Pro Pro Pro Pro Cys Arg Thr His Ser

25 Ala Ser Xaa Gly Ser Ser His Arg Leu His Ser Asp Ala Arg Val Pro 40 Pro Gly Arg Ala Val Gln His Gly Arg Pro Arg Arg Arg Asp Gln Arg His Leu Gly Arg Arg Gly 70 (2) INFORMATION FOR SEQ ID NO:2014: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..54 (D) OTHER INFORMATION: / Ceres Seq. ID 1599734 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014: Met Ala Gln Met Leu Leu Leu Leu Leu Leu Leu Ala Ala Pro Thr Val 10 5 Pro Ala Xaa Ala Ala Ala Thr Ala Ser Thr Pro Thr Leu Val Phe Leu 25 2.0 Leu Ala Gly Gln Ser Asn Met Gly Gly Arg Gly Gly Ala Thr Asn Gly 40 35 Thr Trp Asp Gly Val Val 50 (2) INFORMATION FOR SEQ ID NO:2015: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..51 (D) OTHER INFORMATION: / Ceres Seq. ID 1599735 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015: Met Leu Leu Leu Leu Leu Leu Ala Ala Pro Thr Val Pro Ala Xaa 10 Ala Ala Ala Thr Ala Ser Thr Pro Thr Leu Val Phe Leu Leu Ala Gly 25 2.0 Gln Ser Asn Met Gly Gly Arg Gly Gly Ala Thr Asn Gly Thr Trp Asp 35 Gly Val Val 50 (2) INFORMATION FOR SEQ ID NO:2016: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..147 (D) OTHER INFORMATION: / Ceres Seq. ID 1599740 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016: gaacaacgca gagaaaagaa aaccgctcca atccggaagc tgaaaatagc agaagaatcc agaggegaet ceaggtttgt eggegatget gegageggga ggeaggegge tmetegeeee

ggggeteegt eggeteggee tgggeac

- (2) INFORMATION FOR SEQ ID NO:2017:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..49
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599741
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

Glu Gln Arg Arg Glu Lys Lys Thr Ala Pro Ile Arg Lys Leu Lys Ile 1 5 10 15

Ala Glu Glu Ser Arg Gly Asp Ser Arg Phe Val Gly Asp Ala Ala Ser 20 25 30

Gly Arg Gln Ala Ala Xaa Arg Pro Gly Ala Pro Ser Ala Arg Pro Gly 35 40 45

His

- (2) INFORMATION FOR SEQ ID NO:2018:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..48
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599742
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

Thr Thr Gln Arg Lys Glu Asn Arg Ser Asn Pro Glu Ala Glu Asn Ser 1 10 15

Arg Arg Ile Gln Arg Arg Leu Gln Val Cys Arg Arg Cys Cys Glu Arg

Glu Ala Gly Gly Xaa Ser Pro Arg Gly Ser Val Gly Ser Ala Trp Ala 35 40 45

- (2) INFORMATION FOR SEQ ID NO:2019:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..381
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599746
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

attgattgt togogtoata ttaacgocag ggagggoott ttotetoto tgtgaacgoc 60
aaacagtgto tottttocag ttocagacot gaagaaacto cgaccggoog gtgggoggtg 120
geggcacggo aggatotgtg cogogatggo gacgtogaac acggoggga tggaggacgg
cggcggogac otgoggassa coatcaagaa gtggaatato atotacctg totacctoaa
ctocaagaag acggtogoog agggoogoog catcgoogt gccaaggoot gccaggaccc
cacctgoato gagatogotg actgotgtto gcacctoaag atoccocacg coatcgantt 360

ngaataaggc gtaccctcgg g
(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..73 (D) OTHER INFORMATION: / Ceres Seq. ID 1599747 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020: Met Ala Thr Ser Asn Thr Ala Arg Met Glu Asp Gly Gly Asp Leu 10 Arg Xaa Thr Ile Lys Lys Trp Asn Ile Ile Tyr Pro Val Tyr Leu Asn 25 Ser Lys Lys Thr Val Ala Glu Gly Arg Arg Ile Ala Ala Ala Lys Ala 40 Cys Pro Asp Pro Thr Cys Ile Glu Ile Ala Asp Cys Cys Ser His Leu 55 Lys Ile Pro His Ala Ile Xaa Xaa Glu 70 (2) INFORMATION FOR SEQ ID NO:2021: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..65 (D) OTHER INFORMATION: / Ceres Seq. ID 1599748 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021: Met Glu Asp Gly Gly Gly Asp Leu Arg Xaa Thr Ile Lys Lys Trp Asn 10 Ile Ile Tyr Pro Val Tyr Leu Asn Ser Lys Lys Thr Val Ala Glu Gly 25 2.0 Arg Arg Ile Ala Ala Ala Lys Ala Cys Pro Asp Pro Thr Cys Ile Glu 40 45 Ile Ala Asp Cys Cys Ser His Leu Lys Ile Pro His Ala Ile Xaa Xaa 55 50 Glu (2) INFORMATION FOR SEQ ID NO:2022: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..461 (D) OTHER INFORMATION: / Ceres Seq. ID 1599756 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022: geogeacece acgaetteeg teegagtetg ageteatete caegegeege egeegeeget cgacgcccac cgcgcmssca tggcggnaac agactgagaa ggctttcctc aagcagccta 120 aggtgttcct cagctcaaag aaatctggca agggtaagaa gccaggcaag ggtggcaatc 180 gattttggaa gagcattggc cttggtttca agactcccag ggaagcaatt gaagggacct 240 acattgacaa gaaatgtcca ttcactggaa ccgtttctat cagaggcaga attattgctg 300 gaacatgcca cagtgctaag atgaacagaa ccatcattgt tcgcaggaac tatctccact 360 ttgttaagaa ataccagagg tataaaagag gcactccaac attccagctc acatctcccc 420 atgcttccgt gtgaaggaag gcgaccatgt catcattggc c

(2) INFORMATION FOR SEQ ID NO:2023:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599757
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Ala Ala Pro His Asp Phe Arg Pro Ser Leu Ser Ser Ser Pro Arg Ala

Ala Ala Ala Arg Arg Pro Pro Arg Xaa His Gly Xaa Asn Arg Leu 20 25 30

Arg Arg Leu Ser Ser Ser Ser Leu Arg Cys Ser Ser Ala Gln Arg Asn

Leu Ala Arg Val Arg Ser Gln Ala Arg Val Ala Ile Asp Phe Gly Arg 50 55 60

Ala Leu Ala Leu Val Ser Arg Leu Pro Gly Lys Gln Leu Lys Gly Pro
70 75 80

Thr Leu Thr Arg Asn Val His Ser Leu Glu Pro Phe Leu Ser Glu Ala 85 90 95

Glu Leu Leu Glu His Ala Thr Val Leu Arg 100 105

- (2) INFORMATION FOR SEQ ID NO:2024:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599758
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

Arg Thr Pro Arg Leu Pro Ser Glu Ser Glu Leu Ile Ser Thr Arg Arg

Arg Arg Arg Ser Thr Pro Thr Ala Xaa Xaa Trp Arg Xaa Gln Thr Glu

20 25 30

Plantage Clar Pro Lyc Val Phe Leu Ser Ser Lys Lys Ser

Lys Ala Phe Leu Lys Gln Pro Lys Val Phe Leu Ser Ser Lys Lys Ser 35 40 45

Gly Lys Gly Lys Lys Pro Gly Lys Gly Gly Asn Arg Phe Trp Lys Ser 50 55 60

Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu Ala Ile Glu Gly Thr Tyr
65 70 75 80

Ile Asp Lys Lys Cys Pro Phe Thr Gly Thr Val Ser Ile Arg Gly Arg

Ile Ile Ala Gly Thr Cys His Ser Ala Lys Met Asn Arg Thr Ile Ile
100 105 110

Val Arg Arg Asn Tyr Leu His Phe Val Lys Lys Tyr Gln Arg Tyr Lys 115 120 125

Arg Gly Thr Pro Thr Phe Gln Leu Thr Ser Pro His Ala Ser Val 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2025:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..458
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025: agggaaccat cttcttcttc cccgcgctgc ctgctgcctg ctcgagcttg gagatggcgt 60 120 tggtgcggcg atgcctctgt ggatccgagg aagactgcag agcgcttttg ggcatggaaa atctccggct gttctcctac agagagatca gagcaggcac aaacaacttc gatcagagta 180 acaagcttgg acgaggtggt tttggaactg tctacaaggg agttctaaga gacggcactg 240 300 aatttgccgc gaaggttctg tcctcggaat ccgagcaggg gatcaaggag ttcctagctg agatogagag catotoccag gtgaagcacg cgaacctogt caggetgotg ggctgctgcg 360 420 tgcagaggaa aaaaaggatc ctggtgtacg agtaccttgc gaacaacagc ctcgatcatg cgctcaaagg agcagcagca gatctaccct ggagcacg
- (2) INFORMATION FOR SEQ ID NO: 2026:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599771
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:
- Gly Thr Ile Phe Phe Pro Ala Leu Pro Ala Ala Cys Ser Ser Leu 10
- Glu Met Ala Leu Val Arg Arg Cys Leu Cys Gly Ser Glu Glu Asp Cys 20 25
- Arg Ala Leu Leu Gly Met Glu Asn Leu Arg Leu Phe Ser Tyr Arg Glu
- Ile Arg Ala Gly Thr Asn Asn Phe Asp Gln Ser Asn Lys Leu Gly Arg 55
- Gly Gly Phe Gly Thr Val Tyr Lys Gly Val Leu Arg Asp Gly Thr Glu 70 75
- Phe Ala Ala Lys Val Leu Ser Ser Glu Ser Glu Gln Gly Ile Lys Glu 90 8.5
- Phe Leu Ala Glu Ile Glu Ser Ile Ser Gln Val Lys His Ala Asn Leu 105 100
- Val Arg Leu Leu Gly Cys Cys Val Gln Arg Lys Lys Arg Ile Leu Val 120 125
- Tyr Glu Tyr Leu Ala Asn Asn Ser Leu Asp His Ala Leu Lys Gly Ala 140 135
- Ala Ala Asp Leu Pro Trp Ser Thr 150
- (2) INFORMATION FOR SEQ ID NO:2027:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599772
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

180

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
Met Ala Leu Val Arg Cys Leu Cys Gly Ser Glu Glu Asp Cys Arg
                                    10
Ala Leu Leu Gly Met Glu Asn Leu Arg Leu Phe Ser Tyr Arg Glu Ile
                                25
            2.0
Arg Ala Gly Thr Asn Asn Phe Asp Gln Ser Asn Lys Leu Gly Arg Gly
                            40
Gly Phe Gly Thr Val Tyr Lys Gly Val Leu Arg Asp Gly Thr Glu Phe
                        55
Ala Ala Lys Val Leu Ser Ser Glu Ser Glu Gln Gly Ile Lys Glu Phe
                                        75
                    70
Leu Ala Glu Ile Glu Ser Ile Ser Gln Val Lys His Ala Asn Leu Val
                85
                                    90
Arg Leu Leu Gly Cys Cys Val Gln Arg Lys Lys Arg Ile Leu Val Tyr
                                                   110
                                105
            100
Glu Tyr Leu Ala Asn Asn Ser Leu Asp His Ala Leu Lys Gly Ala Ala
                            120
       115
Ala Asp Leu Pro Trp Ser Thr
                       135
    130
(2) INFORMATION FOR SEQ ID NO:2028:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 115 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
           (B) LOCATION: 1..115
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599773
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:
Met Glu Asn Leu Arg Leu Phe Ser Tyr Arg Glu Ile Arg Ala Gly Thr
                                     10
            5
Asn Asn Phe Asp Gln Ser Asn Lys Leu Gly Arg Gly Gly Phe Gly Thr
                                 25
 Val Tyr Lys Gly Val Leu Arg Asp Gly Thr Glu Phe Ala Ala Lys Val
                             40
```

Leu Ser Ser Glu Ser Glu Gln Gly Ile Lys Glu Phe Leu Ala Glu Ile 5.5 Glu Ser Ile Ser Gln Val Lys His Ala Asn Leu Val Arg Leu Leu Gly 75 70 Cys Cys Val Gln Arg Lys Lys Arg Ile Leu Val Tyr Glu Tyr Leu Ala

90 Asn Asn Ser Leu Asp His Ala Leu Lys Gly Ala Ala Ala Asp Leu Pro

105

Trp Ser Thr

115

- (2) INFORMATION FOR SEQ ID NO: 2029:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..431
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029: gactgggatg tggatgcccc gatggaaatt gtggatgatg aagccaccaa gcctgaggga tggttggatg atgaacctga ggagattgat gatcctgagg cagccaatcc tgaggactgg gacgatgagg aggatggtga atgggaggcg ccaaagattg acaaccccaa gtgtgaagag

gcacctggat gtggcgagtg gaagaggcca atgaagcaga atcetgetta caagggcaag 240 tggcatgcae ctatgattga caaccccaac tacaagggaa tetggaagce teaggagate 300 eccaaccetg agtactttga gettgacaag cetgactttg atceaattge tgetattggg attgagatet ggacaatgca ggatggcate etgtttgaca atatettgat tgetgacgat 420 nagaaggttg c

- (2) INFORMATION FOR SEQ ID NO:2030:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

Asp Trp Asp Val Asp Ala Pro Met Glu Ile Val Asp Asp Glu Ala Thr 1 5 10 15

Lys Pro Glu Gly Trp Leu Asp Asp Glu Pro Glu Glu Ile Asp Asp Pro 20 25 30

Glu Ala Ala Asn Pro Glu Asp Trp Asp Asp Glu Glu Asp Gly Glu Trp 35 40 45

Glu Ala Pro Lys Ile Asp Asn Pro Lys Cys Glu Glu Ala Pro Gly Cys 50 55 60

Gly Glu Trp Lys Arg Pro Met Lys Gln Asn Pro Ala Tyr Lys Gly Lys 65 70 75 80

Trp His Ala Pro Met Ile Asp Asn Pro Asn Tyr Lys Gly Ile Trp Lys 85 90 95

Pro Gln Glu Ile Pro Asn Pro Glu Tyr Phe Glu Leu Asp Lys Pro Asp 100 105 110

Phe Asp Pro Ile Ala Ala Ile Gly Ile Glu Ile Trp Thr Met Gln Asp 115 120 125

- Gly Ile Leu Phe Asp Asn Ile Leu Ile Ala Asp Asp Xaa Lys Val
- (2) INFORMATION FOR SEQ ID NO:2031:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599797
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

Met Glu Ile Val Asp Asp Glu Ala Thr Lys Pro Glu Gly Trp Leu Asp
1 10 15

Asp Glu Pro Glu Glu Ile Asp Asp Pro Glu Ala Ala Asn Pro Glu Asp 20 25 30

Trp Asp Asp Glu Glu Asp Gly Glu Trp Glu Ala Pro Lys Ile Asp Asn 35 40 45

Pro Lys Cys Glu Glu Ala Pro Gly Cys Gly Glu Trp Lys Arg Pro Met
50 55 60

Lys Gln Asn Pro Ala Tyr Lys Gly Lys Trp His Ala Pro Met Ile Asp 70 75 80

Asn Pro Asn Tyr Lys Gly Ile Trp Lys Pro Gln Glu Ile Pro Asn Pro 85 90 95

Glu Tyr Phe Glu Leu Asp Lys Pro Asp Phe Asp Pro Ile Ala Ala Ile 100 105 110

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Gly Ile Glu Ile Trp Thr Met Gln Asp Gly Ile Leu Phe Asp Asn Ile
                            120
Leu Ile Ala Asp Asp Xaa Lys Val
                        135
    130
(2) INFORMATION FOR SEQ ID NO:2032:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 73 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..73
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599798
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:
Met Lys Gln Asn Pro Ala Tyr Lys Gly Lys Trp His Ala Pro Met Ile
                                     10
                5
Asp Asn Pro Asn Tyr Lys Gly Ile Trp Lys Pro Gln Glu Ile Pro Asn
                                                     30
            2.0
Pro Glu Tyr Phe Glu Leu Asp Lys Pro Asp Phe Asp Pro Ile Ala Ala
                            40
                                                 45
        35
Ile Gly Ile Glu Ile Trp Thr Met Gln Asp Gly Ile Leu Phe Asp Asn
                                             60
                        55
Ile Leu Ile Ala Asp Asp Xaa Lys Val
                    70
(2) INFORMATION FOR SEQ ID NO:2033:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 210 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..210
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599813
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:
gcaccaaaaa cccaagcctc ctctgccaca cacacctcgc cagcaccaca gccaccgcca
                                                                         60
bsntcacaca gtcagcgaga gagagcatgg acctgctgaa ccccgagcag atctccgagt
                                                                        120
tccgggaggc gttcgcgttc ttcgacaagg acggcgacgg gtgcatcacg gtggaggagc
                                                                        180
tggcgacggt gatggggtcg ctgcaggggc
 (2) INFORMATION FOR SEQ ID NO: 2034:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 69 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..69
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599814
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:
 His Gln Lys Pro Lys Pro Pro Leu Pro His Thr Pro Arg Gln His His
                                     10
                 5
 Ser His Arg Xaa Xaa His Thr Val Ser Glu Arg Glu His Gly Pro Ala
                                  25
                                                      30
             20
 Glu Pro Arg Ala Asp Leu Arg Val Pro Gly Gly Val Arg Val Leu Arg
                             40
 Gln Gly Arg Arg Val His His Gly Gly Gly Ala Gly Asp Gly Asp
```

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60
                        55
    50
Gly Val Ala Ala Gly
(2) INFORMATION FOR SEQ ID NO:2035:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..69
          (D) OTHER INFORMATION: / Ceres Seq. ID 1599815
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:
Thr Lys Asn Pro Ser Leu Leu Cys His Thr His Leu Ala Ser Thr Thr
                                     10
                5
Ala Thr Ala Xaa Xaa Thr Gln Ser Ala Arg Glu Ser Met Asp Leu Leu
                                                     30
                                 25
            2.0
Asn Pro Glu Gln Ile Ser Glu Phe Arg Glu Ala Phe Ala Phe Phe Asp
                                                 4.5
                            40
Lys Asp Gly Asp Gly Cys Ile Thr Val Glu Glu Leu Ala Thr Val Met
                         55
    50
Gly Ser Leu Gln Gly
65
(2) INFORMATION FOR SEQ ID NO:2036:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 41 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..41
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599816
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:
Met Asp Leu Leu Asn Pro Glu Gln Ile Ser Glu Phe Arg Glu Ala Phe
                                     10
                 5
Ala Phe Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Val Glu Glu Leu
                                 25
             20
 Ala Thr Val Met Gly Ser Leu Gln Gly
 (2) INFORMATION FOR SEQ ID NO:2037:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 459 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..459
           (D) OTHER INFORMATION: / Ceres Seq. ID 1599829
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:
 acaggacgac ccaagcaagc aagcaagcag cgagtacata catactaggc agccaggcag
 ccatggcgcc caccgtgatg atggcctcgt cggccaccgc cgtcgctccg ttccaggggc
                                                                         120
 tcaagtccac cgccagcctc cccatcgccc gccgctcctc cagaagcctc ggcaacgtca
                                                                         240
 gcaacggcgg aaggatccgg tgcatgcagg tgtggccggc ctacggsaac aagaagttcg
 agacgctgtc gtacctgccg ccgctgtcga cggacgacct gctgaagcag tggactacct
                                                                         300
 getgegeaac ggetggatac cetgeetega gtteagearg gteggetteg tgtacegega
                                                                         360
```

gaactecace teecegtget actaegaegg eegetaetgg accatetsga agetgeecat 420 gtteggetge aaegaegeea eeeaggtgta eaaggatet

- (2) INFORMATION FOR SEQ ID NO:2038:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599830
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

Gln Asp Asp Pro Ser Lys Gln Ala Ser Ser Glu Tyr Ile His Thr Arg
1 5 10 15

Gln Pro Gly Ser His Gly Ala His Arg Asp Asp Gly Leu Val Gly His 20 25 30

Arg Arg Arg Ser Val Pro Gly Ala Gln Val His Arg Gln Pro Pro His 35 40 45

Arg Pro Pro Leu Leu Gln Lys Pro Arg Gln Arg Gln Gln Arg Arg Lys
50 55 60

Asp Pro Val His Ala Gly Val Ala Gly Leu Arg Xaa Gln Glu Val Arg

Asp Ala Val Val Pro Ala Ala Val Asp Gly Arg Pro Ala Glu Ala 85 90 95

Val Asp Tyr Leu Leu Arg Asn Gly Trp Ile Pro Cys Leu Glu Phe Ser 100 105 110

Xaa Val Gly Phe Val Tyr Arg Glu Asn Ser Thr Ser Pro Cys Tyr Tyr 115 120 125

Asp Gly Arg Tyr Trp Thr Ile Xaa Lys Leu Pro Met Phe Gly Cys Asn 130 135 140

Asp Ala Thr Gln Val Tyr Lys Asp 145 150

- (2) INFORMATION FOR SEQ ID NO:2039:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

Arg Thr Thr Gln Ala Ser Lys Gln Ala Ala Ser Thr Tyr Ile Leu Gly
1 5 10 15

Ser Gln Ala Ala Met Ala Pro Thr Val Met Met Ala Ser Ser Ala Thr
20
25
30
30

Ala Val Ala Pro Phe Gln Gly Leu Lys Ser Thr Ala Ser Leu Pro Ile 35 40 45

Ala Arg Arg Ser Ser Arg Ser Leu Gly Asn Val Ser Asn Gly Gly Arg 50 55 60

Ile Arg Cys Met Gln Val Trp Pro Ala Tyr Xaa Asn Lys Lys Phe Glu 65 70 75 80

Thr Leu Ser Tyr Leu Pro Pro Leu Ser Thr Asp Asp Leu Leu Lys Gln 85 90 95

Trp Thr Thr Cys Cys Ala Thr Ala Gly Tyr Pro Ala Ser Ser Ser Ala 100 105 110

Xaa Ser Ala Ser Cys Thr Ala Arg Thr Pro Pro Pro Arg Ala Thr Thr

120 115 Thr Ala Ala Thr Gly Pro Ser Xaa Ser Cys Pro Cys Ser Ala Ala Thr 140 135 Thr Pro Pro Arg Cys Thr Arg Ile 150 145 (2) INFORMATION FOR SEQ ID NO:2040: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..132 (D) OTHER INFORMATION: / Ceres Seq. ID 1599832 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040: Met Ala Pro Thr Val Met Met Ala Ser Ser Ala Thr Ala Val Ala Pro 10 5 Phe Gln Gly Leu Lys Ser Thr Ala Ser Leu Pro Ile Ala Arg Arg Ser 25 20 Ser Arg Ser Leu Gly Asn Val Ser Asn Gly Gly Arg Ile Arg Cys Met 40 Gln Val Trp Pro Ala Tyr Xaa Asn Lys Lys Phe Glu Thr Leu Ser Tyr 55 Leu Pro Pro Leu Ser Thr Asp Asp Leu Leu Lys Gln Trp Thr Thr Cys 75 70 Cys Ala Thr Ala Gly Tyr Pro Ala Ser Ser Ser Ala Xaa Ser Ala Ser 90 85 Cys Thr Ala Arg Thr Pro Pro Pro Arg Ala Thr Thr Thr Ala Ala Thr 105 100 Gly Pro Ser Xaa Ser Cys Pro Cys Ser Ala Ala Thr Thr Pro Pro Arg 120 115-Cys Thr Arg Ile 130 (2) INFORMATION FOR SEQ ID NO:2041: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 350 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..350 (D) OTHER INFORMATION: / Ceres Seq. ID 1599833 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041: gegageaace eggegaaase eeccaaacee tegeaceeta aaacagegge geacaagatg tecgaegace ceaecaaegg eggeggeggt gategegtgg aggaegtegt egegeegagg 120 gtgaaacaca acctcgtgat gatggcttsn tcgaaatcca aggataggga caaagataga 180 240 gaaarggaca aggacagaga tcgtcgccga gaccgtgaca gagatcgagg gagagacagg 300 gaccgtgata gggataggga cagggacagg gatcgggaca gagacaagga tcgccaaagt aggcatcacc gtnaaanacg ggaacagcga gaccgtccts atgatcacag (2) INFORMATION FOR SEQ ID NO:2042: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

Ala Ser Asn Pro Ala Lys Xaa Pro Lys Pro Ser His Pro Lys Thr Ala 5 10

Ala His Lys Met Ser Asp Asp Pro Thr Asn Gly Gly Gly Asp Arg 25 20

Val Glu Asp Val Val Ala Pro Arg Val Lys His Asn Leu Val Met Met 40 35

Ala Xaa Ser Lys Ser Lys Asp Arg Asp Lys Asp Arg Glu Xaa Asp Lys 60

Asp Arg Asp Arg Arg Asp Arg Asp Arg Asp Arg Gly Arg Asp Arg 75 70

Asp Arg Asp Lys 90 8.5

Asp Arg Gln Ser Arg His His Arg Xaa Xaa Arg Glu Gln Arg Asp Arg 105 100

Pro Xaa Asp His

115

- (2) INFORMATION FOR SEQ ID NO:2043:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

Met Ser Asp Asp Pro Thr Asn Gly Gly Gly Asp Arg Val Glu Asp 10 5

Val Val Ala Pro Arg Val Lys His Asn Leu Val Met Met Ala Xaa Ser 25 30

Lys Ser Lys Asp Arg Asp Lys Asp Arg Glu Xaa Asp Lys Asp Arg Asp 40

Arg Arg Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp 55

Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Lys Asp Arg Gln 75 70

Ser Arg His His Arg Xaa Xaa Arg Glu Gln Arg Asp Arg Pro Xaa Asp 90

His

- (2) INFORMATION FOR SEQ ID NO: 2044:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

Met Met Ala Xaa Ser Lys Ser Lys Asp Arg Asp Lys Asp Arg Glu Xaa 10 Asp Lys Asp Arg Asp Arg Arg Arg Asp Arg Asp Arg Asp Arg Gly Arg

120

180

240

300

360

Client Docket No. 80146.003 25 30 20 Asp Arg 4.5 40 Asp Lys Asp Arg Gln Ser Arg His His Arg Xaa Xaa Arg Glu Gln Arg 55 Asp Arg Pro Xaa Asp His 70 (2) INFORMATION FOR SEQ ID NO: 2045: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 411 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..411 (D) OTHER INFORMATION: / Ceres Seq. ID 1599853 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045: aaaaagctac agcatctgct cgttcgtcta gcttgggcgg tggaccgaca gaccagccag ctagatggcg cgcagggcgg tcggcgttct cctggccgtg gcgcgctctt cgcgsggccg cgagggcagc agacgacgac gacaagacgc agccctggca gtgcttcagg tcatgctcca gaggetgeca ecaceaceae gaceaegaee aegaeaaegg egetgetgee gtggeggaet tecteteegg ggeegeegee aaggteteeg eegeegteae eegegagtge aagaacaaca gctgccatga caacgcgtgc ttcaaggacc tsccggccat cacctacccg cagtgcgcca tcgccacctg cctcagcctt ccgcaccata gcaaanaraa cggcgtcctt c (2) INFORMATION FOR SEQ ID NO:2046: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..137 (D) OTHER INFORMATION: / Ceres Seq. ID 1599854 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046: Lys Lys Leu Gln His Leu Leu Val Arg Leu Ala Trp Ala Val Asp Arg 10 5 Gln Thr Ser Gln Leu Asp Gly Ala Gln Gly Gly Arg Arg Ser Pro Gly 2.5 Arg Gly Ala Leu Phe Ala Xaa Pro Arg Gly Gln Gln Thr Thr Thr Thr 40 Arg Arg Ser Pro Gly Ser Ala Ser Gly His Ala Pro Glu Ala Ala Thr 55 Thr Thr Thr Thr Thr Thr Thr Thr Ala Leu Leu Pro Trp Arg Thr 75 70 Ser Ser Pro Gly Pro Pro Pro Arg Ser Pro Pro Pro Ser Pro Ala Ser 90 85 Ala Arg Thr Thr Ala Ala Met Thr Thr Arg Ala Ser Arg Thr Xaa Arg 110 105 100 Pro Ser Pro Thr Arg Ser Ala Pro Ser Pro Pro Ala Ser Ala Phe Arg 120 Thr Ile Ala Xaa Xaa Thr Ala Ser Phe 135

- (2) INFORMATION FOR SEQ ID NO: 2047:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:
- Lys Ala Thr Ala Ser Ala Arg Ser Ser Ser Leu Gly Gly Pro Thr 1 5 10 15
- Asp Gln Pro Ala Arg Trp Arg Ala Gly Arg Ser Ala Phe Ser Trp Pro 20 25 30
- Trp Arg Ala Leu Arg Xaa Ala Ala Arg Ala Ala Asp Asp Asp Lys
 35 40 45
- Thr Gln Pro Trp Gln Cys Phe Arg Ser Cys Ser Arg Gly Cys His His
- His His Asp His Asp His Asp Asn Gly Ala Ala Ala Val Ala Asp Phe 65 70 75 80
- Leu Ser Gly Ala Ala Ala Lys Val Ser Ala Ala Val Thr Arg Glu Cys 85 90 95
- Lys Asn Asn Ser Cys His Asp Asn Ala Cys Phe Lys Asp Xaa Pro Ala 100 105 110
- Ile Thr Tyr Pro Gln Cys Ala Ile Ala Thr Cys Leu Ser Leu Pro His 115 120 125
- His Ser Lys Xaa Asn Gly Val Leu 130 135
- (2) INFORMATION FOR SEQ ID NO:2048:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599856
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:
- Met Ala Arg Arg Ala Val Gly Val Leu Leu Ala Val Ala Arg Ser Ser 1 1 5 15
- Xaa Gly Arg Glu Gly Ser Arg Arg Arg Gln Asp Ala Ala Leu Ala 20 25 30
- Val Leu Gln Val Met Leu Gln Arg Leu Pro Pro Pro Pro Arg Pro Arg 35 40 45
- Pro Arg Gln Arg Arg Cys Cys Arg Gly Gly Leu Pro Leu Arg Gly Arg 50 55 60
- Arg Gln Gly Leu Arg Arg Arg His Pro Arg Val Gln Glu Gln Gln Leu 65 75 80
- (2) INFORMATION FOR SEQ ID NO:2049:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..457
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599861
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

acacaccacc accgctgctg ctcgccctca tacatatata accggagcta gaagctcgtc tctgccacca aggagggcct gaagctggac gagagtgagg atgagaagaa gcgcaaggag gageteaagg agaagtttga gggeetetge aaggteatea aggaggtget gggegaeaag 240 gtggagaagg tggtggtctc cgacgcgtgg tggactcccc ctgctgcctg gtgaccggcg agtacggttg gaccgccaac atggagcgga tcatgaaagc ccaggcgctg agggactcca gcatgtctgg gtacatgtcc tccaagaaga cgatggagat caaccccgag aacgccatca tggaggaget ccgcaagegt gccgaggetg acaagaacga caagtccgtt aaggacettn 420 tcatgctgct gttcgagacg gcgctgctca cttctgg

- (2) INFORMATION FOR SEQ ID NO:2050:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599862
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050: Met Arg Arg Ser Ala Arg Arg Ser Ser Arg Arg Ser Leu Arg Ala Ser 10 5 Ala Arg Ser Ser Arg Arg Cys Trp Ala Thr Arg Trp Arg Arg Trp Trp 25 2.0 Ser Pro Thr Arg Gly Gly Leu Pro Leu Leu Pro Gly Asp Arg Arg Val 40 Arg Leu Asp Arg Gln His Gly Ala Asp His Glu Ser Pro Gly Ala Glu 60 55
- Gly Leu Gln His Val Trp Val His Val Leu Gln Glu Asp Asp Gly Asp 70 75 Gln Pro Arg Glu Arg His His Gly Gly Ala Pro Gln Ala Cys Arg Gly
- 90 85
- (2) INFORMATION FOR SEQ ID NO: 2051:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..65
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599863
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:
- Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met Ser 5 10
- Gly Tyr Met Ser Ser Lys Lys Thr Met Glu Ile Asn Pro Glu Asn Ala 30 25
- Ile Met Glu Glu Leu Arg Lys Arg Ala Glu Ala Asp Lys Asn Asp Lys 40 4.5
- Ser Val Lys Asp Leu Xaa Met Leu Leu Phe Glu Thr Ala Leu Leu Thr 55

Ser 65

- (2) INFORMATION FOR SEQ ID NO: 2052:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..61 (D) OTHER INFORMATION: / Ceres Seq. ID 1599864 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052: Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met Ser Gly Tyr Met Ser 10 5 Ser Lys Lys Thr Met Glu Ile Asn Pro Glu Asn Ala Ile Met Glu Glu 30 25 2.0 Leu Arg Lys Arg Ala Glu Ala Asp Lys Asn Asp Lys Ser Val Lys Asp 40 35 Leu Xaa Met Leu Leu Phe Glu Thr Ala Leu Leu Thr Ser 55 (2) INFORMATION FOR SEQ ID NO:2053: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 287 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..287 (D) OTHER INFORMATION: / Ceres Seq. ID 1599885 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053: gatctgagga aatcgtcctt gagaccggag ctgtacacgc cagcctacgg aggcttcttt gagctggacc tggagaagga aaagacggtg gtatctctga gaactttgat cgatcgctct 120 geggtggaga getteggtgg aggeggeagg gtgtgeatea tggeeegggt etateeggeg 180 gegetegteg acgaegege actegeatgt acgegtteaa caatggeact ageacegtea 240 gagtgccccg gctagaagcg tggagcatga ggagggcaca ggttaac (2) INFORMATION FOR SEQ ID NO:2054: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..84 (D) OTHER INFORMATION: / Ceres Seq. ID 1599886 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054: Asp Leu Arg Lys Ser Ser Leu Arg Pro Glu Leu Tyr Thr Pro Ala Tyr 10 5 1. Gly Gly Phe Phe Glu Leu Asp Leu Glu Lys Glu Lys Thr Val Val Ser 30 25 2.0 Leu Arg Thr Leu Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly 4.5 40 35 Gly Arg Val Cys Ile Met Ala Arg Val Tyr Pro Ala Ala Leu Val Asp 55 60 Asp Ala Ala Leu Ala Cys Thr Arg Ser Thr Met Ala Leu Ala Pro Ser

75

(2) INFORMATION FOR SEQ ID NO:2055:

Glu Cys Pro Gly

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid

70

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..332
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599891
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055: taacagtact tgtggtggca tttatgttac aggatggcac tgcgaactac ttgaaaggac 60 120 ttatgctgat cctatgttat ctaatagttg ctgccagttt ctttgttcac gttgatccac 180 aatcaagtga aggctgaagc catatatcct gtaagtaacg cgccaaatac cttttgagac ttaataatct tgttttgttc cgcctgtctc aagccgggtt ccttcatgaa ctgcagaagg 240

aatttttgta ttttgttttg tggatactga tgtgtactag ggtantctcg atgtatacag aaacaagaag tggcagcatg ttatattcga tt

- (2) INFORMATION FOR SEQ ID NO: 2056: (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..37
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599892
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

Asn Ser Thr Cys Gly Gly Ile Tyr Val Thr Gly Trp His Cys Glu Leu 10 5

Leu Glu Arg Thr Tyr Ala Asp Pro Met Leu Ser Asn Ser Cys Cys Gln 20

Phe Leu Cys Ser Arg 35

- (2) INFORMATION FOR SEQ ID NO: 2057:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..44
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599893
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

Thr Val Leu Val Val Ala Phe Met Leu Gln Asp Gly Thr Ala Asn Tyr 10 5

Leu Lys Gly Leu Met Leu Ile Leu Cys Tyr Leu Ile Val Ala Ala Ser 25 20

Phe Phe Val His Val Asp Pro Gln Ser Ser Glu Gly 4.0

- (2) INFORMATION FOR SEQ ID NO:2058:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..37
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599894
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

Met Leu Gln Asp Gly Thr Ala Asn Tyr Leu Lys Gly Leu Met Leu Ile 10 Leu Cys Tyr Leu Ile Val Ala Ala Ser Phe Phe Val His Val Asp Pro 25 20 Gln Ser Ser Glu Gly 35 (2) INFORMATION FOR SEQ ID NO: 2059: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..354 (D) OTHER INFORMATION: / Ceres Seq. ID 1599910 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059: geggaasstg tecagatege gtgatteege atecegtteg ckakegegae acaegetgae 60 120 agetcacgge tgacettece gagtcccgae ggectecage tecatettga ttettgagge gavsccggtg cgtaagagtc tgccatggcc agcgagaata aggtctttgg gttcgaggaa 180 gtegecaage acaaegteae caaggaetne tggateatea tegeeggeaa ggtgtatgae 240 300 gtcactccgt ttatggatga gcatcctggt ggagacgagg ttttgctagc tgtaactggg aaagatgcta cagctgattt cgaagatatt ggccacagtg attccrcaaw ggac (2) INFORMATION FOR SEQ ID NO:2060: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..70 (D) OTHER INFORMATION: / Ceres Seq. ID 1599911 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060: Met Ala Ser Glu Asn Lys Val Phe Gly Phe Glu Glu Val Ala Lys His 10 5 1 Asn Val Thr Lys Asp Xaa Trp Ile Ile Ile Ala Gly Lys Val Tyr Asp 25 Val Thr Pro Phe Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu 40 Ala Val Thr Gly Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His 55 Ser Asp Ser Xaa Xaa Asp 70 (2) INFORMATION FOR SEQ ID NO: 2061: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

gggccctcc gcacgcctgc acacattccg cgcacacccc ggcagccgca aacgccttcg
ccgtcgcgtc ccgctcctcc gcccgcccga cgcgacccct aggacctgga gagagaggtc
ggcatggctg ccgcagtggt cgacgacgct ggtatggacg ccgtccagaa gcgcctcatg

180

(D) OTHER INFORMATION: / Ceres Seq. ID 1599912

(B) LOCATION: 1..385

ttcgaagacg aatgcatttt ggtggacgag taggacaatg ttgttggcca tgagtcaaag 240 tacaactgcc atttgatgga aaagattgat tctgagaatc tgctacatag ggcattcagt 300 gtgttccttt tcaactcaar aatkatgagc tgctacttca gcaaaggtcc gcgacaragg 360 ttacctttss ctttagttgt ggacc

- (2) INFORMATION FOR SEQ ID NO: 2062:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599913
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Gly Pro Ser Ala Arg Leu His Thr Phe Arg Ala His Pro Gly Ser Arg
1 10 15

Lys Arg Leu Arg Arg Arg Val Pro Leu Leu Arg Pro Pro Asp Ala Thr

Pro Arg Thr Trp Arg Glu Arg Ser Ala Trp Leu Pro Gln Trp Ser Thr

Thr Leu Val Trp Thr Pro Ser Arg Ser Ala Ser Cys Ser Lys Thr Asn

Ala Phe Trp Trp Thr Ser Arg Thr Met Leu Leu Ala Met Ser Gln Ser 65 70 75 80

Thr Thr Ala Ile

- (2) INFORMATION FOR SEQ ID NO: 2063:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..76
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599914
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

Ala Pro Pro His Ala Cys Thr His Ser Ala His Thr Pro Ala Ala Ala 1 5 10 15

Asn Ala Phe Ala Val Ala Ser Arg Ser Ser Ala Arg Pro Thr Arg Pro 20 25 30

Leu Gly Pro Gly Glu Arg Gly Arg His Gly Cys Arg Ser Gly Arg Arg 35 40 45

Arg Trp Tyr Gly Arg Arg Pro Glu Ala Pro His Val Arg Arg Met 50 55 60

His Phe Gly Gly Arg Val Gly Gln Cys Cys Trp Pro 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2064:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..43
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599915

Client Docket No. 80146.003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064: Met Glu Lys Ile Asp Ser Glu Asn Leu Leu His Arg Ala Phe Ser Val 10 Phe Leu Phe Asn Ser Xaa Xaa Met Ser Cys Tyr Phe Ser Lys Gly Pro 25 Arg Xaa Arg Leu Pro Xaa Xaa Leu Val Val Asp 35 (2) INFORMATION FOR SEQ ID NO: 2065: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..474 (D) OTHER INFORMATION: / Ceres Seq. ID 1599942 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065: gattctccaa atcctagtag ccgtccgcgc aaaaccctcc ctgctcagac tcgtctgctg cagetectee teegeegeeg tateaaaege acteteette gsngeegtat caaaeteaet 120 180 ctccttcgcy gccgtatcaa acgcactctc ctccgcgngc cgcccgaggc aagatggttc tecagaaega categaeett eteaaeeege eggeagaget egagaagete aageaeaaga 240 agaagcgcct cgtccagtcc cccaactcat tcttcatgga tgtcaagtgc cagggatgct 300 tcagcataac cacggttttc agccactccc agactgttgt tgtgtgccca ggctgccaaa 360 ctgttctctg ccagcccacg ggaggaaagg cgaggctcac ggagggctgc tctttccgcc 420 ggaagggaga ctagagcgag tctgttatta gtactggatc ggttgtsaat ctcc (2) INFORMATION FOR SEQ ID NO:2066: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..102 (D) OTHER INFORMATION: / Ceres Seq. ID 1599943 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066: Asp Ser Pro Asn Pro Ser Ser Arg Pro Arg Lys Thr Leu Pro Ala Gln 1.0 5 Thr Arg Leu Leu Gln Leu Leu Arg Arg Arg Ile Lys Arg Thr Leu 25 Leu Xaa Xaa Arg Ile Lys Leu Thr Leu Leu Arg Xaa Arg Ile Lys Arg 45 40 Thr Leu Leu Arg Xaa Pro Pro Glu Ala Arg Trp Phe Ser Arg Thr Thr 60 55 Ser Thr Phe Ser Thr Arg Arg Gln Ser Ser Arg Ser Ser Ser Thr Arg 75 70 Arg Ser Ala Ser Ser Ser Pro Pro Thr His Ser Ser Trp Met Ser Ser 90 Ala Arg Asp Ala Ser Ala 100 (2) INFORMATION FOR SEQ ID NO:2067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

Ile Leu Gln Ile Leu Val Ala Val Arg Ala Lys Pro Ser Leu Leu Arg
1 5 10 15

Leu Val Cys Cys Ser Ser Ser Ser Ala Ala Val Ser Asn Ala Leu Ser 20 25 30

Phe Xaa Ala Val Ser Asn Ser Leu Ser Phe Xaa Ala Val Ser Asn Ala 35 40 45

Leu Ser Ser Ala Xaa Arg Pro Arg Gln Asp Gly Ser Pro Glu Arg His 50 55 60

Arg Pro Ser Gln Pro Ala Gly Arg Ala Arg Glu Ala Gln Ala Gln Glu 65 70 75 80

Glu Ala Pro Arg Pro Val Pro Gln Leu Ile Leu His Gly Cys Gln Val 85 90 95

Cys Cys Val Pro Arg Leu Pro As
n Cys Ser Leu Pro Ala His Gly Arg 115 120 125

Lys Gly Glu Ala His Gly Gly Leu Leu Phe Pro Pro Glu Gly Arg Leu 130 135 140

Glu Arg Val Cys Tyr

145

- (2) INFORMATION FOR SEQ ID NO:2068:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599945
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser 20 25 30

Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Val 35 40 45

Phe Ser His Ser Gln Thr Val Val Cys Pro Gly Cys Gln Thr Val 50 55 60

Leu Cys Gln Pro Thr Gly Gly Lys Ala Arg Leu Thr Glu Gly Cys Ser 70 75 80

Phe Arg Arg Lys Gly Asp 85

- (2) INFORMATION FOR SEQ ID NO: 2069:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..428
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599954
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

cttccaccac gcagtcactc cogggeogoc gcogcogocg cotcogogaa aaaccctagc

aggettegeg etateactee aaggggegeg accatggtgg ecacaaagaa gacgaagaaa 120 teeacggaca acateaataa eaagetgeag ettgttatga agagtggeaa gtacaetete 180 ggetacaaga eegteeteag gacteteagg aactetaagt egaagetagt gateateget 240 aacaaetgee egeceetteg taagtsstga aattgagtae tatgetatge tggecaaggt eaetggetege eaetgeege ttattgatee tggtnattet gatacatea agaetaeaee 420 gggtgage

- (2) INFORMATION FOR SEQ ID NO:2070:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599955
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

Leu Pro Pro Arg Ser His Ser Arg Ala Ala Ala Ala Ala Ala Ser Ala
1 10 15

Lys Asn Pro Ser Arg Leu Arg Ala Ile Thr Pro Arg Gly Ala Thr Met 20 25 30

Val Ala Thr Lys Lys Thr Lys Lys Ser Thr Asp Asn Ile Asn Asn Lys
35 40 45

Leu Gln Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Thr

Val Leu Arg Thr Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile Ala 65 70 75 80

Asn Asn Cys Pro Pro Leu Arg Lys Xaa 85

- (2) INFORMATION FOR SEQ ID NO:2071:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..52
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599956
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

Phe His His Ala Val Thr Pro Gly Pro Pro Pro Pro Pro Pro Pro Arg
1 5 10 15

Lys Thr Leu Ala Gly Phe Ala Leu Ser Leu Gln Gly Ala Arg Pro Trp 20 25 30

Trp Pro Gln Arg Arg Arg Arg Asn Pro Arg Thr Thr Ser Ile Thr Ser 35 40 45

Cys Ser Leu Leu

50

- (2) INFORMATION FOR SEQ ID NO:2072:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..58

- (D) OTHER INFORMATION: / Ceres Seq. ID 1599957 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072: Met Val Ala Thr Lys Lys Thr Lys Lys Ser Thr Asp Asn Ile Asn Asn 10 Lys Leu Gln Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys 25 2.0 Thr Val Leu Arg Thr Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile 40 4.5 Ala Asn Asn Cys Pro Pro Leu Arg Lys Xaa 55 (2) INFORMATION FOR SEQ ID NO: 2073: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..315 (D) OTHER INFORMATION: / Ceres Seq. ID 1599969 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073: grantgette acaccacca etteraccac caccaccacc accaccagae agggacacgg acggcactag ctcgaggagg gtcggcaagc cagagtcaca gcagaaggtg aaagggagcg 120 qacatgqqqq cqgatcqttt cctgagcqtq qcgnaggqcq gcctcggcqg cgaggcqctc tacttcqcqq tcatcctqtq gctgtccgtc atgtcgtgga tcatcttcac ctgggtcggc 240 qacqqcqqqq aqqacqqqaq qcqqqqqqqq aaqcccqqq qcaqccqcqq cacccqqtqt 300 tcgtcggcgc gtcgg (2) INFORMATION FOR SEQ ID NO: 2074: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..104 (D) OTHER INFORMATION: / Ceres Seq. ID 1599970 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074: Ser Ala Ser His Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Asp 10 Arg Asp Thr Asp Gly Thr Ser Ser Arg Arg Val Gly Lys Pro Glu Ser 20 25 Gln Gln Lys Val Lys Gly Ser Gly Tyr Gly Gly Gly Ser Phe Pro Glu 40 Arg Gly Xaa Gly Arg Pro Arg Arg Gly Ala Leu Leu Arg Gly His Pro Val Ala Val Arg His Val Val Asp His Leu His Leu Gly Arg Arg 70 75 Arg Arg Gly Gly Arg Glu Ala Gly Glu Glu Ala Pro Gly Gln Pro Arg 90 85 His Pro Val Phe Val Gly Ala Ser 100
 - (2) INFORMATION FOR SEQ ID NO:2075:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

180

240

300

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599971
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:
- Met Gly Ala Asp Arg Phe Leu Ser Val Ala Xaa Gly Gly Leu Gly Gly 1 5 10 15
- Glu Ala Leu Tyr Phe Ala Val Ile Leu Trp Leu Ser Val Met Ser Trp 20 25 30
- Ile Ile Phe Thr Trp Val Gly Asp Gly Glu Asp Gly Arg Arg Gly 35 40 45
- Arg Lys Arg Arg Gly Ser Arg Gly Thr Arg Cys Ser Ser Ala Arg Arg 50 55 60
- (2) INFORMATION FOR SEQ ID NO:2076:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..314
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599976
- (xi) SEQUENCE DESCRIPTION: SEQ ID No:2076:

 ccgccccgct ccttgcctcc gatecccaat tectectteg gatetegeat teagegeann aggtgtgaag gaaggggac geggaggaag atggggeteg egttegggaa getetteake eggetetteg ccaagaagga gatgeggate etcatggteg geetegaege egeeggtaaa accaccatec tetacaaget caagetegge gagategtea ecaecatece caecateggt tteaatgttg aaactgttga gtacaagare attagettea etgtetngga tgteggggt caggacaaga teag
- (2) INFORMATION FOR SEQ ID NO:2077:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599977
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:
- Pro Pro Arg Ser Leu Pro Pro Ile Pro Asn Ser Ser Phe Gly Ser Arg

 1 10 15
- Ile Gln Arg Xaa Arg Cys Glu Gly Arg Gly Thr Arg Arg Lys Met Gly
 20 25 30
- Leu Ala Phe Gly Lys Leu Phe Xaa Arg Leu Phe Ala Lys Lys Glu Met 35
- Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu 50 55 60
- Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly 65 70 75 80
- Phe Asn Val Glu Thr Val Glu Tyr Lys Xaa Ile Ser Phe Thr Val Xaa 85 90 95
- Asp Val Gly Gly Gln Asp Lys Ile 100
- (2) INFORMATION FOR SEQ ID NO:2078:
 - (i) SEQUENCE CHARACTERISTICS:

120

(A) LENGTH: 104 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..104 (D) OTHER INFORMATION: / Ceres Seq. ID 1599978 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078: Arg Pro Ala Pro Cys Leu Arg Ser Pro Ile Pro Pro Ser Asp Leu Ala 1.0 5 Phe Ser Ala Xaa Gly Val Lys Glu Gly Gly Arg Gly Arg Trp Gly 25 Ser Arg Ser Gly Ser Ser Ser Xaa Gly Ser Ser Pro Arg Arg Cys 40 Gly Ser Ser Trp Ser Ala Ser Thr Pro Pro Val Lys Pro Pro Ser Ser 60 55 Thr Ser Ser Ser Ser Ala Arg Ser Ser Pro Pro Ser Pro Pro Ser Val 75 70 Ser Met Leu Lys Leu Leu Ser Thr Arg Xaa Leu Ala Ser Leu Ser Xaa 90 85 Met Ser Gly Val Arg Thr Arg Ser 100 (2) INFORMATION FOR SEQ ID NO:2079: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..74 (D) OTHER INFORMATION: / Ceres Seq. ID 1599979 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079: Met Gly Leu Ala Phe Gly Lys Leu Phe Xaa Arg Leu Phe Ala Lys Lys 15 10 5 Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr 30 25 20 Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr 4.5 35 Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Xaa Ile Ser Phe Thr 60 55 Val Xaa Asp Val Gly Gly Gln Asp Lys Ile 70 (2) INFORMATION FOR SEQ ID NO:2080: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080: acagttccac geogecacte ececcaaece gaccaegetg egecteeget tgateccag eegagggagg aatgggtaag ggtacgggca getteggcaa gegeeggaae aagaegeaea egetetgeat eegetgegge egeegeasst tecaeeteea gaagagtace tgeteeteet

(D) OTHER INFORMATION: / Ceres Seq. ID 1599983

geggttacce egeegeege ateegeaagt ataactggag tgtgaaggee ateaggegea 240 agacaacegg tacegaaagg atnaggtaca tgegeeacgt geetegeegt tteaagagea 300 actteagaga agggactssa ggetgeteee aagaagagtg etgeegetge caactaagts 360 stggatettg etateaagaa tetgataag

- (2) INFORMATION FOR SEQ ID NO: 2081:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..74
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599984
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Thr Val Pro Arg Arg His Ser Pro Gln Pro Asp His Ala Ala Pro Pro 1 5 10 15

Leu Asp Pro Gln Pro Arg Glu Glu Trp Val Arg Val Arg Ala Ala Ser 20 25 30

Ala Ser Ala Gly Thr Arg Arg Thr Arg Ser Ala Ser Ala Ala Ala Ala 35 40 45

Ala Xaa Ser Thr Ser Arg Arg Val Pro Ala Pro Pro Ala Val Thr Pro 50 55 60

Pro Pro Ala Ser Ala Ser Ile Thr Gly Val 65

- (2) INFORMATION FOR SEQ ID NO: 2082:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599985
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

Met Gly Lys Gly Thr Gly Ser Phe Gly Lys Arg Arg Asn Lys Thr His

Thr Leu Cys Ile Arg Cys Gly Arg Arg Xaa Phe His Leu Gln Lys Ser 20 25 30

Thr Cys Ser Ser Cys Gly Tyr Pro Ala Ala Arg Ile Arg Lys Tyr Asn $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Trp Ser Val Lys Ala Ile Arg Arg Lys Thr Thr Gly Thr Glu Arg Xaa 50 55 60

Arg Tyr Met Arg His Val Pro Arg Arg Phe Lys Ser Asn Phe Arg Glu 65 70 75 80

Gly Thr Xaa Gly Cys Ser Gln Glu Glu Cys Cys Arg Cys Gln Leu Ser 85 90 95

Xaa Gly Ser Cys Tyr Gln Glu Ser Asp Lys 100 105

- (2) INFORMATION FOR SEQ ID NO:2083:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

 ctccactcgc cctcccabsn cagaaaaccc tagccgccgc caccgaagcg gcctcccagg 60
 taagcaggag cgtccacccc gccgccgtca tgaagcgcaa tccccgcgtc acgagctcc 120
 gccggaagtg ccgcaasgca cttttacggc cccgtcctcc gtccgccgcg ttctcatgtc 180
 cgccgggcts tcgacggagc tccgcacaa gtacaacgtg cgctccatcc cgatccgcaa 240
 gacgacgagg tgcaggtcgt gcgcgcaca gacttcgtca atccatcgcr gctggacaag 300
 cgttccgtcg tanaggtgat cgttgagatg accggcggcg gcgtggacta cagcttcgag 360
 tgcatcggcg tgcsstcggt gatgaccgac gccttcagat gcaccaag
- (2) INFORMATION FOR SEQ ID NO:2084:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599993
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:
- Ser Thr Arg Pro Pro Xaa Xaa Glu Asn Pro Ser Arg Arg His Arg Ser
- Gly Leu Pro Gly Lys Gln Glu Arg Pro Pro Arg Arg Arg His Glu Ala 20 25 30
- Gln Ser Pro Arg His Glu Leu Pro Pro Glu Val Pro Gln Xaa Thr Phe 35 40 45
- Thr Ala Pro Ser Ser Val Arg Arg Val Leu Met Ser Ala Gly Xaa Ser 50 55 60
- Thr Glu Leu Arg His Lys Tyr Asn Val Arg Ser Ile Pro Ile Arg Lys 70 75 80
- Thr Thr Arg Cys Arg Ser Cys Ala Ala Gln Thr Ser Ser Ile His Arg 85 90 95
- Xaa Trp Thr Ser Val Pro Ser Xaa Arg 100 105
- (2) INFORMATION FOR SEQ ID NO:2085:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..107
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1599994
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:
- Pro Leu Ala Leu Pro Xaa Gln Lys Thr Leu Ala Ala Ala Thr Glu Ala

 1 5 10 15
- Ala Ser Gln Val Ser Arg Ser Val His Pro Ala Ala Val Met Lys Arg 20 25 30
- Asn Pro Arg Val Thr Ser Ser Arg Arg Lys Cys Arg Xaa Ala Leu Leu 35 40 45
- Arg Pro Arg Pro Pro Ser Ala Ala Phe Ser Cys Pro Pro Gly Xaa Arg
- Arg Ser Ser Ala Thr Ser Thr Thr Cys Ala Pro Ser Arg Ser Ala Arg 65 70 75 80
- Arg Arg Gly Ala Gly Arg Ala Arg His Arg Leu Arg Gln Ser Ile Xaa 85 90 95
- Ala Gly Gln Ala Phe Arg Arg Xaa Gly Asp Arg

100 (2) INFORMATION FOR SEQ ID NO: 2086: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..78 (D) OTHER INFORMATION: / Ceres Seq. ID 1599995 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086: Met Lys Arg Asn Pro Arg Val Thr Ser Ser Arg Arg Lys Cys Arg Xaa 10 Ala Leu Leu Arg Pro Arg Pro Pro Ser Ala Ala Phe Ser Cys Pro Pro 20 25 Gly Xaa Arg Arg Ser Ser Ala Thr Ser Thr Thr Cys Ala Pro Ser Arg 40 4.5 Ser Ala Arg Arg Arg Gly Ala Gly Arg Ala Arg His Arg Leu Arg Gln 55 Ser Ile Xaa Ala Gly Gln Ala Phe Arg Arg Xaa Gly Asp Arg 70 (2) INFORMATION FOR SEQ ID NO: 2087: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 156 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..156 (D) OTHER INFORMATION: / Ceres Seq. ID 1600027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087: agactecaqt etectetage egtetegege getteacett eeceaeceeg eegeegeeat 60 cgcacgcccg cagccgcatc cgctatgggt gcgtacaagt acgtctcgga gctatggcgg 120 aggaagcagt ccgatgtgat gcggttcgtg cagcgc (2) INFORMATION FOR SEQ ID NO: 2088: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1600028 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088: Arg Leu Gln Ser Pro Leu Ala Val Ser Arg Ala Ser Pro Ser Pro Pro 10 Arg Arg Arg His Arg Thr Pro Ala Ala Ala Ser Ala Met Gly Ala Tyr 25 Lys Tyr Val Ser Glu Leu Trp Arg Arg Lys Gln Ser Asp Val Met Arg 35 40 Phe Val Gln Arg 50 (2) INFORMATION FOR SEQ ID NO: 2089: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

Ser Cys Ser

(B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..51 (D) OTHER INFORMATION: / Ceres Seq. ID 1600029 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089: Thr Pro Val Ser Ser Ser Arg Leu Ala Arg Phe Thr Phe Pro Thr Pro 10 5 Pro Pro Pro Ser His Ala Arg Ser Arg Ile Arg Tyr Gly Cys Val Gln 25 20 Val Arg Leu Gly Ala Met Ala Glu Glu Ala Val Arg Cys Asp Ala Val 35 Arg Ala Ala 50 (2) INFORMATION FOR SEQ ID NO:2090: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..341 (D) OTHER INFORMATION: / Ceres Seq. ID 1600039 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090: ttccccgccg ccnnggcccc cgctcgcttc acttctctag agatggcggt gcgctgctga cgaagaagat cgtgaagaag cgggtcaagc agttcaagag gccccacctc gaccgckaca 120 agtgccttaa gccaagctgg cgcaggccaa agggtattga ttcccgtgtc aggaggaagt 180 tcaagggatg caccttgatg cccaacattg gttatgttct gacaagtcga ccaggcacta 240 cckccccagc aagttcaaga agtttntggt ccacaacgtt tctgagctgg agttgctcat 300 gatgcacaac aggacctact gcgctgaaat tgctcacaac g (2) INFORMATION FOR SEQ ID NO:2091: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..99 (D) OTHER INFORMATION: / Ceres Seq. ID 1600040 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091: Pro Arg Arg Xaa Gly Pro Arg Ser Leu His Phe Ser Arg Asp Gly Gly 10 Ala Leu Leu Thr Lys Lys Ile Val Lys Lys Arg Val Lys Gln Phe Lys 30 25 20 Arg Pro His Leu Asp Arg Xaa Lys Cys Leu Lys Pro Ser Trp Arg Arg 40 Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys Gly Cys Thr 60 55 Leu Met Pro Asn Ile Gly Tyr Val Leu Thr Ser Arg Pro Gly Thr Thr 75 70 Xaa Pro Ala Ser Ser Arg Ser Xaa Trp Ser Thr Thr Phe Leu Ser Trp 90

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(2) INFORMATION FOR SEQ ID NO:2092:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 51 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..51
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600041
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:
Met His Leu Asp Ala Gln His Trp Leu Cys Ser Asp Lys Ser Thr Arg
                                    10
                5
His Tyr Xaa Pro Ser Lys Phe Lys Lys Phe Xaa Val His Asn Val Ser
                                                     30
                                25
Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu Ile
                                                 4.5
                            40
Ala His Asn
    50
(2) INFORMATION FOR SEQ ID NO:2093:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 415 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
           (B) LOCATION: 1..415
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600059
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:
gaccgageta ggagaagege gaacnegtge atgegeagae gttgaggteg agggaeaegg
tatctctgag cttcatcgga gagcgacccg ccaccgccac gcttggccgc aagccgagaa
                                                                        120
gagtgccggg ccgggagacc ggacgattat tgatccgtag cagattcgct aatggcggag
                                                                        180
acggcggaca tggagcggat cttcaagcgg ttcgacacca acggcgacgg taagatctcg
                                                                        240
ctgtcggagc tgacggaggc gctacggacg ctggggtcca cctctgccga cgaggtgcag
                                                                        300
cgcatgatgg ccgagatcga caccgacggc gacggctgta tcgacttcaa cgagttcatc
                                                                        360
accttctgca acgccaaccc ggggctcatg aaggacgtcg caaaggtctt ctgat
 (2) INFORMATION FOR SEQ ID NO:2094:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 52 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..52
           (D) OTHER INFORMATION: / Ceres Seq. ID 1600060
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:
 Thr Glu Leu Gly Glu Ala Arg Xaa Arg Ala Cys Ala Asp Val Glu Val
                                      10
 Glu Gly His Gly Ile Ser Glu Leu His Arg Arg Ala Thr Arg His Arg
                                                      30
                                  25
             20
 His Ala Trp Pro Gln Ala Glu Lys Ser Ala Gly Pro Gly Asp Arg Thr
                                                  45
                              40
         35
 Ile Ile Asp Pro
 (2) INFORMATION FOR SEQ ID NO:2095:
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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600061
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:

Met Ala Glu Thr Ala Asp Met Glu Arg Ile Phe Lys Arg Phe Asp Thr 5 10

Asn Gly Asp Gly Lys Ile Ser Leu Ser Glu Leu Thr Glu Ala Leu Arg 30 25 20

Thr Leu Gly Ser Thr Ser Ala Asp Glu Val Gln Arg Met Met Ala Glu 45 40

Ile Asp Thr Asp Gly Asp Gly Cys Ile Asp Phe Asn Glu Phe Ile Thr 60 55

Phe Cys Asn Ala Asn Pro Gly Leu Met Lys Asp Val Ala Lys Val Phe 75

- (2) INFORMATION FOR SEQ ID NO:2096:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..74
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600062
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

Met Glu Arg Ile Phe Lys Arg Phe Asp Thr Asn Gly Asp Gly Lys Ile 10 5

Ser Leu Ser Glu Leu Thr Glu Ala Leu Arg Thr Leu Gly Ser Thr Ser 25

Ala Asp Glu Val Gln Arg Met Met Ala Glu Ile Asp Thr Asp Gly Asp 45 40

Gly Cys Ile Asp Phe Asn Glu Phe Ile Thr Phe Cys Asn Ala Asn Pro 55

- Gly Leu Met Lys Asp Val Ala Lys Val Phe 70
- (2) INFORMATION FOR SEQ ID NO:2097:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..438
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097: ggctggctcc caccgaattc attccacccc cgtctcctcc gatcggacca ccgggccagc

ageggggegn ategtgaegt cageaggeat ggtgaaggee taccceaegg tgaacgagga ctacctcaag gcggtcgaca aggccaagcg caasstccgc ggcctcatcg ccgagaagaa

180 ttgcgccccg ctcatgctcc gcctcgcatg gcactccgcg ggcaccttcg atgtggccac 240 300

caaaaccggg ggccccttcg gcaccatgaa gaaccccgcc gagcaggsca cggagccaac

geoggaeten gaaattneea teaggetget agageeeate aaggageagt teeceateet 360 ateetaeget gaettetaee agettnetgg agtegtssse agtegaggta aeggeggaee 420 tgatgteeet teeaceee

- (2) INFORMATION FOR SEQ ID NO:2098:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600072
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:
- Gly Trp Leu Pro Pro Asn Ser Phe His Pro Arg Leu Leu Arg Ser Asp
 1 15
- His Arg Ala Ser Ser Gly Ala Xaa Arg Asp Val Ser Arg His Gly Glu 20 25 30
- Gly Leu Pro His Gly Glu Arg Gly Leu Pro Gln Gly Gly Arg Gln Gly 35 40 45
- Gln Ala Gln Xaa Pro Arg Pro His Arg Arg Glu Glu Leu Arg Pro Ala 50 55 60
- His Ala Pro Pro Arg Met Ala Leu Arg Gly His Leu Arg Cys Gly His 65 70 75 80
- Gln Asn Arg Gly Pro Leu Arg His His Glu Glu Pro Arg Arg Ala Xaa 85 90 95
- His Gly Ala Asn Ala Gly Leu Xaa Asn Xaa His Gln Ala Ala Arg Ala 100 105 110
- His Gln Gly Ala Val Pro His Pro Ile Leu Arg 115 120
- (2) INFORMATION FOR SEQ ID NO:2099:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..145
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600073
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:
- Ala Gly Ser His Arg Ile His Ser Thr Pro Val Ser Ser Asp Arg Thr 1 5 10 15
- Thr Gly Pro Ala Ala Gly Xaa Ile Val Thr Ser Ala Gly Met Val Lys
 20 25 30
- Ala Tyr Pro Thr Val Asn Glu Asp Tyr Leu Lys Ala Val Asp Lys Ala 35 40 45
 Lys Arg Xaa Xaa Arg Gly Leu Ile Ala Glu Lys Asn Cys Ala Pro Leu
- Lys Arg Xaa Xaa Arg Gly Leu lie Ala Glu Lys Ash Cys Ala 110 Leu
 50 55 60
- Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp Val Ala Thr 65 70 75 80
 Lys Thr Gly Gly Pro Phe Gly Thr Met Lys Asn Pro Ala Glu Gln Xaa
- 85 90 95

 Thr Glu Pro Thr Pro Asp Xaa Glu Ile Xaa Ile Arg Leu Leu Glu Pro
- 100 105 110

 Ile Lys Glu Gln Phe Pro Ile Leu Ser Tyr Ala Asp Phe Tyr Gln Leu
- 115 120 125

 Xaa Gly Val Xaa Xaa Ser Arg Gly Asn Gly Gly Pro Asp Val Pro Ser
 130 135 140

Thr 145 (2) INFORMATION FOR SEQ ID NO:2100: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..116 (D) OTHER INFORMATION: / Ceres Seq. ID 1600074 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100: Met Val Lys Ala Tyr Pro Thr Val Asn Glu Asp Tyr Leu Lys Ala Val 10 5 Asp Lys Ala Lys Arg Xaa Xaa Arg Gly Leu Ile Ala Glu Lys Asn Cys 30 25 2.0 Ala Pro Leu Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp 40 Val Ala Thr Lys Thr Gly Gly Pro Phe Gly Thr Met Lys Asn Pro Ala 55 60 Glu Gln Xaa Thr Glu Pro Thr Pro Asp Xaa Glu Ile Xaa Ile Arg Leu 75 7.0 Leu Glu Pro Ile Lys Glu Gln Phe Pro Ile Leu Ser Tyr Ala Asp Phe 90 85 Tyr Gln Leu Xaa Gly Val Xaa Xaa Ser Arg Gly Asn Gly Gly Pro Asp 110 105 100 Val Pro Ser Thr 115 (2) INFORMATION FOR SEQ ID NO:2101: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 416 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..416 (D) OTHER INFORMATION: / Ceres Seq. ID 1600077 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101: aagtaaacct cgtttccgca tgccgaccgt aaacgtgaaa tggcagaagg aggtctttcc aggcatagag attgacacta gccagcctcc gattgtkttg aagagtcagc tatacacact 120 aactggtgtg ccacctgaac gccaaaaaat tatggtgaag ggtggattat tgaaggatga 180 tgcagattgg tctactttgg gagtgaaaga tggccaaaag ttaatgatga taggcacagc 240 tgatgagatt gttaaagctc cagagaragg tccactgttt gttgaggatc taccagaaga 300 agagcaagtg gttgcactgg gtcacagtct ggtctttaca atcttnggaa tacatgctat 360 atgadttcca cattgcratg tttgcrttca gttccagagc tgaagtcagc gctgct (2) INFORMATION FOR SEQ ID NO:2102: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1600078

(B) LOCATION: 1..120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

```
      Ser
      Lys
      Pro
      Arg
      Phe
      Arg
      Met
      Pro
      Thr
      Val
      Ass
      Val
      Lys
      Trp
      Gln
      Lys

      Glu
      Val
      Phe
      Pro
      Gly
      Ile
      Glu
      Ile
      Asp
      Thr
      Ser
      Gln
      Pro
      Ile
      Xaa

      Leu
      Lys
      Ser
      Gln
      Leu
      Tyr
      Thr
      Leu
      Thr
      Gly
      Val
      Pro
      Pro
      Glu
      Arg
      Gln

      Lys
      Ile
      Met
      Val
      Lys
      Gly
      Ile
      Lys
      Asp
      Ala
      Asp
      Ala
      Asp
      Ile
      Met
      Ile
      Gly
      Thr
      Ala

      Thr
      Leu
      Gly
      Ile
      I
```

Leu Pro Glu Glu Glu Gln Val Val Ala Leu Gly His Ser Leu Val Phe
100 105 110

Thr Ile Xaa Gly Ile His Ala Ile 115 120

- (2) INFORMATION FOR SEQ ID NO:2103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600079
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Met Pro Thr Val Asn Val Lys Trp Gln Lys Glu Val Phe Pro Gly Ile 1 5 10 15 Glu Ile Asp Thr Ser Gln Pro Pro Ile Xaa Leu Lys Ser Gln Leu Tyr

20 25 30

Thr Leu Thr Gly Val Pro Pro Glu Arg Gln Lys Ile Met Val Lys Gly

35 40 45
Gly Leu Leu Lys Asp Asp Ala Asp Trp Ser Thr Leu Gly Val Lys Asp

50 55 60

Gly Gln Lys Leu Met Met Ile Gly Thr Ala Asp Glu Ile Val Lys Ala
70 75 80

Pro Glu Xaa Gly Pro Leu Phe Val Glu Asp Leu Pro Glu Glu Glu Gln
85 90 95

Val Val Ala Leu Gly His Ser Leu Val Phe Thr Ile Xaa Gly Ile His
100 105 110

Ala Ile

- (2) INFORMATION FOR SEQ ID NO:2104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600080
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

Met Val Lys Gly Gly Leu Leu Lys Asp Asp Ala Asp Trp Ser Thr Leu 1 5 10 15

Gly Val Lys Asp Gly Gln Lys Leu Met Met Ile Gly Thr Ala Asp Glu 20 25 30

Ile Val Lys Ala Pro Glu Xaa Gly Pro Leu Phe Val Glu Asp Leu Pro

240

300

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 4.0 35 Glu Glu Glu Gln Val Val Ala Leu Gly His Ser Leu Val Phe Thr Ile 55 Xaa Gly Ile His Ala Ile (2) INFORMATION FOR SEQ ID NO:2105: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..309 (D) OTHER INFORMATION: / Ceres Seq. ID 1600093 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105: gctatacatc ccgaatccga cgctccatcg agtgtgtgcg gcggcgggag gagacggaag agaacgatgc aggcggtggc acgggcgcgt gggcttgcgg ctgcggctgt ggctgcgcgg ccgtcggcga tggaggcagg gcaccgcggg caggtgcagc aagcccgggg cattgtggtg caggtgaggg acgggaacct ggagcgggcg ctggcggtca tggagcgcaa gatgaggtcc ageggeatgg agegeettat eegagegege acceactace aegtgaaaga eteggagaag cgcgtgctc (2) INFORMATION FOR SEQ ID NO:2106: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..103 (D) OTHER INFORMATION: / Ceres Seq. ID 1600094 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106: Ala Ile His Pro Glu Ser Asp Ala Pro Ser Ser Val Cys Gly Gly 10 5 Arg Arg Arg Lys Arg Thr Met Gln Ala Val Ala Arg Ala Arg Gly Leu 25 Ala Ala Ala Ala Val Ala Ala Arg Pro Ser Ala Met Glu Ala Gly His 40 Arg Gly Gln Val Gln Gln Ala Arg Gly Ile Val Val Gln Val Arg Asp 60 55 Gly Asn Leu Glu Arg Ala Leu Ala Val Met Glu Arg Lys Met Arg Ser 75 70 Ser Gly Met Glu Arg Leu Ile Arg Ala Arg Thr His Tyr His Val Lys 90 85 Asp Ser Glu Lys Arg Val Leu

(2) INFORMATION FOR SEQ ID NO:2107:

100

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600095
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

Leu Gly Glu Ala Arg Ala 100

- (2) INFORMATION FOR SEQ ID NO:2108:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600096
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

 Met Gln Ala Val Ala Arg Ala Arg Gly Leu Ala Ala Ala Ala Val Ala 1

 1
 5
 10
 15
 15

 Ala Arg Pro Ser Ala Met Glu Ala Gly His Arg Gly Gln Val Gln Gln 20
 25
 30

 Ala Arg Gly Ile Val Val Gln Val Arg Asp Gly Asn Leu Glu Arg Ala 35
 40
 45

 Leu Ala Val Met Glu Arg Lys Met Arg Ser Ser Gly Met Glu Arg Leu

50 55 60

Ile Arg Ala Arg Thr His Tyr His Val Lys Asp Ser Glu Lys Arg Val
65 70 75 80

Leu

- (2) INFORMATION FOR SEQ ID NO:2109:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..421
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

 cttggccttg gctggcgctc gcacctcaca gcagcagcag tcaacaacaa cctccactgc gcacaccac cgagaggcga gaccggcggc ggcaaaagga cgatacaaaa gcagccaggg ttgctggcaa cassgtcggt cgcccgcccg ctcgccatgg ggaggtcgcc gtgctgcgag aaggcgcaca ccaacaaggg cgcgtggacc aaggaggagg acgagcgcct ggtcgcgac atcagggcaca acgacgaggg gtgctggcgc tcgctgcca aggccgcgg ctcctggct 300 gcggcaagag ctgccgcctc cgctggatca actacctccg ccccgacctc aagcgggca agctcatcgt caagctgcac asgtccctcg gcaacaagtg 420
- (2) INFORMATION FOR SEQ ID NO:2110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:
- Leu Gly Leu Gly Trp Arg Ser His Leu Thr Ala Ala Ala Val Asn Asn 1 10 15
- Asn Leu His Cys Arg Asn Pro Pro Arg Gly Glu Thr Gly Gly Gly Lys 20 25 30
- Arg Thr Ile Gln Lys Gln Pro Gly Leu Leu Ala Thr Xaa Ser Val Ala 35 40 45
- Arg Pro Leu Ala Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr 50 55 60
- Asn Lys Gly Ala Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ala His 65 70 75 80
- Ile Arg Ala His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala 85 90 95
- Ser Ala Pro Thr Ser Ser Ala Ala Thr Ser Arg Arg Gly Arg Ala 115 120 125
- His Arg Gln Ala Ala Xaa Val Pro Arg Gln Gln Val 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2111:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:
- Leu Ala Leu Ala Gly Ala Arg Thr Ser Gln Gln Gln Gln Ser Thr Thr 1 5 10 15
- Thr Ser Thr Ala Ala Thr His Arg Glu Ala Arg Pro Ala Ala Ala Lys 20 25 30
- Gly Arg Tyr Lys Ser Ser Gln Gly Cys Trp Gln Xaa Xaa Arg Ser Pro
 35 40 45
- Ala Arg Ser Pro Trp Gly Gly Arg Arg Ala Ala Arg Arg Arg Thr Pro 50 55 60
- Thr Arg Ala Arg Gly Pro Arg Arg Thr Ser Ala Trp Ser Arg Thr 65 70 75 80
 Ser Gly Arg Thr Ala Arg Gly Ala Gly Ala Arg Cys Pro Arg Pro
- 85 90 95 Ala Pro Ala Leu Arg Gln Glu Leu Pro Pro Pro Leu Asp Gln Leu Pro
- Pro Pro Arg Pro Gln Ala Arg Gln Leu His Gly Glu Asp Glu Leu
 115 120 125
- Ile Val Lys Leu His Xaa Ser Leu Gly Asn Lys Trp
 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..139
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600108
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

Trp Pro Trp Leu Ala Leu Ala Pro His Ser Ser Ser Gln Gln Gln 1 5 10 15

Pro Pro Leu Pro Gln Pro Thr Glu Arg Arg Asp Arg Arg Arg Gln Lys 20 25 30

Asp Asp Thr Lys Ala Ala Arg Val Ala Gly Asn Xaa Val Gly Arg Pro 35 40 45

Pro Ala Arg His Gly Glu Val Ala Val Leu Arg Glu Gly Ala His Gln 50 55 60

Gln Gly Arg Val Asp Gln Gly Gly Gly Arg Ala Pro Gly Arg Ala His 65 70 75 80

Gln Gly Ala Arg Arg Gly Val Leu Ala Leu Ala Ala Gln Gly Arg Arg 85 90 95

Leu Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu 100 105 110

Arg Pro Asp Leu Lys Arg Gly Asn Phe Thr Glu Glu Arg Thr Ser Ser

Ser Ser Ser Cys Thr Xaa Pro Ser Ala Thr Ser 130 135

- (2) INFORMATION FOR SEQ ID NO:2113:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..432
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600113
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

ttgggcaget gcgagcactg ccatctccat ccacctgcgt tctgagcagt acattccatt 60 ccattccgtc ccatcgatcg gtccactgga cgatggcttc cctcctcctg ttcctgcgag 120 ccattgtcat cagtgccgat gacgaggaac tcacgggcgc ggacgaggag cgggatgcgg 240 aggaggagga ggaggaggag gaggaagaac ggtggctgat ctcctgcctg gagtggcctc gagtgcgacg caagtccgcg tggatgcaga tggttnacg gcctggtga gccaagtgct catcttgctc gccgttgccg cgtgttnttn aagccaraga tsagctccac 420 aggatnctca ac

- (2) INFORMATION FOR SEQ ID NO:2114:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600114
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

Gly Gln Leu Arg Ala Leu Pro Ser Pro Ser Thr Cys Val Leu Ser Ser 1 5 10 15

Thr Phe His Ser Ile Pro Ser His Arg Ser Val His Trp Thr Met Ala

Ser Leu Leu Phe Leu Arg Ala Ile Val Ile Ser Ala Asp Asp Glu 40 45 Glu Leu Thr Gly Ala Asp Glu Gly Arg Asp Ala Ala Arg Glu Arg Arg Pro Glu Asn Cys Ala Phe Gly Pro Ala Ala Ala Arg Asp Thr Glu

75 70

Glu Glu Glu Glu Glu Glu Glu Glu Arg Trp Leu Val Ser Cys Leu 85 90

Glu Trp Pro Arg Val Asp Arg Lys Ser Ala Trp Met Gln Met Val Xaa 105 100

Arg Pro Gly Gly Ala Lys Cys Phe Arg Arg Phe Ile Leu Leu Ala Val 120 115

Ala Ala Cys Xaa Xaa Ser Xaa Arg Xaa Ala Pro Gln Asp Xaa Gln 135 130

- (2) INFORMATION FOR SEQ ID NO:2115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Ala Ser Leu Leu Phe Leu Arg Ala Ile Val Ile Ser Ala Asp 10 5

Asp Glu Glu Leu Thr Gly Ala Asp Glu Gly Arg Asp Ala Ala Arg 25

Glu Arg Arg Pro Glu Asn Cys Ala Phe Gly Pro Ala Ala Ala Arg Asp 40

Thr Glu Glu Glu Glu Glu Glu Glu Glu Glu Arg Trp Leu Val Ser 60 55

Cys Leu Glu Trp Pro Arg Val Asp Arg Lys Ser Ala Trp Met Gln Met 75

Val Xaa Arg Pro Gly Gly Ala Lys Cys Phe Arg Arg Phe Ile Leu Leu 90 85

Ala Val Ala Ala Cys Xaa Xaa Ser Xaa Arg Xaa Ala Pro Gln Asp Xaa 110 100 105

Gln

- (2) INFORMATION FOR SEQ ID NO:2116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

Met Thr Arg Asn Ser Arg Ala Arg Thr Arg Asp Gly Met Arg Arg Arg 10 5

Val Asn Gly Asp Arg Arg Thr Ala Arg Ser Gly Arg Arg Arg Arg Ala 25

Thr Arg Arg Arg Arg Arg Arg Arg Arg Lys Asn Gly Gly Trp Ser 40

Pro Ala Trp Ser Gly Leu Ala Ser Thr Ala Ser Pro Arg Gly Cys Arg 55 Trp Phe Xaa Gly Leu Val Glu Pro Ser Ala Ser Asp Asp Ser Ser Cys 75 70 Ser Pro Leu Pro Arg Val Xaa Xaa Ala Xaa Asp Xaa Leu His Arg Xaa 85 90 Leu Asn (2) INFORMATION FOR SEQ ID NO:2117: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 409 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..409 (D) OTHER INFORMATION: / Ceres Seq. ID 1600117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117: ctaagcaggc aagcatacgc tocattttat aaccaaccgg cggtccatct tgagaggacc 60 120 aagaaacaga gagagcggtt ctacgtccga gtcgtcgcat caggtcccct cgattcgccg 180 gcgssncgcc accaaccaag ctcatacatc tgaattgact agtccaactc agggatttct ttggggacca atcaaactca agaactaagt ttcatgtctg atctcgacgt ccagcttcca 240 tctgcttttg atccgtttgc agaggcaaat sctgaggact ccagtgctgg tgctggatca 300 aaggactatg tgcacgtgcg tattcagcag cgcaacggga aggaanattc tnacaactct 360 tcagggcttc aagaaanagt acagctacaa caagatcctc aaggatctc (2) INFORMATION FOR SEQ ID NO:2118: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..50 (D) OTHER INFORMATION: / Ceres Seq. ID 1600118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118: Leu Ser Arg Gln Ala Tyr Ala Pro Phe Tyr Asn Gln Pro Ala Val His 1.0 Leu Glu Arg Thr Lys Lys Gln Arg Glu Arg Phe Tyr Val Arg Val Val 30 20 25 Ala Ser Gly Pro Leu Asp Ser Pro Ala Xaa Arg His Gln Pro Ser Ser 45 Tyr Ile 50 (2) INFORMATION FOR SEQ ID NO:2119: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:
Met Ser Asp Leu Asp Val Gln Leu Pro Ser Ala Phe Asp Pro Phe Ala
1 5 10 15

(D) OTHER INFORMATION: / Ceres Seq. ID 1600119

Glu Ala Asn Xaa Glu Asp Ser Ser Ala Gly Ala Gly Ser Lys Asp Tyr 25 Val His Val Arg Ile Gln Gln Arg Asn Gly Lys Glu Xaa Ser Xaa Asn 40 35 Ser Ser Gly Leu Gln Glu Xaa Val Gln Leu Gln Gln Asp Pro Gln Gly 55 Ser 65 (2) INFORMATION FOR SEQ ID NO:2120: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..34 (D) OTHER INFORMATION: / Ceres Seq. ID 1600120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120: Met Cys Thr Cys Val Phe Ser Ser Ala Thr Gly Arg Xaa Ile Xaa Thr 10 5 Thr Leu Gln Gly Phe Lys Lys Xaa Tyr Ser Tyr Asn Lys Ile Leu Lys 20 25 Asp Leu (2) INFORMATION FOR SEQ ID NO:2121: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..392 (D) OTHER INFORMATION: / Ceres Seq. ID 1600147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121: aktttttaat agacacatcg atcaacttat tctttgctgt ctttatggtg ttgcaaaggt 60 ttgccaatta gaactctcat tcagggagat actcaacaat tacaaaarag aagcacaatg 120 caaaccagaa gtttttttaa gcatctatat tcgaagtang aatcataatn gggtattaat 180 atcacgccat gttgatatca ttacttttta caatgaggtc tttgttccag cagccaagcc 240 ttktcctggt gtcattaata tcatctggta ctcgtccaga agacaagaag aatkctaatg 300 qccaagttcc tggatcaccg aagctatctc ctttcccaaa tttrccagat atgtccccaa 360 agaragtttc agcttctcat aatgtatatg tg (2) INFORMATION FOR SEQ ID NO:2122: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 98 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..98 (D) OTHER INFORMATION: / Ceres Seq. ID 1600148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122: Xaa Phe Asn Arg His Ile Asp Gln Leu Ile Leu Cys Cys Leu Tyr Gly 10 Val Ala Lys Val Cys Gln Leu Glu Leu Ser Phe Arg Glu Ile Leu Asn

25

20

30

Asn Tyr Lys Xaa Glu Ala Gln Cys Lys Pro Glu Val Phe Leu Ser Ile
35
Tyr Ile Arg Ser Xaa Asn His Asn Xaa Val Leu Ile Ser Arg His Val
50
Asp Ile Ile Thr Phe Tyr Asn Glu Val Phe Val Pro Ala Ala Lys Pro
65
Xaa Pro Gly Val Ile Asn Ile Ile Trp Tyr Ser Ser Arg Arg Gln Glu

90

Glu Xaa

- (2) INFORMATION FOR SEQ ID NO:2123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..68
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600149
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Leu Ile Ser Leu Leu Phe Thr Met Arg Ser Leu Phe Gln Gln Pro 1 5 10 15

Ser Leu Xaa Leu Val Ser Leu Ile Ser Ser Gly Thr Arg Pro Glu Asp 20 25 30

Lys Lys Asn Xaa Asn Gly Gln Val Pro Gly Ser Pro Lys Leu Ser Pro 35 40 45

Phe Pro Asn Xaa Pro Asp Met Ser Pro Lys Xaa Val Ser Ala Ser His 50 55 60

Asn Val Tyr Val

65

- (2) INFORMATION FOR SEQ ID NO:2124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600150
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

Met Arg Ser Leu Phe Gln Gln Pro Ser Leu Xaa Leu Val Ser Leu Ile

5 10 15

Ser Ser Gly Thr Arg Pro Glu Asp Lys Lys Asn Xaa Asn Gly Gln Val 20 25 30

Pro Gly Ser Pro Lys Leu Ser Pro Phe Pro Asn Xaa Pro Asp Met Ser 35 40 45

Pro Lys Xaa Val Ser Ala Ser His Asn Val Tyr Val 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

- (B) LOCATION: 1..441
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600160
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125: ggaacgggta gattgctgat gagaaaaaca agctggcata aatgaataat tcgcaattgg 60 catcttgcag gtgaaaggac tgttgaagga gaagaaggtg gagatgctgg tggacccaga 120 tctcagaaag cctacgagga ggtcgaggtg gagagccgtt attcaggtgg cactcctctg 180 cacgcagggc tccccctgg accgtccaaa gatgtcggag gtggtgagga tgctcgaagg 240 tgacgggctg gcagagcgtt gggacgaatg gcagaaagta gaggtggtga ggcaggaggc 300 tgagtcggca ccgctccgca atgactggat cgtcgattcc acgtacaacc ttcgtgccgt 360 420 ggagctgtcc ggcccaaggt agccactcca cgactccgat garagaraac actgaattcg ccaagattca ntctaattgc t
- (2) INFORMATION FOR SEQ ID NO:2126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600161
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Met Leu Val Asp Pro Asp Leu Arg Lys Pro Thr Arg Arg Ser Arg Trp

Arg Ala Val Ile Gln Val Ala Leu Leu Cys Thr Gln Gly Ser Pro Leu 20 25 30

Asp Arg Pro Lys Met Ser Glu Val Val Arg Met Leu Glu Gly Asp Gly 35 40 45

Leu Ala Glu Arg Trp Asp Glu Trp Gln Lys Val Glu Val Val Arg Gln 50 55 60

Glu Ala Glu Ser Ala Pro Leu Arg Asn Asp Trp Ile Val Asp Ser Thr 65 70 75 80

Tyr Asn Leu Arg Ala Val Glu Leu Ser Gly Pro Arg 85 90

- (2) INFORMATION FOR SEQ ID NO:2127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met Ser Glu Val Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Arg
1 5 10 15

Trp Asp Glu Trp Gln Lys Val Glu Val Val Arg Gln Glu Ala Glu Ser 20 25 30

Ala Pro Leu Arg Asn Asp Trp Ile Val Asp Ser Thr Tyr Asn Leu Arg

Ala Val Glu Leu Ser Gly Pro Arg

- (2) INFORMATION FOR SEQ ID NO:2128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..50 (D) OTHER INFORMATION: / Ceres Seq. ID 1600163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128: Met Leu Glu Gly Asp Gly Leu Ala Glu Arg Trp Asp Glu Trp Gln Lys 10 Val Glu Val Val Arg Gln Glu Ala Glu Ser Ala Pro Leu Arg Asn Asp 25 2.0 Trp Ile Val Asp Ser Thr Tyr Asn Leu Arg Ala Val Glu Leu Ser Gly 40 Pro Ara 50 (2) INFORMATION FOR SEQ ID NO:2129: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..418 (D) OTHER INFORMATION: / Ceres Seq. ID 1600189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129: 60 ctctctgttg catttcccgt cctgtccttc cacccggcgg cttaaaccct agttctcact cccatcgccg cttcagctcc gccgctgcag atggagttct ggggtctcga ggtcaagcct 120 ggttccactg ttaagtgtga gcctggatat ggctttgtgc tgcacctttc ccaggctgct 180 cttggggaat cgaagaagag tgataatgcc ttgatgtatg tcaaaattga tgatcagaaa 240 cttgccattg gaaccctctc tgttgacaag aacccacaca ttcaatttga tctgattttc 300 gataamgagt ttgagctgtc gcacacatca aaaactacca gcgtcttctt cactggctac 360 aaggttgaac agccattcga ggaagatgaa atggatcttg attctgaaga tgaagacg (2) INFORMATION FOR SEQ ID NO:2130: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..109 (D) OTHER INFORMATION: / Ceres Seq. ID 1600190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130: Met Glu Phe Trp Gly Leu Glu Val Lys Pro Gly Ser Thr Val Lys Cys 10 Glu Pro Gly Tyr Gly Phe Val Leu His Leu Ser Gln Ala Ala Leu Gly 30 25 20 Glu Ser Lys Lys Ser Asp Asn Ala Leu Met Tyr Val Lys Ile Asp Asp 45 40 35 Gln Lys Leu Ala Ile Gly Thr Leu Ser Val Asp Lys Asn Pro His Ile 55 60 Gln Phe Asp Leu Ile Phe Asp Xaa Glu Phe Glu Leu Ser His Thr Ser 75 70

Lys Thr Thr Ser Val Phe Phe Thr Gly Tyr Lys Val Glu Gln Pro Phe

Glu Glu Asp Glu Met Asp Leu Asp Ser Glu Asp Glu Asp

90

100 105
(2) INFORMATION FOR SEQ ID NO:2131:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..68
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600191
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

Met Tyr Val Lys Ile Asp Asp Gln Lys Leu Ala Ile Gly Thr Leu Ser 1 $$ 5 $$ 10 $$ 15

Val Asp Lys Asn Pro His Ile Gln Phe Asp Leu Ile Phe Asp Xaa Glu 20 25 30

Phe Glu Leu Ser His Thr Ser Lys Thr Thr Ser Val Phe Phe Thr Gly 35 40 45

Tyr Lys Val Glu Gln Pro Phe Glu Glu Asp Glu Met Asp Leu Asp Ser 50 55 60

Glu Asp Glu Asp

65

- (2) INFORMATION FOR SEQ ID NO:2132:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..426
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600196
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132: cgctcctcct ccatcatagc tcctggctcg cggctcagct tgccactacc agcaarcgct 60 cgtcacccgt cggttctccc cgagtagctc gtcgcgtcgg caatggagaa tttgagatct 120 caaaactgcc accaaggtgt tgccatggag ggcgtcaagt ttgcgccgga gaaggccaac 180 accaaccgga gagccctcag cgacatcaag aacataatag gaggcccaca ccagcacttg 240 gcggtcagca agagggctct gtcagaaaaa ccagctgcta ctgcaaatgc taaagatcaa 300 360 gctggctttg ttggacaccg tcagntcacc aggaaattcg ctgcaacatt sgcaaaccaa cctacagttg cccttctgga cccaattnga agtgaaagac tgaaaagaaa cgctgatacg 420 gcattt
- (2) INFORMATION FOR SEQ ID NO:2133:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600197
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

Leu Leu Leu His His Ser Ser Trp Leu Ala Ala Gln Leu Ala Thr Thr

1 5 10 15

Ser Xaa Arg Ser Ser Pro Val Gly Ser Pro Arg Val Ala Arg Arg Val
20 25 30

Gly Asn Gly Glu Phe Glu Ile Ser Lys Leu Pro Pro Arg Cys Cys His 35 40 45

Gly Gly Arg Gln Val Cys Ala Gly Glu Gly Gln His Gln Pro Glu Ser 50 55 60

Pro Gln Arg His Gln Glu His Asn Arg Arg Pro Thr Pro Ala Leu Gly

65 70 75 80 80 Gly Gln Glu Gly Ser Val Arg Lys Thr Ser Cys Tyr Cys Lys Cys 85 90 95

- (2) INFORMATION FOR SEQ ID NO:2134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600198
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

Met Glu Asn Leu Arg Ser Gln Asn Cys His Gln Gly Val Ala Met Glu 1 5 10 15

Gly Val Lys Phe Ala Pro Glu Lys Ala Asn Thr Asn Arg Arg Ala Leu 20 25 30

Ser Asp Ile Lys Asn Ile Ile Gly Gly Pro His Gln His Leu Ala Val

Ser Lys Arg Ala Leu Ser Glu Lys Pro Ala Ala Thr Ala Asn Ala Lys
50 55 60

Asp Gln Ala Gly Phe Val Gly His Arg Gln Xaa Thr Arg Lys Phe Ala 65 70 75 80

Ala Thr Xaa Ala Asn Gln Pro Thr Val Ala Leu Leu Asp Pro Ile Xaa 85 90 95

Ser Glu Arg Leu Lys Arg Asn Ala Asp Thr Ala Phe 100 105

- (2) INFORMATION FOR SEQ ID NO:2135:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..94
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600199
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

Met Glu Gly Val Lys Phe Ala Pro Glu Lys Ala Asn Thr Asn Arg Arg 1 5 10 15

Ala Leu Ser Asp Ile Lys Asn Ile Ile Gly Gly Pro His Gln His Leu 20 25 30

Ala Val Ser Lys Arg Ala Leu Ser Glu Lys Pro Ala Ala Thr Ala Asn 35 40 45

Ala Lys Asp Gln Ala Gly Phe Val Gly His Arg Gln Xaa Thr Arg Lys 50 55 60

Phe Ala Ala Thr Xaa Ala Asn Gln Pro Thr Val Ala Leu Leu Asp Pro 65 70 75 80

Ile Xaa Ser Glu Arg Leu Lys Arg Asn Ala Asp Thr Ala Phe 85 90

- (2) INFORMATION FOR SEQ ID NO:2136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

Page 1104 Client Docket No. 80146.003 (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..325 (D) OTHER INFORMATION: / Ceres Seq. ID 1600201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136: aaaaccttgc ccctgctcct cacgccgccg ccgccgccgc cgccgccgtc gccgccacca 60 catecgtage geceageege eggagaagag gagggageea geaceageea eeatgggteg 120 cgtccgcacc aagaccgtga agaagacctc caggcaggtg atcgagaagt actactcccg 180 catgaccete gaettecaca ecaacaagaa ggtgetggaa gaggtetega teeteeeete 240 gaagegeete egeaacaagg ttgeeggett caccacceae etgatgegee gnatecageg 300 gggccccgtc cgtggcatct cgctc (2) INFORMATION FOR SEQ ID NO:2137: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..108 (D) OTHER INFORMATION: / Ceres Seq. ID 1600202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137: Lys Pro Cys Pro Cys Ser Ser Arg Arg Arg Arg Arg Arg Arg Arg Arg 10 5 Arg Arg His His Ile Arg Ser Ala Gln Pro Pro Glu Lys Arg Arg Glu 25 20 Pro Ala Pro Ala Thr Met Gly Arg Val Arg Thr Lys Thr Val Lys Lys 40 Thr Ser Arg Gln Val Ile Glu Lys Tyr Tyr Ser Arg Met Thr Leu Asp 55 Phe His Thr Asn Lys Lys Val Leu Glu Glu Val Ser Ile Leu Pro Ser 75 7.0 Lys Arg Leu Arg Asn Lys Val Ala Gly Phe Thr Thr His Leu Met Arg 90 8.5 Xaa Ile Gln Arg Gly Pro Val Arg Gly Ile Ser Leu 105 100 (2) INFORMATION FOR SEQ ID NO:2138: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1600203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138: Met Gly Arg Val Arg Thr Lys Thr Val Lys Lys Thr Ser Arg Gln Val 5 1.0 Ile Glu Lys Tyr Tyr Ser Arg Met Thr Leu Asp Phe His Thr Asn Lys 30 25 Lys Val Leu Glu Glu Val Ser Ile Leu Pro Ser Lys Arg Leu Arg Asn

45

Lys Val Ala Gly Phe Thr Thr His Leu Met Arg Xaa Ile Gln Arg Gly 55 Pro Val Arg Gly Ile Ser Leu

- 70
- (2) INFORMATION FOR SEQ ID NO:2139:

60

120

180 240

300

360

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..392 (D) OTHER INFORMATION: / Ceres Seq. ID 1600215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139: atagcttggc tcgcacggtg tcgctggctc ccctcccctt ccctccccac tgttacatcc agcgagctgt tcacggccgt gcssagctca gtgaggcagc gtttgcgagt ccgggacgag gggageggeg ggegaeatgg ggagggeeg cagegagata aageggateg agaaceecae qcaqcggcag tccaccttct acaagcgcag ggacggcctc ttcaagaagg ctagggagct ctccgttctg tgcgacgtgg acctgctgct gctcctcttc tccacctccg gcaagctcta ccactacete tegeceaceg teceeteegt caaggacetg gtegagaggt acgaggeeae gacgcacacc aaggtctgga ccgacatccg cc (2) INFORMATION FOR SEQ ID NO:2140: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..77 (D) OTHER INFORMATION: / Ceres Seq. ID 1600216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140: Ile Ala Trp Leu Ala Arg Cys Arg Trp Leu Pro Ser Pro Ser Leu Pro 10 5 Thr Val Thr Ser Ser Glu Leu Phe Thr Ala Val Xaa Ser Ser Val Arg 25 2.0 Gln Arg Leu Arg Val Arg Asp Glu Gly Ser Gly Gly Arg His Gly Glu 40 45 Gly Pro Gln Arg Asp Lys Ala Asp Arg Glu Pro His Ala Ala Ala Val 55 His Leu Leu Gln Ala Gln Gly Arg Pro Leu Gln Glu Gly 75 70 (2) INFORMATION FOR SEQ ID NO:2141: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1600217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141: Ser Leu Ala Arg Thr Val Ser Leu Ala Pro Leu Pro Phe Pro Pro His 10 5 Cys Tyr Ile Gln Arg Ala Val His Gly Arg Xaa Xaa Leu Ser Glu Ala 25 Ala Phe Ala Ser Pro Gly Arg Gly Glu Arg Arg Ala Thr Trp Gly Gly
- Ala Ala Arg 50
- (2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..85 (D) OTHER INFORMATION: / Ceres Seq. ID 1600218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142: Met Gly Arg Gly Arg Ser Glu Ile Lys Arg Ile Glu Asn Pro Thr Gln 10 Arg Gln Ser Thr Phe Tyr Lys Arg Arg Asp Gly Leu Phe Lys Lys Ala 30 25 20 Arg Glu Leu Ser Val Leu Cys Asp Val Asp Leu Leu Leu Leu Phe 40 Ser Thr Ser Gly Lys Leu Tyr His Tyr Leu Ser Pro Thr Val Pro Ser 60 55 Val Lys Asp Leu Val Glu Arg Tyr Glu Ala Thr Thr His Thr Lys Val 75 70 Trp Thr Asp Ile Arg 8.5 (2) INFORMATION FOR SEQ ID NO:2143: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..466 (D) OTHER INFORMATION: / Ceres Seq. ID 1600233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143: tgaagggtac gtcgacgagc aaccatacgg caacgatcgt gttcaacagc agtcgttggg 60 gtgaageegt egeegategt ggeageette tegtegegeg gneeeagegt egeeageece 120 ggagtgetga agcccgacat catggcgccg gggctcaaca tactcgccgc gtggccgtcg 180 gaggtgeeeg tegggggeee ceagtegage agetteaacg tegteteegg caegteeatg 240 gcgacgcgca tatcaccggc gtcgggccct cgtcaagaag gtgcacccgg actggtccac 300 cgccgcgatc aagtccgcca tcatgacacg tccagcgccg tcgacaacgc gggcaaccag 360 atcatggacg aggagcaccg gaaggcgagc ttctactccg tcggcgccgg ccacgttgtc 420 ccggcgaagg ccgtaagacc ccggcctggt gtacgacctc ggcgtc (2) INFORMATION FOR SEQ ID NO:2144: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1600234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144: Lys Gly Thr Ser Thr Ser Asn His Thr Ala Thr Ile Val Phe Asn Ser 10 5 Ser Arg Trp Gly Glu Ala Val Ala Asp Arg Gly Ser Leu Leu Val Ala 25 Arg Xaa Gln Arg Arg Gln Pro Arg Ser Ala Glu Ala Arg His His Gly 35

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Client Docket No. 80146.003
Ala Gly Ala Gln His Thr Arg Arg Val Ala Val Gly Gly Ala Arg Arg
                        55
Gly Pro Pro Val Glu Gln Leu Gln Arg Arg Leu Arg His Val His Gly
                                        75
                    70
Asp Ala His Ile Thr Gly Val Gly Pro Ser Ser Arg Arg Cys Thr Arg
                                   90
               85
Thr Gly Pro Pro Pro Arg Ser Ser Pro Pro Ser
                                105
           100
(2) INFORMATION FOR SEQ ID NO:2145:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 108 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..108
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600235
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:
Met Ala Pro Gly Leu Asn Ile Leu Ala Ala Trp Pro Ser Glu Val Pro
                                    10
                5
Val Gly Gly Pro Gln Ser Ser Ser Phe Asn Val Val Ser Gly Thr Ser
           20
                                25
Met Ala Thr Arg Ile Ser Pro Ala Ser Gly Pro Arg Gln Glu Gly Ala
                            40
Pro Gly Leu Val His Arg Arg Asp Gln Val Arg His His Asp Thr Ser
                        55
Ser Ala Val Asp Asn Ala Gly Asn Gln Ile Met Asp Glu Glu His Arg
                                        75
                    70
Lys Ala Ser Phe Tyr Ser Val Gly Ala Gly His Val Val Pro Ala Lys
                                    90
               85
Ala Val Arg Pro Arg Pro Gly Val Arg Pro Arg Arg
                                105
            100
(2) INFORMATION FOR SEQ ID NO:2146:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 76 amino acids
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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..76
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600236
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

Met Ala Thr Arg Ile Ser Pro Ala Ser Gly Pro Arg Gln Glu Gly Ala
1 10 15

Pro Gly Leu Val His Arg Arg Asp Gln Val Arg His His Asp Thr Ser 20 25 30

Ser Ala Val Asp Asn Ala Gly Asn Gln Ile Met Asp Glu Glu His Arg 35 40 45

Lys Ala Ser Phe Tyr Ser Val Gly Ala Gly His Val Val Pro Ala Lys 50 55 60

Ala Val Arg Pro Arg Pro Gly Val Arg Pro Arg Arg

- (2) INFORMATION FOR SEQ ID NO:2147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..446
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

ccaccacaca gcatccatca aagaaacaag agcacacaaa caatacctct ctagctcgcc accaacaatg gcctctaggt tctccatcat gctcgccaca acggcactgg ctacgttttt 120 tgtgattggt tcgtgcacca accatcgcc cttcaaggtc ggcaaaggct ccaagcctgg ctacgttttt tgtggcgatgac ctcacccca acattgccac catctccgaa gtggagatca aggagcacgg 240 tggcgatgac ttctcctttg agctcaagga gggcccggcc ggcacctgga cgcttgacac aaaggccca ctcaagtacc ccctctgcat ccgctttgcc atcaagtctg gcggctaccg 360 catcgccgat gatgtcatcc ctgaaaattt taaggccgac accacctaca agaccacct 420 cagcatctga tcatcctctt atgarg

- (2) INFORMATION FOR SEQ ID NO:2148:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600250
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:
- His Thr His Ala Ser Ile Lys Glu Thr Arg Ala His Lys Gln Tyr Leu
 1 10 15
- Ser Ser Ser Pro Pro Thr Met Ala Ser Arg Phe Ser Ile Met Leu Ala 20 25 30
- Thr Thr Ala Leu Ala Thr Phe Phe Val Ile Gly Ser Cys Thr Thr Pro 35 40 45
- Leu Thr Phe Lys Val Gly Lys Gly Ser Lys Pro Gly His Leu Val Leu 50 55 60
- Thr Pro Asn Ile Ala Thr Ile Ser Glu Val Glu Ile Lys Glu His Gly 65 70 80
- Gly Asp Asp Phe Ser Phe Glu Leu Lys Glu Gly Pro Ala Gly Thr Trp 85 90 95
- Thr Leu Asp Thr Lys Ala Pro Leu Lys Tyr Pro Leu Cys Ile Arg Phe
 100 105 110
- Ala Ile Lys Ser Gly Gly Tyr Arg Ile Ala Asp Asp Val Ile Pro Glu
 115 120 125
- Asn Phe Lys Ala Asp Thr Thr Tyr Lys Thr Thr Leu Ser Ile 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2149:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600251
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:
- Met Ala Ser Arg Phe Ser Ile Met Leu Ala Thr Thr Ala Leu Ala Thr 1 10 15
- Phe Phe Val Ile Gly Ser Cys Thr Thr Pro Leu Thr Phe Lys Val Gly 20 25 30

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Lys Gly Ser Lys Pro Gly His Leu Val Leu Thr Pro Asn Ile Ala Thr 35

Ile Ser Glu Val Glu Ile Lys Glu His Gly Gly Asp Asp Phe Ser Phe 50

Glu Leu Lys Glu Gly Pro Ala Gly Thr Trp Thr Leu Asp Thr Lys Ala 65
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65 70 75 80

Pro Leu Lys Tyr Pro Leu Cys Ile Arg Phe Ala Ile Lys Ser Gly Gly

85 90 95

Tyr Arg Ile Ala Asp Asp Val Ile Pro Glu Asn Phe Lys Ala Asp Thr

100 105 Thr Tyr Lys Thr Thr Leu Ser Ile

Thr Tyr Lys Thr Thr Led Ser 11e 115 120

- (2) INFORMATION FOR SEQ ID NO:2150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150: Met Leu Ala Thr Thr Ala Leu Ala Thr Phe Phe Val Ile Gly Ser Cys 10 5 Thr Thr Pro Leu Thr Phe Lys Val Gly Lys Gly Ser Lys Pro Gly His 25 2.0 Leu Val Leu Thr Pro Asn Ile Ala Thr Ile Ser Glu Val Glu Ile Lys 40 Glu His Gly Gly Asp Asp Phe Ser Phe Glu Leu Lys Glu Gly Pro Ala 55 Gly Thr Trp Thr Leu Asp Thr Lys Ala Pro Leu Lys Tyr Pro Leu Cys 75 70 Ile Arg Phe Ala Ile Lys Ser Gly Gly Tyr Arg Ile Ala Asp Asp Val 90 8.5 Ile Pro Glu Asn Phe Lys Ala Asp Thr Thr Tyr Lys Thr Thr Leu Ser 105 100
- Ile
- (2) INFORMATION FOR SEQ ID NO:2151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..486
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600256
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151: 60 tctaggatga atagattcaa aagaagggct ctaagggtca ttgctgatca tttghctgct gaggaagttg aggatataaa ggatatgttc aagactatgg atactgacaa tgatggaatt 120 gtatcttatg aagaactgaa gactggaata gcaaaacttg gttctcatct tgcggaatca 180 gaagtacaga tgctcattga agctgtggac acaaacggga ggggggcact agactacggg 240 300 gaatttctgg ccgtctcgct ccacctgcag aggatggcga acgacgagca tctccggcgg 360 gccttcctgt tcttcgacaa ggacggcaac ggtttcatcg agcccgagga gcttcgagag gctctggtgg acgacgggc gtccgacdtc atcgaggaag tggtgaacga catactgcaa gaagtcgaca ccgacaagga cggcaagatc agctacgagg agtttgtggc gatgatgaag 480 accggc

- (2) INFORMATION FOR SEQ ID NO:2152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600257
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:
- Ser Arg Met Asn Arg Phe Lys Arg Arg Ala Leu Arg Val Ile Ala Asp 1 5 10 15
- His Leu Xaa Ala Glu Glu Val Glu Asp Ile Lys Asp Met Phe Lys Thr 20 25 30
- Met Asp Thr Asp Asn Asp Gly Ile Val Ser Tyr Glu Glu Leu Lys Thr 35 40 45
- Gly Ile Ala Lys Leu Gly Ser His Leu Ala Glu Ser Glu Val Gln Met 50 55 60
- Leu Ile Glu Ala Val Asp Thr Asn Gly Arg Gly Ala Leu Asp Tyr Gly
 70 75 80
- Glu Phe Leu Ala Val Ser Leu His Leu Gln Arg Met Ala Asn Asp Glu 85 90 95
- His Leu Arg Arg Ala Phe Leu Phe Phe Asp Lys Asp Gly Asn Gly Phe 100 105 110
- Ile Glu Pro Glu Glu Leu Arg Glu Ala Leu Val Asp Asp Gly Ala Ser 115 120 125
- Asp Xaa Ile Glu Glu Val Val Asn Asp Ile Leu Gln Glu Val Asp Thr 130 135 140
- Asp Lys Asp Gly Lys Ile Ser Tyr Glu Glu Phe Val Ala Met Met Lys 145 150 155 160
 Thr Gly
- (2) INFORMATION FOR SEQ ID NO:2153:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600258
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:
- Met Asn Arg Phe Lys Arg Arg Ala Leu Arg Val Ile Ala Asp His Leu
 1 10 15
- Xaa Ala Glu Glu Val Glu Asp Ile Lys Asp Met Phe Lys Thr Met Asp 20 25 30
- Thr Asp Asn Asp Gly Ile Val Ser Tyr Glu Glu Leu Lys Thr Gly Ile 35 40 45
- Ala Lys Leu Gly Ser His Leu Ala Glu Ser Glu Val Gln Met Leu Ile 50 55 60
- Glu Ala Val Asp Thr Asn Gly Arg Gly Ala Leu Asp Tyr Gly Glu Phe 65 70 75 80
- Leu Ala Val Ser Leu His Leu Gln Arg Met Ala Asn Asp Glu His Leu 85 90 95
- Arg Arg Ala Phe Leu Phe Phe Asp Lys Asp Gly Asn Gly Phe Ile Glu 100 105 110
- Pro Glu Glu Leu Arg Glu Ala Leu Val Asp Asp Gly Ala Ser Asp Xaa

		115					120					125			
Ile	Glu	Glu	Val	Val	Asn	Asp	Ile	Leu	Gln	Glu	Val	Asp	Thr	Asp	Lys
	130					135					140				
Asp	Gly	Lys	Ile	Ser	Tyr	Glu	Glu	Phe	Val	Ala	Met	Met	Lys	Thr	Gly
145	_	_			150					155					160

- (2) INFORMATION FOR SEQ ID NO:2154:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600259
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met Phe Lys Thr Met Asp Thr Asp Asn Asp Gly Ile Val Ser Tyr Glu
1 10 15

Glu Leu Lys Thr Gly Ile Ala Lys Leu Gly Ser His Leu Ala Glu Ser 20 25 30

Glu Val Gln Met Leu Ile Glu Ala Val Asp Thr Asn Gly Arg Gly Ala

Leu Asp Tyr Gly Glu Phe Leu Ala Val Ser Leu His Leu Gln Arg Met 50 55 60

Ala Asn Asp Glu His Leu Arg Arg Ala Phe Leu Phe Phe Asp Lys Asp 65 70 75 80

Gly Asn Gly Phe Ile Glu Pro Glu Glu Leu Arg Glu Ala Leu Val Asp $95\,$

Asp Gly Ala Ser Asp Xaa Ile Glu Glu Val Val Asn Asp Ile Leu Gln
100 105 110

Glu Val Asp Thr Asp Lys Asp Gly Lys Ile Ser Tyr Glu Glu Phe Val 115 120 125

Ala Met Met Lys Thr Gly

130

- (2) INFORMATION FOR SEQ ID NO:2155:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..493
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

tcgaaaaaac cttactatgc tgatctcctt gatttgttca atgaggttga gttcaagaca 60 gcttcaggtc agctgctgga ccttatcact acccatgagg gagaaaaaga tctaacaaag 120 tataacataa cagttcacgg tcgaattgtt caatacaaga cagcctatta ttcattttat 180 240 ctgccggttg catgtgccct gctgctctct ggcgagaatt tggacaatta tggtgatgta gagaacatcc ttgttgaaat gggaacatac tttcaagtcc aggatgacta tctggattgt 300 tatggtgatc ctgaatttat cggcaagatt ggaacggaca ttgaagatta caagtgctca 360 tggctagttg tgcaagccct tgagcgtgct gatgagagcc aaaagcgcat tctatttgaa 420 aattatggca agaaagatca gcctgtgtgg caaaagtgaa gaacctctac aaagaacttg acctagaggc ggt

- (2) INFORMATION FOR SEQ ID NO:2156:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids

- (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..152 (D) OTHER INFORMATION: / Ceres Seq. ID 1600270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156: Ser Lys Lys Pro Tyr Tyr Ala Asp Leu Leu Asp Leu Phe Asn Glu Val 10 Glu Phe Lys Thr Ala Ser Gly Gln Leu Leu Asp Leu Ile Thr Thr His 30 2.0 Glu Gly Glu Lys Asp Leu Thr Lys Tyr Asn Ile Thr Val His Gly Arg 40 Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro Val Ala 55 Cys Ala Leu Leu Ser Gly Glu Asn Leu Asp Asn Tyr Gly Asp Val 70 Glu Asn Ile Leu Val Glu Met Gly Thr Tyr Phe Gln Val Gln Asp Asp 90 85 Tyr Leu Asp Cys Tyr Gly Asp Pro Glu Phe Ile Gly Lys Ile Gly Thr 100 105 110 Asp Ile Glu Asp Tyr Lys Cys Ser Trp Leu Val Val Gln Ala Leu Glu 125 120 Arg Ala Asp Glu Ser Gln Lys Arg Ile Leu Phe Glu Asn Tyr Gly Lys 135 Lys Asp Gln Pro Val Trp Gln Lys 150 (2) INFORMATION FOR SEQ ID NO:2157: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..383 (D) OTHER INFORMATION: / Ceres Seq. ID 1600285 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157: atcacaaatc tatctcgctc gctctccagg ctccagctag actgtcctgc tctgcttccg 120 180 agtectgeag egeaacaatg gacaggeetg egeaggegee caegeagetg eegeeggggt tccggttcca ccctaccgac gaggagctgg tcgtgctgta cctccgccgg aagsscctgg 240 ctcgcccgct gccggccgcc gtcatccccg tcgtccacga gtcgccaggc tcgatccgtg 300 ggacgtccct ggggcgagcg aaggggaggg ctacttcttc agcctgcggc gangcgcssg 360 gcgaccggcc gcagagggag ggc
 - (2) INFORMATION FOR SEQ ID NO:2158:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600286
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:
 - Ile Thr Asn Leu Ser Arg Ser Leu Ser Arg Leu Gln Leu Asp Cys Pro

1 5 10 15
Ala Leu Leu Pro Cys Tyr Ser Leu Cys Thr Ala Ser Gln Leu Gln Gln
20 25 30
Ser Pro Ala Arg Leu Ser Ala Ala Ser Pro Ala Ala Gln Gln Trp Thr
35 40 45
Cly Lou Arg Arg Arg Pro Arg Ser Cys Arg Arg Gly Ser Gly Ser Thr

Gly Leu Arg Arg Arg Pro Arg Ser Cys Arg Arg Gly Ser Gly Ser Thr 50 55 60

Leu Pro Thr Arg Ser Trp Ser Cys Cys Thr Ser Ala Gly Xaa Xaa Trp 65 70 75 80

Leu Ala Arg Cys Arg Pro Pro Ser Ser Pro Ser Ser Thr Ser Arg Gln 85 90 95

Ala Arg Ser Val Gly Arg Pro Trp Gly Glu Arg Arg Gly Gly Leu Leu 100 105 110

Leu Gln Pro Ala Ala Xaa Arg Xaa Ala Thr Gly Arg Arg Gly Arg 115 120 125

- (2) INFORMATION FOR SEQ ID NO:2159:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600287
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

His Lys Ser Ile Ser Leu Ala Leu Gln Ala Pro Ala Arg Leu Ser Cys
1 10 15

Ser Ala Ser Val Leu Leu Thr Val His Ser Gln Pro Ala Ser Ala Glu 20 25 30

Ser Gly Ser Ala Val Gly Cys Glu Ser Cys Ser Ala Thr Met Asp Arg

Pro Ala Gln Ala Pro Thr Gln Leu Pro Pro Gly Phe Arg Phe His Pro 50 55 60

Thr Asp Glu Glu Leu Val Val Leu Tyr Leu Arg Arg Lys Xaa Leu Ala 65 70 80

Arg Pro Leu Pro Ala Ala Val Ile Pro Val Val His Glu Ser Pro Gly 85 90 95

Ser Ile Arg Gly Thr Ser Leu Gly Arg Ala Lys Gly Arg Ala Thr Ser 100 105 110

Ser Ala Cys Gly Xaa Ala Xaa Gly Asp Arg Pro Gln Arg Glu Gly 115 120 125

- (2) INFORMATION FOR SEQ ID NO:2160:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

Met Asp Arg Pro Ala Gln Ala Pro Thr Gln Leu Pro Pro Gly Phe Arg

Phe His Pro Thr Asp Glu Glu Leu Val Val Leu Tyr Leu Arg Arg Lys
20 25 30

Xaa Leu Ala Arg Pro Leu Pro Ala Ala Val Ile Pro Val Val His Glu
35 40 45

Ser Pro Gly Ser Ile Arg Gly Thr Ser Leu Gly Arg Ala Lys Gly Arg 50 55 60

Ala Thr Ser Ser Ala Cys Gly Xaa Ala Xaa Gly Asp Arg Pro Gln Arg 65 70 75 80

Glu Gly

- (2) INFORMATION FOR SEQ ID NO:2161:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..482
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600289
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161: tcaaattcag gccaaaggaa ctggaagatt gcatgctaag gcttgaccca gaattgattg 60 gtctgaatac taggctgaaa gagatgaaga aacaaaatgc cagcatctcg gaaatggaga 120 180 ccatacggag gagtatgact attcggatga agcagttgat gcctatttat actcaggttg ccacacgatt tgccgaattg catgacacct ctgctagaat ggccgccaaa ggtgtgatcg 240 gtaaggttgt tgattggaaa gagtctcggg ccttcttcta caggagattg cgaaggagag 300 ttgctgagga tgccctggcc aaggaagtta aagaagctgc tggcgagcag cttttcccac 360 agatcagcat tagactgtat caagaaatgg tatctagcgt ccaaaggaac tgaaggtgat 420 ggtgaaatgt ggaatgatga tgaatctttc tttgctggaa ggatgatccc aaaaactatg 480
- (2) INFORMATION FOR SEQ ID NO:2162:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..136
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600290
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:
- Lys Phe Arg Pro Lys Glu Leu Glu Asp Cys Met Leu Arg Leu Asp Pro 1 5 10 15
- Glu Leu Ile Gly Leu Asn Thr Arg Leu Lys Glu Met Lys Lys Gln Asn 20 25 30
- Ala Ser Ile Ser Glu Met Glu Thr Ile Arg Arg Ser Met Thr Ile Arg 35 40 45
- Met Lys Gln Leu Met Pro Ile Tyr Thr Gln Val Ala Thr Arg Phe Ala 50 55 60
- Glu Leu His Asp Thr Ser Ala Arg Met Ala Ala Lys Gly Val Ile Gly 65 70 75 80
- Lys Val Val Asp Trp Lys Glu Ser Arg Ala Phe Phe Tyr Arg Arg Leu 85 90 95 Arg Arg Val Ala Glu Asp Ala Leu Ala Lys Glu Val Lys Glu Ala
- 100 105 110

 Ala Gly Glu Gln Leu Phe Pro Gln Ile Ser Ile Arg Leu Tyr Gln Glu

- 115 120 Met Val Ser Ser Val Gln Arg Asn 130 135
- (2) INFORMATION FOR SEQ ID NO:2163:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..126
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

Met Leu Arg Leu Asp Pro Glu Leu Ile Gly Leu Asn Thr Arg Leu Lys

1 10 15

Glu Met Lys Lys Gln Asn Ala Ser Ile Ser Glu Met Glu Thr Ile Arg 20 25 30

Arg Ser Met Thr Ile Arg Met Lys Gln Leu Met Pro Ile Tyr Thr Gln 35 40 45

Val Ala Thr Arg Phe Ala Glu Leu His Asp Thr Ser Ala Arg Met Ala 50 60

Ala Lys Gly Val Ile Gly Lys Val Val Asp Trp Lys Glu Ser Arg Ala 65 70 75 80

Phe Phe Tyr Arg Arg Leu Arg Arg Arg Val Ala Glu Asp Ala Leu Ala 85 90 95

Lys Glu Val Lys Glu Ala Ala Gly Glu Gln Leu Phe Pro Gln Ile Ser 100 105 110

Ile Arg Leu Tyr Gln Glu Met Val Ser Ser Val Gln Arg Asn 115 120 125

- (2) INFORMATION FOR SEQ ID NO:2164:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600292
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

Met Lys Lys Gln Asn Ala Ser Ile Ser Glu Met Glu Thr Ile Arg Arg 1 5 10 15

Ser Met Thr Ile Arg Met Lys Gln Leu Met Pro Ile Tyr Thr Gln Val 20 25 30

Ala Thr Arg Phe Ala Glu Leu His Asp Thr Ser Ala Arg Met Ala Ala 35 40 45

Lys Gly Val Ile Gly Lys Val Val Asp Trp Lys Glu Ser Arg Ala Phe
50 55 60

Phe Tyr Arg Arg Leu Arg Arg Arg Val Ala Glu Asp Ala Leu Ala Lys 65 70 75 80 Glu Val Lys Glu Ala Ala Gly Glu Gln Leu Phe Pro Gln Ile Ser Ile

\$85\$ \$90\$ Arg Leu Tyr Gln Glu Met Val Ser Ser Val Gln Arg Asn \$100\$ \$105\$

- (2) INFORMATION FOR SEQ ID NO:2165:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..448
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165: gtggatttaa aagtctaaaa tgtcattttc agaaaatgta ccttgattct tttgtagttt gctatgcatc agcagcattt aatatcatga taataacatt ctctgtacta acagcacatg 120 tggggttgca ggaaaagatt aatgtccatg gaggagctgt gtctctaggg catcctcttg 180 ggtgcagcgg tgctcgcatt ttggtcaccc ttcttggtgt ccttagggaa aagggcggca 240 agateggtgt tgetggtgte tgeaaeggeg gaggtggage ateagetett gttetegaae tegeataaga agtattgget tgaagcactg gatatgtage taattcagte geattcatet atacatgatg aagtattgaa aaaaaaagac cctacgatat ccatgccggg tgccactgtc tgcttaattc amcagaatat gattgtgc (2) INFORMATION FOR SEQ ID NO:2166: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:
- Gly Phe Lys Ser Leu Lys Cys His Phe Gln Lys Met Tyr Leu Asp Ser $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$
- Phe Val Val Cys Tyr Ala Ser Ala Ala Phe Asn Ile Met Ile Ile Thr 20 25 30
- Phe Ser Val Leu Thr Ala His Val Gly Leu Gln Glu Lys Ile Asn Val 35 40 45
- His Gly Gly Ala Val Ser Leu Gly His Pro Leu Gly Cys Ser Gly Ala 50 55 60
- Arg Ile Leu Val Thr Leu Leu Gly Val Leu Arg Glu Lys Gly Gly Lys 65 70 75 80
- Ile Gly Val Ala Gly Val Cys As
n Gly Gly Gly Ala Ser Ala Leu 85 90 95
- Val Leu Glu Leu Ala

- (2) INFORMATION FOR SEQ ID NO:2167:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..90
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600295
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:
- Met Tyr Leu Asp Ser Phe Val Val Cys Tyr Ala Ser Ala Ala Phe Asn 1 5 10 15
- Ile Met Ile Ile Thr Phe Ser Val Leu Thr Ala His Val Gly Leu Gln $20 \\ 25 \\ 30$
- Glu Lys Ile Asn Val His Gly Gly Ala Val Ser Leu Gly His Pro Leu $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$
- Gly Cys Ser Gly Ala Arg Ile Leu Val Thr Leu Leu Gly Val Leu Arg $50 \hspace{1.5cm} 55 \hspace{1.5cm} 60$
- Glu Lys Gly Gly Lys Ile Gly Val Ala Gly Val Cys Asn Gly Gly Gly 65 70 75 80
- Gly Ala Ser Ala Leu Val Leu Glu Leu Ala 85 90
- (2) INFORMATION FOR SEQ ID NO:2168:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids(B) TYPE: amino acid(C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..73
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600296
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

Met Ile Ile Thr Phe Ser Val Leu Thr Ala His Val Gly Leu Gln Glu 1 5 10 15

Lys Ile Asn Val His Gly Gly Ala Val Ser Leu Gly His Pro Leu Gly 20 25 30

Cys Ser Gly Ala Arg Ile Leu Val Thr Leu Leu Gly Val Leu Arg Glu 35 40 45

Lys Gly Gly Lys Ile Gly Val Ala Gly Val Cys Asn Gly Gly Gly Gly 50 55 60

Ala Ser Ala Leu Val Leu Glu Leu Ala 65 70

- (2) INFORMATION FOR SEQ ID NO:2169:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..498
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600310
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169: atccagatec ggaccetace geogatecat ccaaateace etteceette ecettetet

ceaceaceae caceaega cegeckeeks sgtegteete aatteteett tegaatttag 120 aateeeegtg etgagagttg agtgeegeet tegetgetee gtaetggaet egatteetea 180 tegeageaga ageateeegt eeeeteeget teteettget etgetetgae aaaaaaaatag 240 cateatgteg gaggtgaagg acteeaatgt geetgetgea ettgatggaa ateeteaaee 300 tatggaecaa actgaagaca attetatgee etcageaega caacaggaag aageaateaa 360 gaagaagttt ggaggaetaa tgeecaaaaa geeceeaete ateteaaagg ateatgggeg ggeetatttt gattetgetg actgggetet agggaageaa ggtgttgeea aaceaaaagg 480 acegetggag geacttag

- (2) INFORMATION FOR SEQ ID NO:2170:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..75
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600311
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

Ser Arg Ser Gly Pro Tyr Arg Arg Ser Ile Gln Ile Thr Leu Pro Leu 1 5 10 15

Pro Leu Leu Phe His His His His Gln Ala Ala Xaa Val Val 20 25 30

Leu Asn Ser Pro Phe Glu Phe Arg Ile Pro Val Leu Arg Val Glu Cys 35 40 45

Arg Leu Gly Cys Ser Val Leu Asp Ser Ile Pro His Arg Ser Arg Ser

Ile Pro Ser Pro Pro Leu Leu Leu Ala Leu Leu 7.0

- (2) INFORMATION FOR SEQ ID NO:2171:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600312
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

Met Ser Glu Val Lys Asp Ser Asn Val Pro Ala Ala Leu Asp Gly Asn 10

Pro Gln Pro Met Asp Gln Thr Glu Asp Asn Ser Met Pro Ser Ala Gln 25 20

Gln Gln Glu Glu Ala Ile Lys Lys Phe Gly Gly Leu Met Pro Lys 40

Lys Pro Pro Leu Ile Ser Lys Asp His Glu Arg Ala Tyr Phe Asp Ser 50 55 60

Ala Asp Trp Ala Leu Gly Lys Gln Gly Val Ala Lys Pro Lys Gly Pro 70

Leu Glu Ala Leu

- (2) INFORMATION FOR SEO ID NO:2172:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..65
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600313
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

Met Asp Gln Thr Glu Asp Asn Ser Met Pro Ser Ala Gln Gln Glu Glu 10

Glu Ala Ile Lys Lys Phe Gly Gly Leu Met Pro Lys Lys Pro Pro 20 25

Leu Ile Ser Lys Asp His Glu Arg Ala Tyr Phe Asp Ser Ala Asp Trp 40 45

Ala Leu Gly Lys Gln Gly Val Ala Lys Pro Lys Gly Pro Leu Glu Ala 55

Leu

- (2) INFORMATION FOR SEQ ID NO:2173:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600322
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

caagttccgc atgtcactgg gtctaccggt ggcggccacg gtgaactgcg cggacaacac 120 gggcgcgaag aacctctaca tcatctccgt caagggaatc aagggccgcc tcaaccgcct 180 cccgtccgcc tgcgtcggcg acatggtcat ggccaccgtc aagaagggaa agcccgacct 240 caggaagaaa gtgatgcctg ccgtcatcgt ccgccagcgc aagccgtggc gtcgcaagga 300 cggtgtctac atgtacttcg aagataatgc tggagtgatt gtgaatccca agggtgagat 360 gaaaggttct gcaatcactg gacctatcgg caaggagtgt gctgaccttt ggcctaggat 420 cgctagtgca gcaaatgcca tcgtttgaga gcttgttgga atgtgtttag acttgagtat 480 qatcatctca attgtgtgtt g

- (2) INFORMATION FOR SEQ ID NO:2174:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600323
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

Glu Asn Pro Thr Gln Ala Ala Val Met Ser Lys Arg Gly Arg Gly Gly 1 5 10 15

Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala Ala 20 25 30

Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile Ile 35 40 45

Ser Val Lys Gly Ile Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala Cys 50 55 60

Val Gly Asp Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp Leu 65 70 75 80

Arg Lys Lys Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Pro Trp 85 90 95

Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly Val
100 105 110

Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly Pro 115 120 125

Ile Gly Lys Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala Ala 130 135 140

Asn Ala Ile Val

145

- (2) INFORMATION FOR SEQ ID NO:2175:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600324
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

Met Ser Lys Arg Gly Arg Gly Gly Ser Ala Gly Asn Lys Phe Arg Met 1 $$ 5 $$ 10 $$ 15

Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr $20 \\ 25 \\ 30$

Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg 35 40 45

Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr 50 60

Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val

420

480

65 70 75 Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr Met 85 90 95 Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met 100 105 110 Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu 115 120 125 Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val 130 135 (2) INFORMATION FOR SEQ ID NO:2176: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..125 (D) OTHER INFORMATION: / Ceres Seq. ID 1600325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176: Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn 10 Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly 25 Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala 40 Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala 55 Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp 100 105 Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val 115 120 (2) INFORMATION FOR SEQ ID NO:2177: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 490 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..490 (D) OTHER INFORMATION: / Ceres Seq. ID 1600326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177: aatcaattct ccagaccctc cccggcaacc gcgtccggcc gtccgcttcc gtttccttgg 60 ataaccacga cgcccgcccg cccccggca agcgaaagcg aagcgagcca acccagccat 120 ggagaaggeg ategategge agegggteet eetggegeae etecteeet eeceeteege 180 egecteeteg eagecteage ttgeggegte ggegtgegeg geeggggaea gegeegeeta 240 ccagaggtcc tectecttcg gggacgatgt cgtcgtcgtc gctgcctaca ggacgccgat 300 atgcaaggcc aagcgaggag gcttcaagga cacctaccca gaggacctcc tcactgttgt 360

(2) INFORMATION FOR SEQ ID NO:2178:

ttgctggatt

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids

totcaaggot gttotggaca acactagaat caatccagot gacatcggtg acatcgtcgt

tgggacggtg ctcggccctg gttcccagcg tgcaaacgag tgcaggatgg ctgcgcttgt

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:
- Asn Gln Phe Ser Arg Pro Ser Pro Ala Thr Ala Ser Gly Arg Pro Leu
 1 10 15
- Pro Phe Pro Trp Ile Thr Thr Thr Pro Ala Arg Pro Pro Ala Ser Glu 20 25 30
- Ser Glu Ala Ser Gln Pro Ser His Gly Glu Gly Asp Arg Ser Ala Ala
- Gly Pro Pro Gly Ala Pro Pro Pro Leu Pro Leu Arg Arg Leu Leu Ala
- Ala Ser Ala Cys Gly Val Gly Val Arg Gly Arg Gly Gln Arg Arg Leu
 65 70 75 80
- Pro Glu Val Leu Leu Arg Gly Arg Cys Arg Arg Arg Cys Leu 85 90 95
- Gln Asp Ala Asp Met Gln Gly Gln Ala Arg Arg Leu Gln Gly His Leu 100 105 110
- Pro Arg Gly Pro Pro His Cys Cys Ser Gln Gly Cys Ser Gly Gln His
 115 120 125
- (2) INFORMATION FOR SEQ ID NO:2179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600328
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:
- Ser Ile Leu Gln Thr Leu Pro Gly Asn Arg Val Arg Pro Ser Ala Ser 1 5 10 15
- Val Ser Leu Asp Asn His Asp Ala Arg Pro Pro Pro Gly Lys Arg Lys 20 25 30
- Arg Ser Glu Pro Thr Gln Pro Trp Arg Arg Arg Ser Ile Gly Ser Gly 35 40 45
- Ser Ser Trp Arg Thr Ser Ser Pro Pro Pro Pro Pro Pro Pro Pro Arg Ser 50 55 60
- Leu Ser Leu Arg Arg Arg Arg Ala Arg Pro Gly Thr Ala Pro Pro Thr 65 70 80
- Arg Gly Pro Pro Ser Gly Thr Met Ser Ser Ser Ser Leu Pro Thr
 85 90 95
- Gly Arg Arg Tyr Ala Arg Pro Ser Glu Glu Ala Ser Arg Thr Pro Thr
- Gln Arg Thr Ser Ser Leu Leu Phe Ser Arg Leu Phe Trp Thr Thr Leu 115 120 125
- Glu Ser Ile Gln Leu Thr Ser Val Thr Ser Ser Leu Gly Arg Cys Ser 130 135 140
- Ala Leu Val Pro Ser Val Gln Thr Ser Ala Gly Trp Leu Arg Leu Phe 145 150 155 160
- Ala Gly

(2) INFORMATION FOR SEQ ID NO:2180: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..124 (D) OTHER INFORMATION: / Ceres Seq. ID 1600329 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180: Met Glu Lys Ala Ile Asp Arg Gln Arg Val Leu Leu Ala His Leu Leu 10 5 Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro Gln Leu Ala Ala Ser Ala 25 20 Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln Arg Ser Ser Ser Phe Gly 45 40 Asp Asp Val Val Val Ala Ala Tyr Arg Thr Pro Ile Cys Lys Ala 60 55 Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro Glu Asp Leu Leu Thr Val 70 75 Val Leu Lys Ala Val Leu Asp Asn Thr Arg Ile Asn Pro Ala Asp Ile 90 8.5 Gly Asp Ile Val Val Gly Thr Val Leu Gly Pro Gly Ser Gln Arg Ala 110 100 105 Asn Glu Cys Arg Met Ala Ala Leu Val Cys Trp Ile 120 115 (2) INFORMATION FOR SEQ ID NO:2181: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..447 (D) OTHER INFORMATION: / Ceres Seq. ID 1600333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181: actcacaget caaaagcage caaaacgeta getagetgea gegatgatgt etegeteetg 60 ctgcctcgcc gtgtcggtcc ttctcgcggt cgcgcgacag ccagcggcgc catcgcgccg 120 gcgttgctgc acgagggcg cctcgaggat atcgacgcgt gctccgccga gtgcgaggtc 180 cacategege aggagtgget tgacaagetg ceaceacegt cetaegagga gegataegtg 240 300 ctcacgcgcg cgtccaggaa ccgcgagctc aacaagcacg cgcgcctggg ctgccaggtc gtcctcgcgc cggagctgca ggggatggtc gtcgccatcc ccgagcctaa gccgtgggac 360 atcccataat ggcctgccga cgaaaggtaa ggtgcggctt ttgacgctgt gagccttcct 420 taattccctt ggctgtcaag ctgtgcg (2) INFORMATION FOR SEQ ID NO:2182: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..122 (D) OTHER INFORMATION: / Ceres Seq. ID 1600334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182:

Thr His Ser Ser Lys Ala Ala Lys Thr Leu Ala Ser Cys Ser Asp Asp

1 5 10 15

Val Ser Leu Leu Leu Pro Arg Arg Val Gly Pro Ser Arg Gly Arg Ala
20 25 30

Thr Ala Ser Gly Ala Ile Ala Pro Ala Leu Leu His Glu Gly Arg Leu

35 40 45

Glu Asp Ile Asp Ala Cys Ser Ala Glu Cys Glu Val His Ile Ala Gln 50 55 60

Glu Trp Leu Asp Lys Leu Pro Pro Pro Ser Tyr Glu Glu Arg Tyr Val 65 70 75 80

Leu Thr Arg Ala Ser Arg Asn Arg Glu Leu Asn Lys His Ala Arg Leu 85 90 95

Gly Cys Gln Val Val Leu Ala Pro Glu Leu Gln Gly Met Val Val Ala 100 105 110

Ile Pro Glu Pro Lys Pro Trp Asp Ile Pro 115 120

- (2) INFORMATION FOR SEQ ID NO:2183:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

Ala Arg Gln Pro Ala Ala Pro Ser Arg Arg Cys Cys Thr Arg Gly
20 25 30

21 25 Ser Ala Arg Ser Thr Ser

Ala Ser Arg Ile Ser Thr Arg Ala Pro Pro Ser Ala Arg Ser Thr Ser 35 40 45
Arg Arg Ser Gly Leu Thr Ser Cys His His Arg Pro Thr Arg Ser Asp

50 55 60
Thr Cys Ser Arg Ala Arg Pro Gly Thr Ala Ser Ser Thr Ser Thr Arg

65 70 75 80
Ala Trp Ala Ala Arg Ser Ser Ser Arg Arg Ser Cys Arg Gly Trp Ser

85 90 95
Ser Pro Ser Pro Ser Leu Ser Arg Gly Thr Ser His Asn Gly Leu Pro
100 105 110

Thr Lys Gly Lys Val Arg Leu Leu Thr Leu
115 120

- (2) INFORMATION FOR SEQ ID NO:2184:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..121
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

Met Ser Arg Ser Cys Cys Leu Ala Val Ser Val Leu Leu Ala Val Ala 1 5 10 15

Arg Gln Pro Ala Ala Pro Ser Arg Arg Cys Cys Thr Arg Gly Ala
20 25 30

Ser Arg Ile Ser Thr Arg Ala Pro Pro Ser Ala Arg Ser Thr Ser Arg

```
Arg Ser Gly Leu Thr Ser Cys His His Arg Pro Thr Arg Ser Asp Thr 50 55 60
```

Cys Ser Arg Ala Arg Pro Gly Thr Ala Ser Ser Thr Ser Thr Arg Ala 65 70 75 80

Trp Ala Ala Arg Ser Ser Ser Arg Arg Ser Cys Arg Gly Trp Ser Ser 85 90 95

Pro Ser Pro Ser Leu Ser Arg Gly Thr Ser His Asn Gly Leu Pro Thr $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Lys Gly Lys Val Arg Leu Leu Thr Leu 115 120

- (2) INFORMATION FOR SEQ ID NO:2185:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..503
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600346
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

aaaaaaacca gcgactcaca caccegegeg cegettetgt agggeeccaa ceaacegege 60 agggagaaaa ccaccacage acatgcageg cctcgcctcc tcccggaggc tcctccaggc 120 egegetegee eeeggeeeggg ceaacteeag ceteteegeg geegeegteg eeggeeege 180 qccaqcqaat ggcgccttcc cgaagatgcc ggccttcgac tacacgccgc cgccgtacga 240 cqqqccqcqc qccqaqqaqa tcttccqqaa qcqcqctcaq ttcctcaqcc catccctttt 300 tcatttctac gatcgcccat tgaacatagt cgaaggaaag atgcagtacc tatttgatga 360 ggatggccgt cgttacctgg atgctttcgg tggcattgca acagtttgtt gtgggcactg 420 ccatccagat gtgttgaage catagtaaac caggcaaage ggatccagea etecacagtt 480 ctatatctca atcatgcaat tgc

- (2) INFORMATION FOR SEQ ID NO:2186:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..147
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600347
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

Lys Lys Pro Ala Thr His Thr Pro Ala Arg Arg Phe Cys Arg Ala Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Thr Asn Arg Ala Gly Arg Lys Pro Pro Gln His Met Gln Arg Leu Ala 20 25 30

Ser Ser Arg Arg Leu Leu Gln Ala Ala Leu Ala Pro Ala Arg Ala Asn 35 40 45

Ser Ser Leu Ser Ala Ala Ala Val Ala Ala Pro Ala Pro Ala Asn Gly 50 55 60

Ala Phe Pro Lys Met Pro Ala Phe Asp Tyr Thr Pro Pro Pro Tyr Asp 65 70 75 80

Gly Pro Arg Ala Glu Glu Ile Phe Arg Lys Arg Ala Gln Phe Leu Ser 85 90 95

Pro Ser Leu Phe His Phe Tyr Asp Arg Pro Leu Asn Ile Val Glu Gly 100 105

Lys Met Gln Tyr Leu Phe Asp Glu Asp Gly Arg Arg Tyr Leu Asp Ala 115 120 125

Phe Gly Gly Ile Ala Thr Val Cys Cys Gly His Cys His Pro Asp Val 130 135 140 Leu Lys Pro 145 (2) INFORMATION FOR SEQ ID NO:2187: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..106 (D) OTHER INFORMATION: / Ceres Seq. ID 1600348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187: Lys Asn Gln Arg Leu Thr His Pro Arg Ala Ala Ser Val Gly Pro Gln 10 5 Pro Thr Ala Gln Gly Glu Asn His His Ser Thr Cys Ser Ala Ser Pro 30 25 20 Pro Pro Gly Gly Ser Ser Arg Pro Arg Ser Pro Pro Pro Gly Pro Thr 40 35 Pro Ala Ser Pro Arg Pro Pro Ser Pro Arg Pro Arg Gln Arg Met Ala 55 Pro Ser Arg Arg Cys Arg Pro Ser Thr Thr Arg Arg Arg Arg Thr Thr 75 70 Gly Arg Ala Pro Arg Arg Ser Ser Gly Ser Ala Leu Ser Ser Ser Ala 85 90 His Pro Phe Phe Ile Ser Thr Ile Ala His 105 100 (2) INFORMATION FOR SEQ ID NO:2188: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..120 (D) OTHER INFORMATION: / Ceres Seq. ID 1600349 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188: Met Gln Arg Leu Ala Ser Ser Arg Arg Leu Leu Gln Ala Ala Leu Ala 10 Pro Ala Arg Ala Asn Ser Ser Leu Ser Ala Ala Ala Val Ala Ala Pro 30 25 Ala Pro Ala Asn Gly Ala Phe Pro Lys Met Pro Ala Phe Asp Tyr Thr 4.5 40 Pro Pro Pro Tyr Asp Gly Pro Arg Ala Glu Glu Ile Phe Arg Lys Arg 55 60 Ala Gln Phe Leu Ser Pro Ser Leu Phe His Phe Tyr Asp Arg Pro Leu 75 Asn Ile Val Glu Gly Lys Met Gln Tyr Leu Phe Asp Glu Asp Gly Arg 90 Arg Tyr Leu Asp Ala Phe Gly Gly Ile Ala Thr Val Cys Cys Gly His 105 100 Cys His Pro Asp Val Leu Lys Pro 115 (2) INFORMATION FOR SEQ ID NO:2189: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..484
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600361
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

gttgttgttg atccaaaaag ccacctccc ccaacccaat cccgtcgtca ctctctcact 60 ccactgcctc cggaacaccc tagcaatgga gcccaactcc agcatccctc ccccggtgat 120 gggcgcggcg gtggcgtacc ctccggcggc cggcgccgcg tactccgccg ggccgtacgc 180 gcacgcgcac gcggcgttgg gcgcgctgta cccgcctccc ccggcgccgg gtcccccctc 240 ctcgcaccag ggcggcacgg cggcggcac gctgcagctg ttctgggcgg agcagtaccg 300 cgagatcgag gcgacgacgg acttcaagaa ccacaacctg ccgctggccc gcatcaagaa 360 gateatgaag geggaegagg aegtgegeat gategeegee gaggegeegg tggtgttege 420 ccgcgcctgc gagatgttca tcctggagct gacccaccgc ggctgggcgc acgcggagga 480 gaac

- (2) INFORMATION FOR SEQ ID NO:2190:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600362
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:
- Val Val Val Asp Pro Lys Ser His Leu Pro Pro Thr Gln Ser Arg Arg

 1 10 15
- His Ser Leu Thr Pro Leu Pro Pro Glu His Pro Ser Asn Gly Ala Gln 20 25 30
- Leu Gln His Pro Ser Pro Gly Asp Gly Arg Gly Gly Val Pro Ser 35 40 45
- Gly Gly Arg Arg Arg Val Leu Arg Arg Ala Val Arg Ala Arg 50 55 60
- Gly Val Gly Arg Ala Val Pro Ala Ser Pro Gly Ala Gly Ser Pro Leu
 65 70 75 80
- Leu Ala Pro Gly Arg His Gly Gly Gly Ala Ala Ala Ala Val Leu Gly $85 \\ 90 \\ 95$
- Gly Ala Val Pro Arg Asp Arg Gly Asp Asp Gly Leu Gln Glu Pro Gln $100 \,$ $105 \,$ $110 \,$
- Pro Ala Ala Gly Pro His Gln Glu Asp His Glu Gly Gly Arg Gly Arg 115 120 125
- Ala His Asp Arg Arg Gly Ala Gly Gly Val Arg Pro Arg Leu Arg 130 135 140
- Asp Val His Pro Gly Ala Asp Pro Pro Arg Leu Gly Ala Arg Gly Gly 145 150 155 160
- (2) INFORMATION FOR SEQ ID NO:2191:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191: Leu Leu Leu Ile Gln Lys Ala Thr Ser Pro Gln Pro Asn Pro Val Val 10 Thr Leu Ser Leu His Cys Leu Arg Asn Thr Leu Ala Met Glu Pro Asn 25 Ser Ser Ile Pro Pro Pro Val Met Gly Ala Ala Val Ala Tyr Pro Pro 40 Ala Ala Gly Ala Ala Tyr Ser Ala Gly Pro Tyr Ala His Ala His Ala 55 Ala Leu Gly Ala Leu Tyr Pro Pro Pro Pro Ala Pro Gly Pro Pro Ser 70 Ser His Gln Gly Gly Thr Ala Ala Ala Gln Leu Gln Leu Phe Trp Ala 8.5 Glu Gln Tyr Arg Glu Ile Glu Ala Thr Thr Asp Phe Lys Asn His Asn 100 105 Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val 120 125 115 Arg Met Ile Ala Ala Glu Ala Pro Val Val Phe Ala Arg Ala Cys Glu 140 130 135 Met Phe Ile Leu Glu Leu Thr His Arg Gly Trp Ala His Ala Glu Glu 155 150 Asn

- (2) INFORMATION FOR SEQ ID NO:2192:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600364
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:
- Met Glu Pro Asn Ser Ser Ile Pro Pro Pro Val Met Gly Ala Ala Val

 5 10 15

 15 20 Ala Ala Cly Pro Tyr Ala
- Ala Tyr Pro Pro Ala Ala Gly Ala Ala Tyr Ser Ala Gly Pro Tyr Ala 20 25 30
- His Ala His Ala Ala Leu Gly Ala Leu Tyr Pro Pro Pro Pro Ala Pro 35 40 45 Gly Pro Pro Ser Ser His Gln Gly Gly Thr Ala Ala Ala Gln Leu Gln
- 50 55 60 50 50 Fro Ser Ser HIS GIR GIY GIY THE ALL THE CIN Det Cin Det
- Leu Phe Trp Ala Glu Gln Tyr Arg Glu Ile Glu Ala Thr Thr Asp Phe 65 70 75 80
- Lys Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala 85 90 95
- Asp Glu Asp Val Arg Met Ile Ala Ala Glu Ala Pro Val Val Phe Ala 100 105 110
- Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr His Arg Gly Trp Ala 115 120 125
- His Ala Glu Glu Asn 130
- (2) INFORMATION FOR SEQ ID NO:2193:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600383
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193: gggccaagtc gcagacgcgg agccaccgcc attttttta ctcccgaaac caggcaggag 60 ggaggaggcg acgacatcgc catcacacca gatcactgaa gaagagagag gcgcgtcgag 120 tctccccaaa gaacgagcta gtacaaagtc tcctcttcct ttgactccga atcccctaga 180 ccattgatgg ttgcgggggc accggaagga gccactgacg atgggcctct gctcctcctc 240 cacegoogce egggeogcet ecgacecegg egeogcagee gegggtgatg eegeogegge 300 aaagaagggg cgcgggatcg tcgcgtgcgg gaagcggacc gacttcggat acgacaagga 360 tttcgaggtg cgctactcgc ttgggaagct tttgggccac ggccagttcg gctacacctt 420 tgccgccgtc gatcgcgcct ccaccgagcg cgtcg
- (2) INFORMATION FOR SEQ ID NO:2194:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..61
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600384
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Gly Gln Val Ala Asp Ala Glu Pro Pro Pro Phe Phe Leu Leu Pro Lys
1 10 15

Pro Gly Arg Arg Glu Glu Ala Thr Thr Ser Pro Ser His Gln Ile Thr 20 25 30

Glu Glu Glu Arg Gly Ala Ser Ser Leu Pro Lys Glu Arg Ala Ser Thr 35 40 45

Lys Ser Pro Leu Pro Leu Thr Pro Asn Pro Leu Asp His 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2195:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600385
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

Met Gly Leu Cys Ser Ser Ser Thr Ala Ala Arg Ala Ala Ser Asp Pro

1 5 10 15

Gly Ala Ala Ala Gly Asp Ala Ala Ala Lys Lys Gly Arg Gly
20 25 30

Ile Val Ala Cys Gly Lys Arg Thr Asp Phe Gly Tyr Asp Lys Asp Phe 35 40 45

Glu Val Arg Tyr Ser Leu Gly Lys Leu Leu Gly His Gly Gln Phe Gly 50 55 60

Tyr Thr Phe Ala Ala Val Asp Arg Ala Ser Thr Glu Arg Val 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2196:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600386
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:
- Met Pro Pro Arg Gln Arg Arg Gly Ala Gly Ser Ser Arg Ala Gly Ser 1 10 15
- Gly Pro Thr Ser Asp Thr Thr Arg Ile Ser Arg Cys Ala Thr Arg Leu 20 25 30
- Gly Ser Phe Trp Ala Thr Ala Ser Ser Ala Thr Pro Leu Pro Pro Ser 35 40 45
- Ile Ala Pro Pro Pro Ser Ala Ser 50 55
- (2) INFORMATION FOR SEQ ID NO:2197:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..502
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600395
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:
- ctcccgcaga gcagccgaca actctctacc gtccgagacc ccaagcacca gcgcggcggc 120 ggcggcggcg gcgaccatgg ctgtcgggaa gaacaagagg atctccaagg gaaagaaggg 180 tggcaagaaa aagaccgtcg accetttete taagaaggat tggtatgaca tcaaggcace gtcggtgttc agtgtgcgca acatcgggaa ccgccgccga cgccgcagga ggagacgcat 240 cgagtttagc acgcgaagaa gcgaccatga gggccaagtg gaagaagaag cgcatgagga 300 ggctcaagag gaagcgcaga aagatgaggc agagatccaa gtaggcagat cgagatggat 360 tgtggacctg atgacatgcg tgggtacata catttcttcg gatgcgttgg tgtgcctgtg 420 gagagatgte aacetgeeat ggtgteaegg teegeeatea gttgaaegte tigeetgeae 480 ttcagtaggc catttttcat gg
- (2) INFORMATION FOR SEQ ID NO:2198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..167
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600396
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:
- Ser Arg Arg Ala Ala Asp Asn Ser Leu Pro Ser Glu Thr Pro Ser Thr 1 5 10 15
- Ser Ala Ala Ala Ala Ala Ala Thr Met Ala Val Gly Lys Asn Lys $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$
- Arg Ile Ser Lys Gly Lys Lys Gly Gly Lys Lys Lys Thr Val Asp Pro 35 40
- Phe Ser Lys Lys Asp Trp Tyr Asp Ile Lys Ala Pro Ser Val Phe Ser 50 55 60
- Val Arg Asn Ile Gly Asn Arg Arg Arg Arg Arg Arg Arg Arg Ile
 65 70 75 80
- Glu Phe Ser Thr Arg Arg Ser Asp His Glu Gly Gln Val Glu Glu Glu 85 90 95
- Ala His Glu Glu Ala Gln Glu Glu Ala Gln Lys Asp Glu Ala Glu Ile 100 105 110
- Gln Val Gly Arg Ser Arg Trp Ile Val Asp Leu Met Thr Cys Val Gly

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 125 120 115 Thr Tyr Ile Ser Ser Asp Ala Leu Val Cys Leu Trp Arg Asp Val Asn 135 140 Leu Pro Trp Cys His Gly Pro Pro Ser Val Glu Arg Leu Ala Cys Thr 155 150 Ser Val Gly His Phe Ser Trp 165 (2) INFORMATION FOR SEQ ID NO:2199: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..113 (D) OTHER INFORMATION: / Ceres Seq. ID 1600397 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199: Pro Ala Glu Gln Pro Thr Thr Leu Tyr Arg Pro Arg Pro Gln Ala Pro 10 5 Ala Arg Arg Arg Arg Arg Arg Pro Trp Leu Ser Gly Arg Thr Arg 20 25 Gly Ser Pro Arg Glu Arg Arg Val Ala Arg Lys Arg Pro Ser Thr Leu 40 Ser Leu Arg Arg Ile Gly Met Thr Ser Arg His Arg Arg Cys Ser Val 55 Cys Ala Thr Ser Gly Thr Ala Ala Asp Ala Ala Gly Gly Asp Ala Ser 70 75 Ser Leu Ala Arg Glu Glu Ala Thr Met Arg Ala Lys Trp Lys Lys 90 85 Arg Met Arg Arg Leu Lys Arg Lys Arg Lys Met Arg Gln Arg Ser 105 100 Lys (2) INFORMATION FOR SEQ ID NO:2200: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..142 (D) OTHER INFORMATION: / Ceres Seq. ID 1600398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200: Met Ala Val Gly Lys Asn Lys Arg Ile Ser Lys Gly Lys Lys Gly Gly 1.0 Lys Lys Lys Thr Val Asp Pro Phe Ser Lys Lys Asp Trp Tyr Asp Ile 25 20 Lys Ala Pro Ser Val Phe Ser Val Arg Asn Ile Gly Asn Arg Arg 40

60

120 180

240 300

360 420

Cys Leu Trp Arg Asp Val Asn Leu Pro Trp Cys His Gly Pro Pro Ser

115
120
125
127

Val Glu Arg Leu Ala Cys Thr Ser Val Gly His Phe Ser Trp 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..449
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600399
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

 aaaagaaaaa ggaaattttc ttgggcgttc ttcggcttca ttgtcacaag gttcgagttc
 gtcaccgtct agtacgactg tgcgagggag gaagaggcga ggagaagatg cagatcttcg
 tgaagaccct gacggggaag accatcaccc tcgaggtgga gagcagcgac accgtcgaca
 acgtcaaggc caaaatccag gacaaggaag ggattccccc agatcaacag cgactgatat
 tcgctggcaa gcagctggag gaatcccttc ctcatccagt gttctgtcct agcgccgccg
 ccgccccagc tcgccttgcg tgactgarag ctcgtcggct tccgtccacg cgtgaagcga

gagcatggac acccaggtga agcttgctgt tgtggtgaag gtgatgggca ggacggctca

- ggggtcaggt gacccaggtc agagtgaag (2) INFORMATION FOR SEQ ID NO:2202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600400
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:
- Lys Glu Lys Gly Asn Phe Leu Gly Arg Ser Ser Ala Ser Leu Ser Gln

 10 15

Gly Ser Ser Ser Pro Ser Ser Thr Thr Val Arg Gly Arg Lys Arg 20 25 30

Arg Gly Glu Asp Ala Asp Leu Arg Glu Asp Pro Asp Gly Glu Asp His 35 40 45

His Pro Arg Gly Gly Glu Gln Arg His Arg Arg Gln Arg Gln Gly Gln 50 55 60

Asn Pro Gly Gln Gly Arg Asp Ser Pro Arg Ser Thr Ala Thr Asp Ile
65 70 75 80

Arg Trp Gln Ala Ala Gly Gly Ile Pro Ser Ser Ser Ser Val Leu Ser 85 90 95

- (2) INFORMATION FOR SEQ ID NO:2203:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203: Lys Lys Lys Glu Ile Phe Leu Gly Val Leu Arg Leu His Cys His Lys 10 Val Arg Val Arg His Arg Leu Val Arg Leu Cys Glu Gly Gly Arg Gly 25 Glu Glu Lys Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile 40 Thr Leu Glu Val Glu Ser Ser Asp Thr Val Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe 70 75 Ala Gly Lys Gln Leu Glu Glu Ser Leu Pro His Pro Val Phe Cys Pro 90 85 Ser Ala Ala Ala Pro Ala Arg Leu Ala 100 (2) INFORMATION FOR SEQ ID NO:2204: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1600402 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204: Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu 10 5 Val Glu Ser Ser Asp Thr Val Asp Asn Val Lys Ala Lys Ile Gln Asp 25 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys 40 Gln Leu Glu Glu Ser Leu Pro His Pro Val Phe Cys Pro Ser Ala Ala 55 Ala Ala Pro Ala Arg Leu Ala 70 (2) INFORMATION FOR SEQ ID NO:2205: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 510 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..510 (D) OTHER INFORMATION: / Ceres Seq. ID 1600434 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205: gtcactagta gagccgtaga gggcaagagg cgacggaatg acggagcggc aggtggcgga 60 gctgggtccc gggacggcgt gctgcggctg gaaccactgt ggccgccgcc tcgccgctgg 120 cgccgtcgat ggctccgtct ccgtctatga ctcccagccg ccaccetcgt tcaagtggca 180 ggcccatgag caagccattg tgaatgtcgt ctggcttcct ccagagtatg gggatgctat 240 agcttgtgtt tgtgctgatg ggacactgtc tttgtgggag gaggttgctg ctgatgatca 300 acttccaacc tggagaaatt gtaaaatctt cgaggatggc aactctcata tactaaatgt 360 acattttgga ttacatctgg gaattctgaa aatggttact gcatactcag atggccaagt 420 caaggtctac gagctcttgg attcattgga attagacaag tggcagcttc aggcagagtt 480 ccaaaacatt actgatccaa tctctagatt

- (2) INFORMATION FOR SEQ ID NO:2206:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..157
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600435
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:
- Met Thr Glu Arg Gln Val Ala Glu Leu Gly Pro Gly Thr Ala Cys Cys $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$
- Gly Trp Asn His Cys Gly Arg Arg Leu Ala Ala Gly Ala Val Asp Gly 20 25 30
- Ser Val Ser Val Tyr Asp Ser Gln Pro Pro Pro Ser Phe Lys Trp Gln 35 40 45
- Ala His Glu Gln Ala Ile Val Asn Val Val Trp Leu Pro Pro Glu Tyr 50 55 60
- Gly Asp Ala Ile Ala Cys Val Cys Ala Asp Gly Thr Leu Ser Leu Trp 65 70 75 80
- Glu Glu Val Ala Ala Asp Asp Gln Leu Pro Thr Trp Arg Asn Cys Lys 85 90 95
- Ile Phe Glu Asp Gly Asn Ser His Ile Leu Asn Val His Phe Gly Leu 100 105 110
- His Leu Gly Ile Leu Lys Met Val Thr Ala Tyr Ser Asp Gly Gln Val 115 120 125
- Lys Val Tyr Glu Leu Leu Asp Ser Leu Glu Leu Asp Lys Trp Gln Leu 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2207:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..452
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600436
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:
- geogtgeeae acateegtkt geetetkete eetettgeeg gteeegaata aagageagea 60 gegeaagagg teggtagase gagaagaagg caatggegge egagacette etttteacet 120 eggagteegt gaacgagggg cacceegaca agetgtgega eeaggtgteeg gaegeegtge 180 ttgacgeatg eeteggeag gaeceegaca geaaggtgge etgegagaee tgeaecaaga 240 eeaacatggt gayggtgtye ggegagatea egaceaagge gaecgtggae taegagaaga 300 tegtgeega eacetgeege ragateggt teaecteega egacgtgge etgagaeeg 360 aeegetgeaa ggtgetggtg aacategage ageagteeee egacategeg eagggegtge 420 aeegggeaett eacgaagegg eeegagagaa te
- (2) INFORMATION FOR SEQ ID NO:2208:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600437
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

Cys Leu Ala Gl
n Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys Thr $35 \ \ \, 40 \ \ \, 45$

Lys Thr Asn Met Val Xaa Val Xaa Gly Glu Ile Thr Thr Lys Ala Thr 50 55 60

Val Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Xaa Ile Gly Phe 65 70 75 80

Thr Ser Asp Asp Val Gly Leu Asp Ala Asp Arg Cys Lys Val Leu Val 85 90 95

Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His 100 105 110

Phe Thr Lys Arg Pro Glu Glu Ile 115 120

- (2) INFORMATION FOR SEQ ID NO:2209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600438
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

Met Pro Arg Ala Gly Pro Arg Gln Gln Gly Gly Leu Arg Asp Leu His
1 10 15

Gln Asp Gln His Gly Xaa Gly Xaa Arg Arg Asp His Asp Gln Gly Asp 20 25 30

Arg Gly Leu Arg Glu Asp Arg Ala Arg His Leu Pro Xaa Asp Arg Val 35 40 45

His Leu Arg Arg Arg Gly Pro Arg Arg Pro Leu Gln Gly Ala Gly 50 55 60

Glu His Arg Ala Ala Val Pro Arg His Arg Ala Gly Arg Ala Arg Ala 65 70 75 80

Leu His Glu Ala Ala Arg Gly Asp 85

- (2) INFORMATION FOR SEQ ID NO:2210:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Met Val Xaa Val Xaa Gly Glu Ile Thr Thr Lys Ala Thr Val Asp Tyr 1 5 10 15 15 Glu Lys Ile Val Arg Asp Thr Cys Arg Xaa Ile Gly Phe Thr Ser Asp

Glu Lys Ile Val Arg Asp Thr Cys Arg Xaa Ile Gly Phe Thr Ser Asp 20 25 30

Asp Val Gly Leu Asp Ala Asp Arg Cys Lys Val Leu Val Asn Ile Glu 35 40 45

Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His Phe Thr Lys 50 55 60

Arg Pro Glu Glu Ile

(2) INFORMATION FOR SEO ID NO:2211: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 456 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..456 (D) OTHER INFORMATION: / Ceres Seq. ID 1600444 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211: ctctcggcga gtctttctct ttccccacct tcacttggcc gtcctcccga gctgcqqcqq cqcatcqatt qctaqqatqa aaatccqttc tcccqqcqat ttttqqctct cgqqaacaqa 120 caqqaqqatc cqcqqgaagq attcqqctqc gtcctagtgt agtgtcgaca tgqctqggcg 180 caaggagacc gcactcgacc tggcgaagtt cgtcgacaag ggcgtccagg tgaagctcac 240 cggcggccgc caagtgacag gaactttaaa gggatatgac cagctactca acctagtgct 300 agatgaagca gttgaatatg aaagagagca agatgaccca ttgaagctat cagggaaaac 360 cagacagett ggeeteattg tgtgeagagg caeggeagte atgetggtet caeegactga 420 tggaacctga tgasatcgcc aacccttttc ttgcgg (2) INFORMATION FOR SEQ ID NO:2212: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..51 (D) OTHER INFORMATION: / Ceres Seq. ID 1600445 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212: Ser Arg Arg Val Phe Leu Phe Pro His Leu His Leu Ala Val Leu Pro 10 Ser Cys Gly Gly Ala Ser Ile Ala Arg Met Lys Ile Arg Ser Pro Gly 20 25 Asp Phe Trp Leu Ser Gly Thr Asp Arg Arg Ile Arg Gly Lys Asp Ser 40 Ala Ala Ser 50 (2) INFORMATION FOR SEQ ID NO:2213: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..86 (D) OTHER INFORMATION: / Ceres Seq. ID 1600446 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213: Met Ala Gly Arg Lys Glu Thr Ala Leu Asp Leu Ala Lys Phe Val Asp 10 Lys Gly Val Gln Val Lys Leu Thr Gly Gly Arg Gln Val Thr Gly Thr 25 Leu Lys Gly Tyr Asp Gln Leu Leu Asn Leu Val Leu Asp Glu Ala Val 40

Glu Tyr Glu Arg Glu Gln Asp Asp Pro Leu Lys Leu Ser Gly Lys Thr

55

Arg Gln Leu Gly Leu Ile Val Cys Arg Gly Thr Ala Val Met Leu Val 65 70 75 80

Ser Pro Thr Asp Gly Thr 85

- (2) INFORMATION FOR SEQ ID NO:2214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..477
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600451
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

 acaaaaacct teeggegeeg eegeetgate getecagege eetegeegte ggeagetegg 60

 cegeegtact eeegetaceg agetaggagg eateacette geeggteeaa eatgggtaag 120

 acacgtggta tgggagetgg gegeaagete aagacceaca gaaggaacca gaggtggget 180

 gacaaaageet acaagaagag eeatetegge aacgagtgga agaaaceett tgetgggtea 240

 teteacgeaa agggaategt eettgagaag ateggeattg aggetaagea geetaactet geetateegta agtgeeteg tgtecagetg gtgaagaacg ggaagaagat tgetgeettt gaceaaceg atggtegta agggeeteg tgteggagat atteeggeg ateggtegt gattgetga 420

 teeggtegta agggeeatge tgtgggagat atteecggeg teegttteaa ggtegtg
- (2) INFORMATION FOR SEQ ID NO:2215: (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600452
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:
- Thr Lys Thr Phe Arg Arg Arg Arg Leu Ile Ala Pro Ala Pro Ser Pro 1 5 10 15 Ser Ala Ala Arg Pro Pro Tyr Ser Arg Tyr Arg Ala Arg Arg His His
- 20 25 30
 Leu Arg Arg Ser Asn Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg
- 45
 Lys Leu Lys Thr His Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr
- 50 55 60 Lys Lys Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser
- 65 70 75 80 Ser His Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys
- 85 90 95
 Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys
 100 105 110
- Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn 115 120 125
- Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys 130 135 140
- Gly His Ala Val Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val 145
- (2) INFORMATION FOR SEQ ID NO: 2216:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:
- Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$
- Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu 20 25 30
- Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly $35 \hspace{1cm} 40 \hspace{1cm} 45$
- Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala 50 55 60
- Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile 65 70 75 80
- Ala Ala Phe Val Pro As
n Asp Gly Cys Leu As
n Tyr Ile Glu Glu As
n 85 90 95
- Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly 100 105 110
- Asp Ile Pro Gly Val Arg Phe Lys Val Val 115 120
- (2) INFORMATION FOR SEQ ID NO: 2217:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:
- Met Gly Ala Gly Arg Lys Leu Lys Thr His Arg Arg Asn Gln Arg Trp 1 5 10 15
- Ala Asp Lys Ala Tyr Lys Lys Ser His Leu Gly Asn Glu Trp Lys Lys 20 25 30
- Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Val Leu Glu Lys Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$
- Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg 50 55 60
- Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn 65 70 75 80
- Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala 85 90 95
- Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg 100 105 110

Phe Lys Val Val

115

- (2) INFORMATION FOR SEQ ID NO:2218:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1600459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:	
ctteetteet tteecegete tteteccaea caaacgecae egeegeateg aateegagae	60
geogateteg gattegeogt caccacacge tgeoctegte gegetetece geogeogeog	120
ctcgtctcgt cagccatggc aggattggca ccagaagggt cgcaatttga tgacaagcag	180
tatgacaaga aaatgcagga gatattaact gaagacttct tcacttcata tgatgatgtt	240
tatgacaaga aaatgcagga gatattaact gaagacatta tagagagaat ctatgactat	300
tgtgaaagtt ttgacagcat gggactgcaa gagaaccttc tgagaggcat ctatgcctat	360
ggttttgaga agccatcggc tattcagcaa aggggaatag ttcccttctg caaggggctt	420
gacgtgattc agcaagctca gtctggaact ggaaaaacag ctaccttctg ttctggaatc	
ttgcagcaac ttgattatgg attggttgaa tgccaggcat tggttcttgc tccaacccgt	480
qaqcttqctc aqcaaattga g	

- (2) INFORMATION FOR SEQ ID NO:2219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..167
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

Leu Pro Ser Phe Pro Arg Ser Ser Pro Thr Gln Thr Pro Pro Pro His 1 5 5 10 10 15 15 Arg Ile Arg Asp Ala Asp Leu Gly Phe Ala Val Thr Thr Arg Cys Pro

20 25 30

Arg Arg Ala Leu Pro Pro Pro Pro Leu Val Ser Ser Ala Met Ala Gly
35
40
45

Leu Ala Pro Glu Gly Ser Gln Phe Asp Asp Lys Gln Tyr Asp Lys Lys
50 55 60

Met Gln Glu Ile Leu Thr Glu Asp Phe Phe Thr Ser Tyr Asp Asp Val 65 70 75 80

Cys Glu Ser Phe Asp Ser Met Gly Leu Gln Glu Asn Leu Leu Arg Gly
85
90
95

Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly
100 105 110

Ile Val Pro Phe Cys Lys Gly Leu Asp Val Ile Gln Gln Ala Gln Ser 115 120 125 125 Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser Gly Ile Leu Gln Gln Leu

Asp Tyr Gly Leu Val Glu Cys Gln Ala Leu Val Leu Ala Pro Thr Arg 145 150 155 160

Glu Leu Ala Gln Gln Ile Glu

165

- (2) INFORMATION FOR SEQ ID NO:2220:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

Met Ala Gly Leu Ala Pro Glu Gly Ser Gln Phe Asp Asp Lys Gln Tyr 1 5 10 15

Asp Lys Lys Met Gln Glu Ile Leu Thr Glu Asp Phe Phe Thr Ser Tyr 20 25 30

420

```
Asp Asp Val Cys Glu Ser Phe Asp Ser Met Gly Leu Gln Glu Asn Leu
                       40
Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln
                     55
                              60
Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp Val Ile Gln Gln
                  70 75
Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser Gly Ile Leu
              85
                   90
Gln Gln Leu Asp Tyr Gly Leu Val Glu Cys Gln Ala Leu Val Leu Ala
          100
                             105
Pro Thr Arg Glu Leu Ala Gln Gln Ile Glu
       115
                         120
(2) INFORMATION FOR SEQ ID NO:2221:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 103 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..103
         (D) OTHER INFORMATION: / Ceres Seq. ID 1600462
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:
Met Gln Glu Ile Leu Thr Glu Asp Phe Phe Thr Ser Tyr Asp Asp Val
                                10
            5
Cys Glu Ser Phe Asp Ser Met Gly Leu Gln Glu Asn Leu Leu Arg Gly
          20
                             25
Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly
                         40
Ile Val Pro Phe Cys Lys Gly Leu Asp Val Ile Gln Gln Ala Gln Ser
                      55
Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser Gly Ile Leu Gln Gln Leu
                 70
                      75 80
Asp Tyr Gly Leu Val Glu Cys Gln Ala Leu Val Leu Ala Pro Thr Arg
              85
Glu Leu Ala Gln Gln Ile Glu
          100
(2) INFORMATION FOR SEQ ID NO:2222:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 478 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
         (A) NAME/KEY: -
          (B) LOCATION: 1..478
         (D) OTHER INFORMATION: / Ceres Seq. ID 1600463
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:
                                                                   60
aaaqqaaaqc cccacaaaac ctcqqttqct ccccttqqcc cttqccatcc tcqttcctat
                                                                  120
egecagtteg ecaceteett tgetetegee tegegegege teececege geategtgee
                                                                  180
gttegecace geacegegee gatggaggte geegeegtge ceagateege egeggeetge
cgtgcggcgc ccctgctccc ggycgtccga gccgctgcgt gccacctggc cctgccccgg
                                                                  240
                                                                  300
egegegttet eegeateegt egeggeggea eggegegeg eegetegeeg etegtegege
                                                                  360
tgcggatggt gacagcgtgg agacggcgcc ggaggcggtc cccagttgag aaaaggttcc
```

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

ctcccttccc gagcgtcatg gacatcaacc agatccgcga gatcctcccc cacaggttcc

attccttttg gttgatagag taattgaata caaggbtgga gaatatgcag tggggatc

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Lys Gly Lys Pro His Lys Thr Ser Val Ala Pro Leu Gly Pro Cys His
1 10 15

Pro Arg Ser Tyr Arg Gln Phe Ala Thr Ser Phe Ala Leu Ala Ser Arg

Ala Leu Pro Pro Ala His Arg Ala Val Arg His Arg Thr Ala Pro Met 35 40

Glu Val Ala Ala Val Pro Arg Ser Ala Ala Ala Cys Arg Ala Ala Pro 50 55 60

Leu Leu Pro Xaa Val Arg Ala Ala Ala Cys His Leu Ala Leu Pro Arg 65 70 75 80

Arg Ala Phe Ser Ala Ser Val Ala Ala Ala Arg Arg Arg Ala Ala Arg 85 90 95

Arg Ser Ser Arg Cys Gly Trp 100

- (2) INFORMATION FOR SEQ ID NO:2224:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600465
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Lys Glu Ser Pro Thr Lys Pro Arg Leu Leu Pro Leu Ala Leu Ala Ile 1 5 10 15

Leu Val Pro Ile Ala Ser Ser Pro Pro Pro Leu Leu Ser Pro Arg Ala 20 25 30

Arg Ser Pro Pro Arg Ile Val Pro Phe Ala Thr Ala Pro Arg Arg Trp 35 40 45

Arg Ser Pro Pro Cys Pro Asp Pro Pro Arg Pro Ala Val Arg Arg Pro 50 55 60

Cys Ser Arg Xaa Ser Glu Pro Leu Arg Ala Thr Trp Pro Cys Pro Gly 65 70 80

Ala Arg Ser Pro His Pro Ser Arg Arg His Gly Ala Ala Pro Leu Ala 85 90 95

Ala Arg Arg Ala Ala Asp Gly Asp Ser Val Glu Thr Ala Pro Glu Ala 100 105 110

Val Pro Ser

115

- (2) INFORMATION FOR SEQ ID NO:2225:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1600466 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225: Arg Lys Ala Pro Gln Asn Leu Gly Cys Ser Pro Trp Pro Leu Pro Ser 10 5 Ser Phe Leu Ser Pro Val Arg His Leu Leu Cys Ser Arg Leu Ala Arg 25 30 20 Ala Pro Pro Arg Ala Ser Cys Arg Ser Pro Pro His Arg Ala Asp Gly 40 Gly Arg Arg Ala Gln Ile Arg Arg Gly Leu Pro Cys Gly Ala Pro 55 Ala Pro Xaa Arg Pro Ser Arg Cys Val Pro Pro Gly Pro Ala Pro Ala 75 70 Arg Val Leu Arg Ile Arg Arg Gly Gly Thr Ala Pro Arg Arg Ser Pro 90 85 Leu Val Ala Leu Arg Met Val Thr Ala Trp Arg Arg Arg Arg Arg Arg 110 105 Ser Pro Val Glu Lys Arg Phe Pro Pro Phe Pro Ser Val Met Asp Ile 125 120 Asn Gln Ile Arg Glu Ile Leu Pro His Arg Phe His Ser Phe Trp Leu 140 135 130 Ile Glu 145 (2) INFORMATION FOR SEQ ID NO:2226: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 468 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..468 (D) OTHER INFORMATION: / Ceres Seq. ID 1600471 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226: tttagcaaag gatatgacgg caaggatgtg gtggtccaga acttgcgcca agtttgtgtc 60 tttaaggttg ctaaggagca caagaagcct tggttatggt gggactacgt tactgatttt 120 gcgattcggt gcccgatgaa ggaaaagaag tacacaaagg agtgtgccga tggagttatc 180 aagtcacttg gccttgatca taaagcaata gataagtgta ttggtgatcc agatgcagat 240 gaggaaaacc atgttctgaa agctgaacag gatgcacaga ttggcaaggg ttctcgtggt 300 gatgttacca tcttaccaac tctggtaatc aacaatagac aatacagagg gaagcttgac 360 aaaggagcag ttcttaaagc actttgysst ggnctttagg gaaaccaccg agccagccgt 420 ttgcttgagt gatgatatac aaacaaacga gtgcctagag aacaatgg (2) INFORMATION FOR SEQ ID NO:2227: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..132 (D) OTHER INFORMATION: / Ceres Seq. ID 1600472 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227: Phe Ser Lys Gly Tyr Asp Gly Lys Asp Val Val Gln Asn Leu Arg 10 1 Gln Val Cys Val Phe Lys Val Ala Lys Glu His Lys Lys Pro Trp Leu 30 25 Trp Trp Asp Tyr Val Thr Asp Phe Ala Ile Arg Cys Pro Met Lys Glu 40 Lys Lys Tyr Thr Lys Glu Cys Ala Asp Gly Val Ile Lys Ser Leu Gly

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Attorney Docket No. 2750-1237P
Client Docket No. 80146.003
                        55
    50
Leu Asp His Lys Ala Ile Asp Lys Cys Ile Gly Asp Pro Asp Ala Asp
                                       75
                    70
Glu Glu Asn His Val Leu Lys Ala Glu Gln Asp Ala Gln Ile Gly Lys
                                    90
                85
Gly Ser Arg Gly Asp Val Thr Ile Leu Pro Thr Leu Val Ile Asn Asn
                                                    110
                               105
           100
Arg Gln Tyr Arg Gly Lys Leu Asp Lys Gly Ala Val Leu Lys Ala Leu
                            120
        115
Xaa Xaa Xaa Leu
    130
(2) INFORMATION FOR SEQ ID NO:2228:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 87 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..87
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600473
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:
Met Lys Glu Lys Lys Tyr Thr Lys Glu Cys Ala Asp Gly Val Ile Lys
                                    1.0
Ser Leu Gly Leu Asp His Lys Ala Ile Asp Lys Cys Ile Gly Asp Pro
                                2.5
Asp Ala Asp Glu Glu Asn His Val Leu Lys Ala Glu Gln Asp Ala Gln
```

40 Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu Pro Thr Leu Val

Ile Asn Asn Arg Gln Tyr Arg Gly Lys Leu Asp Lys Gly Ala Val Leu

55

70 Lys Ala Leu Xaa Xaa Xaa Leu 85

- (2) INFORMATION FOR SEQ ID NO:2229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..491
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229: atettcaace tetagetgat tgatetetge ageatggaca egaegagtga caagegtgeg teatecatge tggcccctaa ceetggcaag gecacgatee tegecettgg ceaegeette ccgcagcagc ttgtcatgca ggactacgtc gtcgacggct tcatgaagaa caccaactgt gacgacccgg agctcaagga gaagctcacc agactctgca agacgacgac cgtgaggact 240 cggtacgtgg tgatgtcgga tgagatcctc aagaactacc cggagctggc ccaggagggg 300 ctgccgacga tgaaccagcg tctggacatc tcgaacgcgg cggtgacgca gatggcgacg gaggcgtccc tgtcgtgcgt ccgctcgtgg ggcggcgcgc tctcgtccat tacccacctg 420 gtgtacgtct cgtcgagcga ggcgcgcttc ccgggcggcg acctgcacct ggcgcgcgcg ctggggctga g

60

75

- (2) INFORMATION FOR SEQ ID NO:2230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600479
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:
- Pro Gly Lys Ala Thr Ile Leu Ala Leu Gly His Ala Phe Pro Gln Gln 20 25 30
- Leu Val Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Asn 35 40 45
- Cys Asp Asp Pro Glu Leu Lys Glu Lys Leu Thr Arg Leu Cys Lys Thr 50 55 60
- Thr Thr Val Arg Thr Arg Tyr Val Val Met Ser Asp Glu Ile Leu Lys 65 70 75 80
- Asn Tyr Pro Glu Leu Ala Gln Glu Gly Leu Pro Thr Met Asn Gln Arg 85 90 95
- Leu Asp Ile Ser Asn Ala Ala Val Thr Gln Met Ala Thr Glu Ala Ser 100 105 110
- Leu Ser Cys Val Arg Ser Trp Gly Gly Ala Leu Ser Ser Ile Thr His 115 120 125
- Leu Val Tyr Val Ser Ser Ser Glu Ala Arg Phe Pro Gly Gly Asp Leu 130 135 140
- His Leu Ala Arg Ala Leu Gly Leu 145 150
- (2) INFORMATION FOR SEQ ID NO:2231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..141
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:
- Met Leu Ala Pro Asn Pro Gly Lys Ala Thr Ile Leu Ala Leu Gly His 1 5 10 15
- Ala Phe Pro Gln Gln Leu Val Met Gln Asp Tyr Val Val Asp Gly Phe 20 25 30
- Met Lys Asn Thr Asn Cys Asp Asp Pro Glu Leu Lys Glu Lys Leu Thr 35 40 45
- Arg Leu Cys Lys Thr Thr Thr Val Arg Thr Arg Tyr Val Val Met Ser 50 60
- Asp Glu Ile Leu Lys Asn Tyr Pro Glu Leu Ala Gln Glu Gly Leu Pro
 65 75 80
- Thr Met Asn Gln Arg Leu Asp Ile Ser Asn Ala Ala Val Thr Gln Met 85 90 95
- Ala Thr Glu Ala Ser Leu Ser Cys Val Arg Ser Trp Gly Gly Ala Leu 100 105 110
- Ser Ser Ile Thr His Leu Val Tyr Val Ser Ser Ser Glu Ala Arg Phe 115 120 125
- Pro Gly Gly Asp Leu His Leu Ala Arg Ala Leu Gly Leu 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2232:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600481
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Asn Cys Asp 1 5 10 15

Asp Pro Glu Leu Lys Glu Lys Leu Thr Arg Leu Cys Lys Thr Thr Thr 20 25 30

Val Arg Thr Arg Tyr Val Val Met Ser Asp Glu Ile Leu Lys Asn Tyr

Pro Glu Leu Ala Gln Glu Gly Leu Pro Thr Met Asn Gln Arg Leu Asp 50 55 60

Ile Ser Asn Ala Ala Val Thr Gln Met Ala Thr Glu Ala Ser Leu Ser 65 70 75 80

Cys Val Arg Ser Trp Gly Gly Ala Leu Ser Ser Ile Thr His Leu Val

Tyr Val Ser Ser Ser Glu Ala Arg Phe Pro Gly Gly Asp Leu His Leu 100 105 110

Ala Arg Ala Leu Gly Leu

115

- (2) INFORMATION FOR SEQ ID NO:2233:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..511
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600496
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

gegeacaegg cagaeggeae acaeaceaea ceacaeetee tegetteeae teegetegte 60 tgacatoteg tocogtoott togtttogaa gootogogag cocogacgat ggooacogog 120 qcqqtgtcqq tcqacqaqaa gctcqacaag cttcqcqccq aggtcqccaa gctcqaccag 180 atcagcgaga acgagaagtc cgggttcatc agcctcgtgt cacgctacct cagtggggaa 240 gcggagcaga tcgagtggag caagatccag acccctacgg atgaggtggt ggtgccctac 300 gataccgtcg cgtcgcctcc cgaagatetc gaggagacga agaagetget ggataagetc 360 gttgtgctca agcttaacgg agggctcggg acgaccatgg gctgcactgg gcccaagtct 420 gtcattgaag tccgcaatgg gttcacattc cttgacctta ttgtgattca aattgagtcc ctgaacaaga agtatggatg caatgtccct t

- (2) INFORMATION FOR SEQ ID NO:2234:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600497
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

Arg Thr Arg Gln Thr Ala His Thr Pro His His Thr Ser Ser Leu Pro 1 5 10 15

Leu Arg Ser Ser Asp Ile Ser Ser Arg Pro Phe Val Ser Lys Pro Arg

```
Glu Pro Arg Arg Trp Pro Pro Arg Arg Cys Arg Ser Thr Arg Ser Ser 35 40 45
```

Thr Ser Phe Ala Pro Arg Ser Pro Ser Ser Thr Arg Ser Ala Arg Thr 50 55 60

Arg Ser Pro Gly Ser Ser Ala Ser Cys His Ala Thr Ser Val Gly Lys 65 70 75 80

Arg Ser Arg Ser Ser Gly Ala Arg Ser Arg Pro Leu Arg Met Arg Trp 85 90 95

Trp Cys Pro Thr Ile Pro Ser Arg Arg Leu Pro Lys Ile Ser Arg Arg 100 105 110

Arg Arg Ser Cys Trp Ile Ser Ser Leu Cys Ser Ser Leu Thr Glu Gly 115 120 125

Ser Gly Arg Pro Trp Ala Ala Leu Gly Pro Ser Leu Ser Leu Lys Ser 130 135 140

Ala Met Gly Ser His Ser Leu Thr Leu Leu 145 150

- (2) INFORMATION FOR SEQ ID NO:2235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600498
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

Ser Ala Arg Leu Thr Ser Arg Pro Val Leu Ser Phe Arg Ser Leu Ala 20 25 30

Ser Pro Asp Asp Gly His Arg Gly Gly Val Gly Arg Arg Glu Ala Arg 35 40 45

Gln Ala Ser Arg Arg Gly Arg Gln Ala Arg Pro Asp Gln Arg Glu Arg 50 55 60

Glu Val Arg Val His Gln Pro Arg Val Thr Leu Pro Gln Trp Gly Ser 70 75 80

- Gly Ala Asp Arg Val Glu Gln Asp Pro Asp Pro Tyr Gly 85 90
- (2) INFORMATION FOR SEQ ID NO:2236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600499
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

Met Ala Thr Ala Ala Val Ser Val Asp Glu Lys Leu Asp Lys Leu Arg
1 10 15

Ala Glu Val Ala Lys Leu Asp Gln Ile Ser Glu Asn Glu Lys Ser Gly 20 25 30

Phe Ile Ser Leu Val Ser Arg Tyr Leu Ser Gly Glu Ala Glu Gln Ile 35 40 45

Glu Trp Ser Lys Ile Gln Thr Pro Thr Asp Glu Val Val Pro Tyr 50 55 60

Asp Thr Val Ala Ser Pro Pro Glu Asp Leu Glu Glu Thr Lys Lys Leu

75 70 65 Leu Asp Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr 90 85 Met Gly Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Phe 105 100 Thr Phe Leu Asp Leu Ile Val Ile Gln Ile Glu Ser Leu Asn Lys Lys 120

Tyr Gly Cys Asn Val Pro 130

- (2) INFORMATION FOR SEQ ID NO: 2237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..458
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600500
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

aacccagaaa gatcgcacta cccggcgctc gcgcggcttt ctttcccaac tccgacgaag 60 gctagctaca ccacctggtg cgggctcgtc tccatcgccc gccacccgct ccgtcgtcgt 120 cgtccccgcc gcgccgatcc cgaatcgaat ggggagcctg gcgtccgaga ggaaggtggt 180 cgggtgggcc gccagggacg ccaccggaca cctctccccc tactcctaca ccctcaggaa 240 cacaggeeet gaagatgtgg tggtgaaggt getetaetge gggatetgee acaeggaeat 300 ccaccaggec aagaaccacc teggggette aaagtateet atggteeetg ggeacgaggt 360 ggtcggcgag gtggtggagg tcgggcccga ggtggccaag tacggcgtcg gcgacgtggt 420 aggcgtcggg gtgatcgtgt gctgccgcga gtgcagcc

- (2) INFORMATION FOR SEQ ID NO:2238:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..83
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600501
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

Asn Pro Glu Arg Ser His Tyr Pro Ala Leu Ala Arg Leu Ser Phe Pro 10

Thr Pro Thr Lys Ala Ser Tyr Thr Thr Trp Cys Gly Leu Val Ser Ile 30 25 20

Ala Arg His Pro Leu Arg Arg Arg Arg Pro Arg Arg Ala Asp Pro Glu 40

Ser Asn Gly Glu Pro Gly Val Arg Glu Glu Gly Gly Arg Val Gly Arg 60 55

Gln Gly Arg His Arg Thr Pro Leu Pro Leu Leu Leu His Pro Gln Glu 75 70

His Arg Pro

- (2) INFORMATION FOR SEQ ID NO:2239:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:

Thr Gln Lys Asp Arg Thr Thr Arg Arg Ser Arg Gly Phe Leu Ser Gln 1 5 10

Leu Arg Arg Leu Ala Thr Pro Pro Gly Ala Gly Ser Ser Pro Ser 20 25 30

Pro Ala Thr Arg Ser Val Val Val Val Pro Ala Ala Pro Ile Pro Asn 35 40 45

Arg Met Gly Ser Leu Ala Ser Glu Arg Lys Val Val Gly Trp Ala Ala 50 55 60

Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Ser Tyr Thr Leu Arg Asn 70 75 80

Thr Gly Pro Glu Asp Val Val Val Lys Val Leu Tyr Cys Gly Ile Cys 85 90 95

His Thr Asp Ile His Gln Ala Lys Asn His Leu Gly Ala Ser Lys Tyr
100 105 110

Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Gly 115 120 125

Pro Glu Val Ala Lys Tyr Gly Val Gly Asp Val Val Gly Val Gly Val 130 135 140

Ile Val Cys Cys Arg Glu Cys Ser

145

150

- (2) INFORMATION FOR SEQ ID NO:2240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..103
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:

Met Gly Ser Leu Ala Ser Glu Arg Lys Val Val Gly Trp Ala Ala Arg

1 5 10 15

15 10 Arg Asp Thr

Asp Ala Thr Gly His Leu Ser Pro Tyr Ser Tyr Thr Leu Arg Asn Thr 20 c 25 c 30 Gly Pro Glu Asp Val Val Val Lys Val Leu Tyr Cys Gly Ile Cys His

35 40 45
Thr Asp Ile His Gln Ala Lys Asn His Leu Gly Ala Ser Lys Tyr Pro

Thr Asp Ile His Gln Ala Lys Asn His Leu Gly Ala Ser Lys Tyl Flo 50 55 60 Met Val Pro Gly His Glu Val Val Gly Glu Val Glu Val Gly Pro

65 70 75 80
Glu Val Ala Lys Tyr Gly Val Gly Asp Val Val Gly Val Gly Val Ile
85 90 95

Val Cys Cys Arg Glu Cys Ser

100

- (2) INFORMATION FOR SEQ ID NO:2241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..513
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:	
aaaaccaaat tcccaattcc caaaccccta gtagacccac gtctccggtc cccctctcct	60
cgcgcccgcc atggcagcct gcggcggcgc cggcgccggc tgcgggccgc agtgctcgtc	120
ctcctcctcc gcgggcggcc aggaggatgc tctggcggag agcatgggac gcctttcgac	180
cgcctccgcc gccgccgcgt gcggcaagtg cgacggcggc ggcgcggccg tcgcggtggc	240
cggcggcgtc ggcatgtgcg ccggctgctt ccgggctcac ctcttcggca agttcaagct	300
ctccgtcacg agcaacgcca tggtgcgccc cacagacgcc gtcctcctcg ccttctccgg	360
cggtcccgcc tccagggtgg ctctgcagtt catacacgag atgcagtcca aggcgatcca	420
gagetgggag gegageaact ceeaggeest geeggtette ageettegge gtegtgtteg	480
togacgagag gagogtocto toagogagto tto	

- (2) INFORMATION FOR SEQ ID NO:2242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..171
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600505
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

Lys Thr Lys Phe Pro Ile Pro Lys Pro Leu Val Asp Pro Arg Leu Arg

1 15 15

Ser Pro Ser Pro Arg Ala Arg His Gly Ser Leu Arg Arg Arg Arg 20 25 30

Arg Leu Arg Ala Ala Val Leu Val Leu Leu Leu Arg Gly Arg Pro Gly 35 45

Gly Cys Ser Gly Gly Glu His Gly Thr Pro Phe Asp Arg Leu Arg Arg 50 55 60

Arg Arg Val Arg Gln Val Arg Arg Arg Arg Gly Arg Arg Gly Gly 65

Arg Arg Arg Arg His Val Arg Arg Leu Leu Pro Gly Ser Pro Leu Arg 85 90 95
Gln Val Gln Ala Leu Arg His Glu Gln Arg His Gly Ala Pro His Arg

100 105 110

Arg Arg Pro Pro Arg Leu Leu Arg Arg Ser Arg Leu Gln Gly Gly Ser

115 120 125 Ala Val His Thr Arg Asp Ala Val Gln Gly Asp Pro Glu Leu Gly Gly

130 135 140
Glu Gln Leu Pro Gly Pro Ala Gly Leu Gln Pro Ser Ala Ser Cys Ser

145 150 155
Ser Thr Arg Gly Ala Ser Ser Gln Arg Val Phe
165 170

- (2) INFORMATION FOR SEQ ID NO:2243:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..170
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Asn Gln Ile Pro Asn Ser Gln Thr Pro Ser Arg Pro Thr Ser Pro Val

1 10 15

Pro Leu Ser Ser Arg Pro Pro Trp Gln Pro Ala Ala Ala Pro Ala Pro 20 25 30

Ala Ala Gly Arg Ser Ala Arg Pro Pro Pro Pro Arg Ala Ala Arg Arg

35 40 Met Leu Trp Arg Arg Ala Trp Asp Ala Phe Arg Pro Pro Pro Pro 55 Pro Arg Ala Ala Ser Ala Thr Ala Ala Ala Arg Pro Ser Arg Trp Pro 75 70 Ala Ala Ser Ala Cys Ala Pro Ala Ala Ser Gly Leu Thr Ser Ser Ala 90 8.5 Ser Ser Ser Pro Ser Arg Ala Thr Pro Trp Cys Ala Pro Gln Thr 100 105 Pro Ser Ser Ser Pro Ser Pro Ala Val Pro Pro Pro Gly Trp Leu Cys 115 120 125 Ser Ser Tyr Thr Arg Cys Ser Pro Arg Arg Ser Arg Ala Gly Arg Arg 135 140 Ala Thr Pro Arg Pro Cys Arg Ser Ser Ala Phe Gly Val Val Phe Val 150 155 Asp Glu Arg Ser Val Leu Ser Ala Ser Leu 165 (2) INFORMATION FOR SEQ ID NO:2244: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..147 (D) OTHER INFORMATION: / Ceres Seq. ID 1600507 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244: Met Ala Ala Cys Gly Gly Ala Gly Ala Gly Cys Gly Pro Gln Cys Ser 10 5 Ser Ser Ser Ser Ala Gly Gly Gln Glu Asp Ala Leu Ala Glu Ser Met 25 Gly Arg Leu Ser Thr Ala Ser Ala Ala Ala Ala Cys Gly Lys Cys Asp 40 Gly Gly Gly Ala Ala Val Ala Val Ala Gly Gly Val Gly Met Cys Ala 60 55 Gly Cys Phe Arg Ala His Leu Phe Gly Lys Phe Lys Leu Ser Val Thr 75 80 70 Ser Asn Ala Met Val Arg Pro Thr Asp Ala Val Leu Leu Ala Phe Ser 90 95 Gly Gly Pro Ala Ser Arg Val Ala Leu Gln Phe Ile His Glu Met Gln 100 105 110 Ser Lys Ala Ile Gln Ser Trp Glu Ala Ser Asn Ser Gln Ala Leu Pro 115 120 125 Val Phe Ser Leu Arg Arg Arg Val Arg Arg Arg Glu Glu Arg Pro Leu 135 130 Ser Glu Ser 145 (2) INFORMATION FOR SEQ ID NO:2245: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1600512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

(A) NAME/KEY: (B) LOCATION: 1..452

ategatecge ageagtgee aaagaggaag agageaagea aggtgtettt ggeaaegete 60 ateagatea acacecege gegtgetage tagetaget etgtgtagga teetetegee 120 ageeggeggeg tegateete ggegeetee teeeggegte tgteateate egeeggeegg tggtateate agtacgtact tetgetgett egttaagta gtageteate getteaeegge eeggtgggge teeegeegg etteeggte eagagaggag agaeagateg gtateateat ggtgaaetae taeetgaage geaagateea egggetgaag ategagetgg acateatee tgagggtegae etetaeagg gg

- (2) INFORMATION FOR SEQ ID NO:2246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600513
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

Ile Asp Pro Gln Gln Cys Pro Lys Arg Lys Arg Ala Ser Lys Val Ser 1 5 10 15

Leu Ala Thr Leu Ile Arg Ser His Thr Pro Ala Arg Ala Ser 20 25 30

- (2) INFORMATION FOR SEQ ID NO: 2247:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..31
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600514
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Ser Ile Arg Ser Ser Ala Gln Arg Gly Arg Glu Gln Ala Arg Cys Leu

1 10 15

10 15

Trp Gln Arg Ser Ser Asp His Thr Pro Pro Arg Val Leu Ala Ser 20 25 30

- (2) INFORMATION FOR SEQ ID NO:2248:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..49
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600515
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

Met Ala Pro Val Gly Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp 1 5 10 15

Glu Glu Leu Val Asn Tyr Tyr Leu Lys Arg Lys Ile His Gly Leu Lys
20 25 30

Ile Glu Leu Asp Ile Ile Pro Glu Val Asp Leu Tyr Lys Cys Glu Pro
35 40 45

Trp

(2) INFORMATION FOR SEQ ID NO:2249:

60

120

180

240 300

360

420

480

Client Docket No. 80146.003 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 500 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..500 (D) OTHER INFORMATION: / Ceres Seq. ID 1600528 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249: aaggegetea tegaeteeag eeageegeee aaaaateeag gegeaaatea eaacetegea tectettetg tecegtetee agetettegt tegtteeeet etegeegeee gteteeeeeg cggtcgagga gccgccaata gcaaggagag ggtttcctcc tccctccacg gctccaccga gctccccgat ccctccgccc caaatcccac acacccggtt ggccaccgcn tcgccatgga tttggatctg tggatctcca aggtcaagga gggtcagcac ctcgcctagc acgagcttca gtccctctgc gaatatgtga aggagatcct catcgaagag tcgaacgtgc aaccagtgaa cageccegtg aeggtttgeg gtgatateea tgggeagtte catgacetaa tgaagetett cgcgacgggt ggccacgtcc cagagacgaa ctatattttc atgggtgatt ttgtggaccg tggcttcaat agtctagagg (2) INFORMATION FOR SEQ ID NO:2250: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..95 (D) OTHER INFORMATION: / Ceres Seq. ID 1600529 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250: Arg Arg Ser Ser Thr Pro Ala Ser Arg Pro Lys Ile Gln Ala Gln Ile 10 5 Thr Thr Ser His Pro Leu Leu Ser Arg Leu Gln Leu Phe Val Arg Ser 25 30 Pro Leu Ala Ala Arg Leu Pro Arg Gly Arg Gly Ala Ala Asn Ser Lys 45 35 Glu Arg Val Ser Ser Ser Leu His Gly Ser Thr Glu Leu Pro Asp Pro 60 55 50 Ser Ala Pro Asn Pro Thr His Pro Val Gly His Arg Xaa Ala Met Asp 75 70 Leu Asp Leu Trp Ile Ser Lys Val Lys Glu Gly Gln His Leu Ala 85 (2) INFORMATION FOR SEQ ID NO:2251: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..105 (D) OTHER INFORMATION: / Ceres Seq. ID 1600530 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251: Gly Ala His Arg Leu Gln Pro Ala Ala Gln Lys Ser Arg Arg Lys Ser 15 10 5

Gln Pro Arg Ile Leu Phe Cys Pro Val Ser Ser Ser Ser Phe Val Pro 20 25 30 Leu Ser Pro Pro Val Ser Pro Ala Val Glu Pro Pro Ile Ala Arg

60

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 35 40 Arg Gly Phe Pro Pro Pro Ser Thr Ala Pro Pro Ser Ser Pro Ile Pro 60 55 Pro Pro Gln Ile Pro His Thr Arg Leu Ala Thr Xaa Ser Pro Trp Ile 75 70 Trp Ile Cys Gly Ser Pro Arg Ser Arg Arg Val Ser Thr Ser Pro Ser 90 8.5 Thr Ser Phe Ser Pro Ser Ala Asn Met 100 105 (2) INFORMATION FOR SEQ ID NO:2252: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 503 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..503 (D) OTHER INFORMATION: / Ceres Seq. ID 1600535 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252: ttctctctcc gccttccgag aggcccgacc cctgatacca cgctgagggc ggtggtatta 120 ggagattagc gatggcgagg tggcggccgg cggcgctgct ggtagtggct ctggcggcgg 180 ttctatcggc ggcgtggcgg gcggatgcgc tatcggttac ggtgaccgac accgagtgca 240 tccacgagtt cgtgccctat gagggcgaca ccgtgtccgg gaacttcgtc gtcgtcgacc 300 acgacatett etggagetee gaccacceag gaategacet caeggtaaeg teaecaggtg 360 gcaacactgt gtacacattg aagggaaaat ctggtgagaa atttgagttt aaagctccaa 420 gaggtggcat gtataagttc tgcttccata acccatatgg agcacctgaa actgtttctt 480 tctacatcca tgttggggca cat (2) INFORMATION FOR SEQ ID NO:2253: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..124 (D) OTHER INFORMATION: / Ceres Seq. ID 1600536 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253: Met Ala Arg Trp Arg Pro Ala Ala Leu Leu Val Val Ala Leu Ala Ala 5 10 Val Leu Ser Ala Ala Trp Arg Ala Asp Ala Leu Ser Val Thr Val Thr 25 Asp Thr Glu Cys Ile His Glu Phe Val Pro Tyr Glu Gly Asp Thr Val 40 Ser Gly Asn Phe Val Val Val Asp His Asp Ile Phe Trp Ser Ser Asp 55

His Pro Gly Ile Asp Leu Thr Val Thr Ser Pro Gly Gly Asn Thr Val 70 75 Tyr Thr Leu Lys Gly Lys Ser Gly Glu Lys Phe Glu Phe Lys Ala Pro 90 85 Arg Gly Gly Met Tyr Lys Phe Cys Phe His Asn Pro Tyr Gly Ala Pro 105 100 Glu Thr Val Ser Phe Tyr Ile His Val Gly Ala His

115 (2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..392
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:

 actttggcag getgegagea gtetgacage tacacacaca ggcagacgee gtteegegg 60
 ggaaaggtge ggacgeetga atecteteca acteeggeae egeattegea egeeeggaa 120
 geeeegaate ggagaggaca gaggagteat ggacgeggeg geggeggegg etgeggetge 180
 gageeeeaeg ageaagagga tegegetggt gaegggaggg aacaagggea tegggetega 240
 gaegtgeegg eagetggegt eeagggegt eagggtegte etgaeggega ggaacgagge 300
 gaggggtttg gaageggteg agegegteag gtgegeeege ggegaegeeg aggtttaett 360
 ceaceagete gaegteaeeg acceetgeag eg
- (2) INFORMATION FOR SEQ ID NO:2255:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600538
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

Thr Leu Ala Gly Cys Glu Gln Ser Asp Ser Tyr Thr His Arg Gln Thr 1 5 10 15

Pro Phe Arg Gly Gly Lys Val Arg Thr Pro Glu Ser Ser Pro Thr Pro 20 25 30

Ala Pro His Ser His Ala Arg Glu Ala Pro Asn Arg Arg Gly Gln Arg
35 40 45

Ser His Gly Arg Gly Gly Gly Gly Cys Gly Cys Glu Pro His Glu
50 55 60

Gln Glu Asp Arg Ala Gly Asp Gly Arg Glu Gln Gly His Arg Ala Arg
65 70 75 80

Asp Val Pro Ala Ala Gly Val Gln Gly Arg Gln Gly Arg Pro Asp Gly 85 90 95 Glu Glu Arg Gly Glu Gly Phe Gly Ser Gly Arg Ala Arg Gln Val Arg

100 105 110
Pro Arg Arg Arg Gly Leu Leu Pro Pro Ala Arg Arg His Arg Pro

Pro Arg Arg Arg Gly Leu Leu Pro Pro Ara Arg Arg 113 Arg 1 115 120 125

Leu Gln 130

- (2) INFORMATION FOR SEQ ID NO:2256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600539
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

Leu Trp Gln Ala Ala Ser Ser Leu Thr Ala Thr His Thr Gly Arg Arg

1 5 10 15

Arg Ser Ala Gly Glu Arg Cys Gly Arg Leu Asn Pro Leu Gln Leu Arg

```
25
           2.0
His Arg Ile Arg Thr Pro Ala Lys Pro Arg Ile Gly Glu Asp Arg Gly
                          40
                                              45
Val Met Asp Ala Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Thr Ser
                       55
Lys Arg Ile Ala Leu Val Thr Gly Gly Asn Lys Gly Ile Gly Leu Glu
                  70
                                      75
Thr Cys Arg Gln Leu Ala Ser Arg Gly Val Arg Val Val Leu Thr Ala
               85
                                  90
Arg Asn Glu Ala Arg Gly Leu Glu Ala Val Glu Arg Val Arg Cys Ala
           100
                             105
Arg Gly Asp Ala Glu Val Tyr Phe His Gln Leu Asp Val Thr Asp Pro
                           120
Cys Ser
   130
(2) INFORMATION FOR SEQ ID NO:2257:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

Met Asp Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Thr Ser Lys 1 5 10 15

Arg Ile Ala Leu Val Thr Gly Gly Asn Lys Gly Ile Gly Leu Glu Thr 20 25 30

Cys Arg Gln Leu Ala Ser Arg Gly Val Arg Val Val Leu Thr Ala Arg 35 40 45

Asn Glu Ala Arg Gly Leu Glu Ala Val Glu Arg Val Arg Cys Ala Arg 50 55 60

Gly Asp Ala Glu Val Tyr Phe His Gln Leu Asp Val Thr Asp Pro Cys 65 70 75 80 Ser

- (2) INFORMATION FOR SEQ ID NO:2258:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..462
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600552
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

ategtetegt tteagtteet egtegeete geeacttege egeegeeget ttggeteeae 60 ceagteeget teeggeatee geecatgget geggeeeeg eeegeeaeet egeegeggee 120 tteaeggeeg eegetgega eeagegget gegtteagge gegteeaggt eegggeeeeg 180 tgtgteegee tetetetet teeegeegeg eeateeegeg acatteegeg geagggeeag 240 cetegeetge eeegeegeg eetetetate egteeeetee ggegeegege eteegggete 300 egtgeeatte aaceteetge egeeegaete egaeeette ategagtggg accegeece 360 gggegaetee geeeetege egetegetgg eggeggtget geeggggtg eeaegetggt 420 egtgetgete ggetggeteg gegeggeea gaageaeetg eg

- (2) INFORMATION FOR SEQ ID NO:2259:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600553
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:
- Ile Val Ser Phe Gln Phe Leu Val Ala Leu Ala Thr Ser Pro Pro Pro 1 10 15
- Leu Trp Leu His Pro Val Arg Phe Arg His Pro Pro Met Ala Ala Ala 20 25 30
- Pro Ala Arg His Leu Ala Ala Ala Phe Thr Ala Ala Ala Ala His Gln 35 40 45
- Arg Val Ala Phe Arg Arg Val Gln Val Arg Ala Pro Cys Val Arg Leu 50 55 60
- Ser Leu Leu Pro Ala Ala Pro Ser Arg Asp Ile Ser Arg Gln Gly Gln 65 70 75 80
- Pro Arg Leu Pro Arg Arg Arg Leu Ser Ile Arg Pro Leu Arg Arg Arg 85 90 95
- Ala Ser Gly Leu Arg Ala Ile Gln Pro Pro Ala Ala Arg Leu Arg Pro
 100 105 110
- Phe His Arg Val Gly Pro Ala Pro Gly Arg Leu Arg Pro Leu Ala Ala 115 120 125
- Arg Trp Arg Cys Cys Arg Gly Cys His Ala Gly Arg Ala Ala Arg 130 135 140
- Leu Ala Arg Arg Ala Pro Glu Ala Pro Ala 145
- (2) INFORMATION FOR SEQ ID NO:2260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600554
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:
- Ser Ser Arg Phe Ser Ser Ser Ser Pro Ser Pro Leu Arg Arg Arg 1 5 10 15
- Phe Gly Ser Thr Gln Ser Ala Ser Gly Ile Arg Pro Trp Leu Arg Pro 20 25 30
- Pro Pro Ala Thr Ser Pro Arg Pro Ser Arg Pro Pro Leu Arg Thr Ser
- Ala Ser Arg Ser Gly Ala Ser Arg Ser Gly Pro Arg Val Ser Ala Ser 50 55 60
- Leu Ser Phe Pro Pro Arg His Pro Ala Thr Phe Arg Gly Arg Ala Ser 75 80
- Leu Ala Cys Pro Ala Ala Ala Ser Leu Ser Val Pro Ser Gly Ala Ala 85 90 95
- Pro Pro Gly Ser Val Pro Phe Asn Leu Leu Pro Pro Asp Ser Asp Pro 100 105 110
- Phe Ile Glu Trp Asp Pro Pro Pro Gly Asp Ser Ala Pro Ser Pro Leu 115 120 125
- Ala Gly Gly Ala Ala Gly Gly Ala Thr Leu Val Val Leu Leu Gly 130 135 140
- Trp Leu Gly Ala Arg Gln Lys His Leu

(ix) FEATURE:

(A) NAME/KEY: peptide

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150
145
(2) INFORMATION FOR SEQ ID NO:2261:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 153 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..153
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600555
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:
Arg Leu Val Ser Val Pro Arg Arg Pro Arg His Phe Ala Ala Ala
                                   10
               5
Leu Ala Pro Pro Ser Pro Leu Pro Ala Ser Ala His Gly Cys Gly Pro
                               25
Arg Pro Pro Pro Arg Arg Gly Leu His Gly Arg Arg Cys Ala Pro Ala
                           40
Arg Arg Val Gln Ala Arg Pro Gly Pro Gly Pro Val Cys Pro Pro Leu
                                           60
                       55
Ser Pro Ser Arg Arg Ala Ile Pro Arg His Phe Ala Ala Gly Pro Ala
                                       75
                   70
Ser Pro Ala Pro Pro Pro Leu Tyr Pro Ser Pro Pro Ala Pro Arg
                                   90
                8.5
Leu Arg Ala Pro Cys His Ser Thr Ser Cys Arg Pro Thr Pro Thr Leu
                                                   110
                               105
            100
Ser Ser Ser Gly Thr Arg Pro Arg Ala Thr Pro Pro Pro Arg Arg Ser
                                               125
                           120
Leu Ala Ala Val Leu Pro Gly Val Pro Arg Trp Ser Cys Cys Ser Ala
                                           140
                       135
    130
Gly Ser Ala Arg Ala Arg Ser Thr Cys
                    150
145
 (2) INFORMATION FOR SEQ ID NO:2262:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 409 base pairs
          (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..409
           (D) OTHER INFORMATION: / Ceres Seq. ID 1600559
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:
 aagaactgca actaggaacg gktcgccaca aaaaaagaac gtacggctat gaagacgagg
                                                                      120
 cgcggtgcct gccacgcggc ggcggcggcc acggcgccgg gcgagkggcc kgatggcgca
                                                                      180
 acgccggaag cggcgcagga cggcggcggc cgaggggtcg ccagcggcgg ccggcactcc
                                                                      240
 aggtgtccgc ccggtgggca gagacatgtt cgagagagct gcctgacgat ctcgtcgtct
                                                                      300
 ccatactacg ggacgtcgcc gcgtccgcca gttcgccggc cgatctcgcc ggcgccatgc
                                                                      360
 tcacgtgcaa gaggttcagg gagctcgggc agagcaaggt ggtgctggc
 (2) INFORMATION FOR SEQ ID NO:2263:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 135 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
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- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

Asn Arg Tyr Arg His Pro Leu Leu Ser Ser Pro Leu Xaa Ser Leu Pro 1 5 10 15

Leu Xaa Xaa Glu Leu Gln Leu Gly Thr Xaa Arg His Lys Lys Arg 20 25 30

Thr Tyr Gly Tyr Glu Asp Glu Ala Arg Cys Leu Pro Arg Gly Gly Gly 35 40 45

Gly His Gly Ala Gly Arg Xaa Ala Xaa Trp Arg Asn Ala Gly Ser Gly 50 60

Ala Gly Arg Arg Pro Arg Gly Arg Gln Arg Arg Pro Ala Leu Gln 65 70 75 80

Val Ser Ala Arg Trp Ala Glu Thr Cys Ser Arg Glu Leu Pro Asp Asp 85 90 95

Leu Val Val Ser Ile Leu Arg Asp Val Ala Ala Ser Ala Ser Ser Pro $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Ala Asp Leu Ala Gly Ala Met Leu Thr Cys Lys Arg Phe Arg Glu Leu 115 120 125

Gly Gln Ser Lys Val Val Leu 130 135

- (2) INFORMATION FOR SEQ ID NO: 2264:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..100
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

Met Lys Thr Arg Gly Ala Cys His Ala Ala Ala Ala Ala Thr Ala 1 $$ 5 $$ 10 $$ 15

Pro Gly Glu Xaa Xaa Asp Gly Ala Thr Pro Glu Ala Ala Gl
n Asp Gly 20 25 30

Gly Gly Arg Gly Val Ala Ser Gly Gly Arg His Ser Arg Cys Pro Pro $35 \hspace{1cm} 40 \hspace{1cm} 45$

Gly Gly Gln Arg His Val Arg Glu Ser Cys Leu Thr Ile Ser Ser Ser 50 55 60

Pro Tyr Tyr Gly Thr Ser Pro Arg Pro Pro Val Arg Arg Pro Ile Ser 65 70 75 80

Pro Ala Pro Cys Ser Arg Ala Arg Gly Ser Gly Ser Ser Gly Arg Ala 85 90 95

Arg Trp Cys Trp

(2) INFORMATION FOR SEQ ID NO:2265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

acattttgga aggagagaga gagaggcaga gggagagatt ggagggaggc cctgcccaag gcaagagaaa ccgcggcgcg cggagaggga ggaagggcag cacgcagacg cagacggrac

gaacaagatgagggagatcatcagcatccacatcggccaggccgggatccaggtcggcaa180cgcctgctgggagctctactgcctcgagcacggcatcgagcacgatggcaccatgcccag240tgattcctcggttggcgtcgcacatgatgccttcaacacgttcttcagcgagactggttc300cggcaagcatgtgccccagggccatcttcgtcgaccttgagcccactgtcatcgacgag360ttcgcactggctcgtaccgccagctcttccacccagagcagctcatctcggggaaggagg420atgcagctaacacttggaccgtgtgcgcragc480

- (2) INFORMATION FOR SEQ ID NO:2266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

Thr Phe Trp Lys Glu Arg Glu Arg Gly Arg Gly Arg Asp Trp Arg Glu 1 5 15

Ala Leu Pro Lys Ala Arg Glu Thr Ala Ala Arg Gly Glu Gly Arg
20 25 30

Ala Ala Arg Arg Arg Arg Xaa Glu Gln Asp Glu Gly Asp His Gln 35 40 45

His Pro His Arg Pro Gly Arg Asp Pro Gly Arg Gln Arg Leu Leu Gly 50 55 60

Ala Leu Leu Pro Arg Ala Arg His Arg Ala Arg Trp His His Ala Gln 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:2267:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600564
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:

His Phe Gly Arg Arg Glu Arg Glu Ala Glu Gly Glu Ile Gly Gly Arg
1 5 10 15

Pro Cys Pro Arg Gln Glu Lys Pro Arg Arg Ala Glu Arg Glu Glu Gly 20 25 30

Gln His Ala Asp Ala Asp Xaa Thr Asn Lys Met Arg Glu Ile Ile Ser

Ile His Ile Gly Gln Ala Gly Ile Gln Val Gly Asn Ala Cys Trp Glu 50 55 60

Leu Tyr Cys Leu Glu His Gly Ile Glu His Asp Gly Thr Met Pro Ser 65 70 75 80

Asp Ser Ser Val Gly Val Ala His Asp Ala Phe Asn Thr Phe Phe Ser 85 90 95

Glu Thr Gly Ser Gly Lys His Val Pro Gln Gly His Leu Arg Arg Pro 100 105 110

- (2) INFORMATION FOR SEQ ID NO:2268:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

Met Ala Pro Cys Pro Val Ile Pro Arg Leu Ala Ser His Met Met Pro 1 5 10 15

Ser Thr Arg Ser Ser Ala Arg Leu Val Pro Ala Ser Met Cys Pro Arg 20 25 30

Ala Ile Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Val Arg Thr 35 40 45

Gly Ser Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Ser Gly Lys 50 55 60

Glu Asp Ala Ala Asn Asn Phe Ala Arg Gly His Tyr Thr Val Gly Lys 65 70 75 80

Glu Ile Val Asp Leu Cys Leu Asp Arg Val Arg 85 90

- (2) INFORMATION FOR SEQ ID NO:2269:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..508
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600574
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

aattteetet teteeaaace ceaeteaceg caacgageeg ceggateeat ggeeggeaaa 60 gacggctccg tcccttcccc gcctcctcsc cggctcccat cctaccctga gatgatcgtg 120 gaggcaatcc gggcgctggg actcgagaac ggctgcaaca agactgcgat ctcggactac 180 atcaaqqqca qctacqqctc caacctccct gcccagcaca acgccgtcct cacgggccac 240 300 ctcqcccqca tqaaqqctac cqqtqaqctc qccttcctca qqaacaacta tctcctcccc 360 aacqaqqacq aaqcctcccc qctqaqcacc qqtggqcaca agggccccgc cgccgccgag 420 gagtetactg gegtgttgga egttggtgac gatgtgttge ttgetteece tetegteate qacqctqacq ccgtcqacat tgacgtgcct gctccagctc ccgttgtcac sgctgatgtc 480 gacgactttg acgtgcttgc ctccagct

- (2) INFORMATION FOR SEQ ID NO:2270:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..169
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600575
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

Asn Phe Leu Phe Ser Lys Pro His Ser Pro Gln Arg Ala Ala Gly Ser 1 5 10 15

Met Ala Gly Lys Asp Gly Ser Val Pro Ser Pro Pro Pro Xaa Arg Leu 20 25 30

Pro Ser Tyr Pro Glu Met Ile Val Glu Ala Ile Arg Ala Leu Gly Leu 35 40 45

```
Glu Asn Gly Cys Asn Lys Thr Ala Ile Ser Asp Tyr Ile Lys Gly Ser 50 55 60

Tyr Gly Ser Asn Leu Pro Ala Gln His Asn Ala Val Leu Thr Gly His
```

65 70 75

Leu Ala Arg Met Lys Ala Thr Gly Glu Leu Ala Phe Leu Arg Asn Asn 85 90 95

Tyr Leu Leu Pro Asn Glu Asp Glu Ala Ser Pro Leu Ser Thr Gly Gly 100 105 110

His Lys Gly Pro Ala Ala Ala Glu Glu Ser Thr Gly Val Leu Asp Val 115 120 125

Gly Asp Asp Val Leu Leu Ala Ser Pro Leu Val Ile Asp Ala Asp Ala 130 135 140

Val Asp Ile Asp Val Pro Ala Pro Ala Pro Val Val Xaa Ala Asp Val 145 150 150

Asp Asp Phe Asp Val Leu Ala Ser Ser 165

- (2) INFORMATION FOR SEQ ID NO:2271:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

Met Ala Gly Lys Asp Gly Ser Val Pro Ser Pro Pro Pro Xaa Arg Leu 1 5 10

Pro Ser Tyr Pro Glu Met Ile Val Glu Ala Ile Arg Ala Leu Gly Leu 20 25 30

Glu Asn Gly Cys Asn Lys Thr Ala Ile Ser Asp Tyr Ile Lys Gly Ser 35 40 45

Tyr Gly Ser Asn Leu Pro Ala Gln His Asn Ala Val Leu Thr Gly His 50 55 60

Leu Ala Arg Met Lys Ala Thr Gly Glu Leu Ala Phe Leu Arg Asn Asn 65 70 75 80

Tyr Leu Leu Pro Asn Glu Asp Glu Ala Ser Pro Leu Ser Thr Gly Gly 85 90 95
His Lys Gly Pro Ala Ala Ala Glu Glu Ser Thr Gly Val Leu Asp Val

100 105 110 Gly Asp Asp Val Leu Leu Ala Ser Pro Leu Val Ile Asp Ala Asp Ala

GIY ASP ASP VAL LEU LEU ALA SER PRO LEU VAL ILE ASP ALA ASP ALA

115

Val Asp Ile Asp Val Pro Ala Pro Ala Pro Val Val Xaa Ala Asp Val

140

130 135
Asp Asp Phe Asp Val Leu Ala Ser Ser
145 150

- (2) INFORMATION FOR SEQ ID NO:2272:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

Met Ile Val Glu Ala Ile Arg Ala Leu Gly Leu Glu Asn Gly Cys Asn

```
Client Docket No. 80146.003
                                   10
                5
Lys Thr Ala Ile Ser Asp Tyr Ile Lys Gly Ser Tyr Gly Ser Asn Leu
                               25
Pro Ala Gln His Asn Ala Val Leu Thr Gly His Leu Ala Arg Met Lys
                            40
Ala Thr Gly Glu Leu Ala Phe Leu Arg Asn Asn Tyr Leu Leu Pro Asn
                        55
Glu Asp Glu Ala Ser Pro Leu Ser Thr Gly Gly His Lys Gly Pro Ala
                    70
Ala Ala Glu Glu Ser Thr Gly Val Leu Asp Val Gly Asp Asp Val Leu
                                   90
Leu Ala Ser Pro Leu Val Ile Asp Ala Asp Ala Val Asp Ile Asp Val
                               105
Pro Ala Pro Ala Pro Val Val Xaa Ala Asp Val Asp Asp Phe Asp Val
                                                125
                            120
       115
Leu Ala Ser Ser
    130
(2) INFORMATION FOR SEQ ID NO:2273:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 557 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
```

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..557
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273: atttttcact ataaagtttc actgtatctt tcaaacttag tcttatttct tattttgcca gcaggaaaaa ccttgccacg agtcgccgac actccatccc ggaagagcta acgaggtgac 120 accccaccgc gcccatgggt gacagccagt actccttctc cctcaccacc ttcagtccgt 180 240 cggggaaget cgtgcagatt gagcacgege teacggetgt cggatecggg cagacetege tcgggatcaa agctgccaat ggtgtagtca ttgccactga gaagaagctg ccttctattt 300 tagtggatga aacatctgtg caaaagattc aggcactaac acctaatatt ggagttgtct 360 atagtgggat gggtccagat ttccgtgttc tggtgagaaa aagtcgaaag caggcacaac 420 aatattatcg gttgtacaag ggaacatata cctgtaacac agcttgtacg agagactgct 480 gctgtcatgc aggagttcac acagtcaggt ggtgtgagac atttggagta tcactgttga 540 ttgctgggta tgatgac
- (2) INFORMATION FOR SEQ ID NO:2274:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..141
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600600
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:
- Met Gly Asp Ser Gln Tyr Ser Phe Ser Leu Thr Thr Phe Ser Pro Ser 10
- Gly Lys Leu Val Gln Ile Glu His Ala Leu Thr Ala Val Gly Ser Gly 2.0 2.5
- Gln Thr Ser Leu Gly Ile Lys Ala Ala Asn Gly Val Val Ile Ala Thr 45 40
- Glu Lys Lys Leu Pro Ser Ile Leu Val Asp Glu Thr Ser Val Gln Lys 55 60
- Ile Gln Ala Leu Thr Pro Asn Ile Gly Val Val Tyr Ser Gly Met Gly 75 70

Pro Asp Phe Arg Val Leu Val Arg Lys Ser Arg Lys Gln Ala Gln Gln 90 Tyr Tyr Arg Leu Tyr Lys Gly Thr Tyr Thr Cys Asn Thr Ala Cys Thr 110 105 100 Arg Asp Cys Cys Cys His Ala Gly Val His Thr Val Arg Trp Cys Glu 125 120 115 Thr Phe Gly Val Ser Leu Leu Ile Ala Gly Tyr Asp Asp 135 130 (2) INFORMATION FOR SEQ ID NO: 2275: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..360 (D) OTHER INFORMATION: / Ceres Seq. ID 1600603 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275: gagecatecg gteceaaaag tagaaaaggg caagegaega geaeageaca geaegeette 120 cqttttggga aggcgaggag aggggaaccc gnggagagtt gggggatcgg cggcggagga gatggaggag egggagaage tegtgtgeet ggeeaagett geegageagg eggassggta 180 240 cgacgatatg gtggaattca tgaagaatct tgctaggatg gacgtggata tgagtgctga agaraggcat ttgttctcag ttggtttcaa gaacactatt ggagcaaaga gagcatcatg 300 360 gagaatcatt tgttcacatg agcaaaaggt cgcagctgat cgtcanactg gtgtgatgat (2) INFORMATION FOR SEQ ID NO:2276: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..71 (D) OTHER INFORMATION: / Ceres Seq. ID 1600604 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276: Glu Pro Ser Gly Pro Lys Ser Arg Lys Gly Gln Ala Thr Ser Thr Ala 10 Gln His Ala Phe Arg Phe Gly Lys Ala Arg Arg Gly Glu Pro Xaa Glu 20 25 Ser Trp Gly Ile Gly Gly Gly Asp Gly Gly Ala Gly Glu Ala Arg 40 Val Pro Gly Gln Ala Cys Arg Ala Gly Gly Xaa Val Arg Arg Tyr Gly Gly Ile His Glu Glu Ser Cys 70 (2) INFORMATION FOR SEQ ID NO:2277: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1600605

(B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

```
Ser His Pro Val Pro Lys Val Glu Lys Gly Lys Arg Arg Ala Gln His
                                    10
Ser Thr Pro Ser Val Leu Gly Arg Arg Gly Glu Gly Asn Pro Xaa Arg
                                25
           2.0
Val Gly Gly Ser Ala Ala Glu Glu Met Glu Glu Arg Glu Lys Leu Val
                            40
        35
Cys Leu Ala Lys Leu Ala Glu Gln Ala Xaa Xaa Tyr Asp Asp Met Val
                                            60
                        55
Glu Phe Met Lys Asn Leu Ala Arg Met Asp Val Asp Met Ser Ala Glu
                                        75
                    7.0
Xaa Arg His Leu Phe Ser Val Gly Phe Lys Asn Thr Ile Gly Ala Lys
                                    90
               8.5
Arg Ala Ser Trp Arg Ile Ile Cys Ser His Glu Gln Lys Val Ala Ala
                                                    110
                                105
            100
Asp Arg Xaa Thr Gly Val Met
        115
```

- (2) INFORMATION FOR SEQ ID NO:2278:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600606
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278: Met Glu Glu Arg Glu Lys Leu Val Cys Leu Ala Lys Leu Ala Glu Gln

1 5 10 15 Ala Xaa Xaa Tyr Asp Asp Met Val Glu Phe Met Lys Asn Leu Ala Arg 20 25 30

Met Asp Val Asp Met Ser Ala Glu Xaa Arg His Leu Phe Ser Val Gly

Phe Lys Asn Thr Ile Gly Ala Lys Arg Ala Ser Trp Arg Ile Ile Cys
50 55 60

Ser His Glu Gln Lys Val Ala Ala Asp Arg Xaa Thr Gly Val Met 65 70 75

- (2) INFORMATION FOR SEQ ID NO: 2279:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..430
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279: agcagtcagc agtgaccaac tcgaagcttg cgttcttgta gtagaggtcg gcagcaagcg 60 gtagagcgag acgtcgagaa gatgaagagc agcactctgt tggcgatcct agttctccag 120 gcccttctgg tctctacggc cgtggcaaag gacctgcagg gccgaagaag cagtgctggt 180 gcggcgagtg caccasstgg tcgggcgtgt ggacctgcga cgacctcctc accaagtgcg 240 ccgccacctg cragaactgc gtccccgtct ccacggacaa gggcgccacc aagtacagat 300 gccgcgactt cctccccgaa aactgcggct gcaagatcca ctagactcat ccacagcggc 360 acageegatg gateetteea tgeteeteeg teegteegee ttnetacaag caggeageea 420 ccaatrrgct
- (2) INFORMATION FOR SEQ ID NO:2280:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..115
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

Met Lys Ser Ser Thr Leu Leu Ala Ile Leu Val Leu Gln Ala Leu Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Val Ser Thr Ala Val Ala Lys Asp Leu Gln Gly Arg Arg Ser Ser Ala 20 25 30

Gly Ala Ala Ser Ala Pro Xaa Gly Arg Ala Cys Gly Pro Ala Thr Thr $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ser Ser Pro Ser Ala Pro Pro Pro Xaa Arg Thr Ala Ser Pro Ser Pro 50 55 60

Arg Thr Arg Ala Pro Pro Ser Thr Asp Ala Ala Thr Ser Ser Pro Lys 65 70 75 80

Thr Ala Ala Arg Ser Thr Arg Leu Ile His Ser Gly Thr Ala Asp 85 90 95

Gly Ser Phe His Ala Pro Pro Ser Val Arg Leu Xaa Thr Ser Arg Gln $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Pro Pro Xaa

115

- (2) INFORMATION FOR SEQ ID NO:2281:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..392
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600634
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

atcttectta tecagatgge ggegegeea actecaceae etteteegge gaegtgtggg 60 eggaegteeg etggeegaeg ecegekaegt geegeacate eacegeetea tacaceatat 120 ggeogagtte gagetgetea ecgacetett egeegeeaee gaagagetee teaegteeae 180 getetteeea tegeogaege egeeteett eaceteette acageeeteg teettgaeet 240 atcececace eccateetee eggaeteete tteeaeeate geeteeegee ggetegaeet 300 groegegtee eggetggege gegeaeette geeteeegee geggeggegg 360 groegegteae ggeegggtte gtgatetget te

- (2) INFORMATION FOR SEQ ID NO:2282:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600635
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

Arg Arg Val Gly Gly Arg Pro Leu Ala Asp Ala Arg Xaa Val Pro His 20 25 30

Ile His Arq Leu Ile His His Met Ala Glu Phe Glu Leu Leu Thr Asp

40 35 Leu Phe Ala Ala Thr Glu Glu Leu Leu Thr Ser Thr Leu Phe Pro Ser 55 Pro Thr Pro Pro Pro Phe Thr Ser Phe Thr Ala Leu Val Leu Asp Leu 75 70 Ser Pro Thr Pro Ile Leu Pro Asp Ser Ser Ser Thr Ile Ala Ser Arg 90 85 Arg Leu Asp Leu Ser Ala Ser Pro Leu Ala Asp Pro Glu Ala Ala Thr 105 Phe Ala Ser Pro Arg Gly Gly Gly Xaa Arg His Gly Arg Val Arg Asp 120 Leu Leu 130 (2) INFORMATION FOR SEQ ID NO:2283: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..130 (D) OTHER INFORMATION: / Ceres Seq. ID 1600636 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283: Leu Pro Tyr Pro Asp Gly Gly Ala Ala Asn Ser Thr Thr Phe Ser Gly 10 5 Asp Val Trp Ala Asp Val Arg Trp Pro Thr Pro Xaa Thr Cys Arg Thr 20 25 Ser Thr Ala Ser Tyr Thr Ile Trp Pro Ser Ser Ser Cys Ser Pro Thr 45 40 Ser Ser Pro Pro Pro Lys Ser Ser Ser Arg Pro Arg Ser Ser His Arg 55 60 Arg Arg Arg Leu Pro Ser Pro Pro Ser Gln Pro Ser Ser Leu Thr Tyr 70 75 Pro Pro Pro Pro Ser Ser Arg Thr Pro Leu Pro Pro Ser Pro Pro Ala 90 85 Gly Ser Thr Ser Pro Arg Pro Arg Ser Gln Thr Arg Arg Pro Pro Pro 100 105 110 Ser Pro Pro Arg Ala Ala Ala Xaa Arg Val Thr Ala Gly Phe Val Ile 120 Cys Phe (2) INFORMATION FOR SEQ ID NO:2284: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..91 (D) OTHER INFORMATION: / Ceres Seq. ID 1600637 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284: Met Ala Glu Phe Glu Leu Leu Thr Asp Leu Phe Ala Ala Thr Glu Glu 10 5 Leu Leu Thr Ser Thr Leu Phe Pro Ser Pro Thr Pro Pro Pro Phe Thr 25 20

Ser Phe Thr Ala Leu Val Leu Asp Leu Ser Pro Thr Pro Ile Leu Pro

40

45

15

Asp Ser Ser Ser Thr Ile Ala Ser Arg Arg Leu Asp Leu Ser Ala Ser 60 55 Pro Leu Ala Asp Pro Glu Ala Ala Thr Phe Ala Ser Pro Arg Gly Gly 75 70 Gly Xaa Arg His Gly Arg Val Arg Asp Leu Leu 85 (2) INFORMATION FOR SEQ ID NO:2285: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..220 (D) OTHER INFORMATION: / Ceres Seq. ID 1600638 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285: acacacaaca gaaacaccac ctccaggctt cccaaatccc aacaagggct accgcccacc 60 ggccaccacc ccacgcgcgt ctcacgccat gggcagcgcg tcgtccccgc catctcacag 120 geggtggage tggggetegg egetggeggg egeggegaeg aeggeegeeg eeaeggeeet 180 agtgctgtgc cggccgcggg acccssgttc gagctcatct (2) INFORMATION FOR SEQ ID NO:2286: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..73 (D) OTHER INFORMATION: / Ceres Seq. ID 1600639 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286: Thr His Asn Arg Asn Thr Thr Ser Arg Leu Pro Lys Ser Gln Gln Gly 15 10 5 Leu Pro Pro Thr Gly His His Pro Thr Arg Val Ser Arg His Gly Gln 30 25 2.0 Arg Val Val Pro Ala Ile Ser Gln Ala Val Glu Leu Gly Leu Gly Ala 4.5 40 Gly Gly Arg Gly Asp Asp Gly Arg Arg His Gly Pro Ser Ala Val Pro 60 50 Ala Ala Gly Pro Xaa Phe Glu Leu Ile 70 (2) INFORMATION FOR SEQ ID NO:2287: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..73 (D) OTHER INFORMATION: / Ceres Seq. ID 1600640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287: His Thr Thr Glu Thr Pro Pro Pro Gly Phe Pro Asn Pro Asn Lys Gly

10

Tyr Arg Pro Pro Ala Thr Thr Pro Arg Ala Ser His Ala Met Gly Ser 25

Ala Ser Ser Pro Pro Ser His Arg Arg Trp Ser Trp Gly Ser Ala Leu

5

2.0

40 35 Ala Gly Ala Ala Thr Thr Ala Ala Ala Thr Ala Leu Val Leu Cys Arg 60 55 Pro Arg Asp Xaa Xaa Ser Ser Ser 70 (2) INFORMATION FOR SEQ ID NO:2288: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..59 (D) OTHER INFORMATION: / Ceres Seq. ID 1600641 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288: Thr Gln Gln Lys His His Leu Gln Ala Ser Gln Ile Pro Thr Arg Ala 10 5 Thr Ala His Arg Pro Pro Pro His Ala Arg Leu Thr Pro Trp Ala Ala 30 25 Arg Arg Pro Arg His Leu Thr Gly Gly Gly Ala Gly Ala Arg Arg Trp 40 Arg Ala Arg Arg Arg Pro Pro Pro Arg Pro 55 (2) INFORMATION FOR SEQ ID NO:2289: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 448 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..448 (D) OTHER INFORMATION: / Ceres Seq. ID 1600644 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289: agrettgtge gecateacae acaagacaea accecaetea eceggeagga ggecetette gtcggcggag gccatggttt ccctcaagcc gcagaagagg ctcgccgcgg gagtcctaaa atgtggcaag gggaaggtgt ggcttgaccc caacgaggtc tacgagatct cgatggctaa 180 ctcgcgtcag aacattcgta agctggtgaa ggatggattc ataattaaga agccacagaa 240 aatccactca aggtcccggg caaggaggc ccatgaggcc aagcagaagg ggaggcactc 300 tggttacggt aagcgcaggg gtaccaggga ggctaggctc cccaccaaga tcctttggat 360 gcgcaggatg sktntcctca ggcgtctgct gcgcaagtrt cgtnaancaa agaaaatcga caaacacatg taccacnata tctatatc (2) INFORMATION FOR SEQ ID NO:2290: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..149 (D) OTHER INFORMATION: / Ceres Seq. ID 1600645 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290: Xaa Leu Cys Ala Ile Thr His Lys Thr Gln Pro His Ser Pro Gly Arg 10 Arg Pro Ser Ser Ser Ala Glu Ala Met Val Ser Leu Lys Pro Gln Lys 30 25 2.0

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Arg Leu Ala Ala Gly Val Leu Lys Cys Gly Lys Gly Lys Val Trp Leu
                           40
Asp Pro Asn Glu Val Tyr Glu Ile Ser Met Ala Asn Ser Arg Gln Asn
                                          60
                       55
Ile Arg Lys Leu Val Lys Asp Gly Phe Ile Ile Lys Lys Pro Gln Lys
                                      75
Ile His Ser Arg Ser Arg Ala Arg Arg Ala His Glu Ala Lys Gln Lys
                                  90
               85
Gly Arg His Ser Gly Tyr Gly Lys Arg Arg Gly Thr Arg Glu Ala Arg
                                                  110
          100
                              105
Leu Pro Thr Lys Ile Leu Trp Met Arg Arg Met Xaa Xaa Leu Arg Arg
      115 120
                                             125
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Leu Leu Arg Lys Xaa Arg Xaa Xaa Lys Lys Ile Asp Lys His Met Tyr 140 135

His Xaa Ile Tyr Ile

145

- (2) INFORMATION FOR SEQ ID NO:2291:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..125
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

Met Val Ser Leu Lys Pro Gln Lys Arg Leu Ala Ala Gly Val Leu Lys 1.0 5 Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Val Tyr Glu Ile

25 Ser Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val Lys Asp Gly 4.5 40

Phe Ile Ile Lys Lys Pro Gln Lys Ile His Ser Arg Ser Arg Ala Arg

55 Arg Ala His Glu Ala Lys Gln Lys Gly Arg His Ser Gly Tyr Gly Lys 75 70

Arg Arg Gly Thr Arg Glu Ala Arg Leu Pro Thr Lys Ile Leu Trp Met 90

Arg Arg Met Xaa Xaa Leu Arg Arg Leu Leu Arg Lys Xaa Arg Xaa Xaa 100 105

Lys Lys Ile Asp Lys His Met Tyr His Xaa Ile Tyr Ile 120 115

- (2) INFORMATION FOR SEQ ID NO:2292:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val Lys Asp Gly Phe 15 10

Ile Ile Lys Lys Pro Gln Lys Ile His Ser Arg Ser Arg Ala Arg Arg 25 20

Ala His Glu Ala Lys Gln Lys Gly Arg His Ser Gly Tyr Gly Lys Arg

Page 1169 Client Docket No. 80146.003 45 40 35 Arg Gly Thr Arg Glu Ala Arg Leu Pro Thr Lys Ile Leu Trp Met Arg 60 55 Arg Met Xaa Xaa Leu Arg Arg Leu Leu Arg Lys Xaa Arg Xaa Xaa Lys 75 70 Lys Ile Asp Lys His Met Tyr His Xaa Ile Tyr Ile 85 (2) INFORMATION FOR SEQ ID NO:2293: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 455 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..455 (D) OTHER INFORMATION: / Ceres Seq. ID 1600652 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293: 60 aggttccagt atttcaccac gcggcgtcgc ctgccgaacc ccgaaccttc tcgaggtcga ggcccctccc ctttcgccag gagaaaacaa tgagcaggcg caacagccgt accatctatg 120 taggcaatct ccctggggac atccgtgaga gggaggttga ggatctcttc tacaagtatg 180 geogtatttt ggatattgae ttgaaaatae eteegagaee teetggatae geattesstt 240 gagtttgagg atccacgtga tgctgatgat gcaatttatg gccgtgatgg gtataacttt 300 gatggctaca ggttgagggt tnaattagct catggtggca gaggccagts sttattctta 360 tgakcgttca agcagctata gcagtgcatg ccgtggaggt gtttctaggc gctctgattt 420 ccqtqttatq qtcactggtt tacctcatcg gcatc (2) INFORMATION FOR SEQ ID NO:2294: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..48 (D) OTHER INFORMATION: / Ceres Seq. ID 1600653 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294: Gly Ser Ser Ile Ser Pro Arg Gly Val Ala Cys Arg Thr Pro Asn Leu 10 Leu Glu Val Glu Ala Pro Pro Leu Ser Pro Gly Glu Asn Asn Glu Gln 25 Ala Gln Gln Pro Tyr His Leu Cys Arg Gln Ser Pro Trp Gly His Pro 4.0 (2) INFORMATION FOR SEQ ID NO:2295: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600654
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295: Val Pro Val Phe His His Ala Ala Ser Pro Ala Glu Pro Arg Thr Phe 1.0

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Ser Arg Ser Arg Pro Leu Pro Phe Arg Gln Glu Lys Thr Met Ser Arg
                                25
Arg Asn Ser Arg Thr Ile Tyr Val Gly Asn Leu Pro Gly Asp Ile Arg
                            40
Glu Arg Glu Val Glu Asp Leu Phe Tyr Lys Tyr Gly Arg Ile Leu Asp
                                             60
                        55
Ile Asp Leu Lys Ile Pro Pro Arg Pro Pro Gly Tyr Ala Phe Xaa
                                         75
                    70
(2) INFORMATION FOR SEQ ID NO: 2296:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..50
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600655
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:
Met Ser Arg Arg Asn Ser Arg Thr Ile Tyr Val Gly Asn Leu Pro Gly
                5
                                     10
Asp Ile Arg Glu Arg Glu Val Glu Asp Leu Phe Tyr Lys Tyr Gly Arg
                                                     3.0
                                 25
            20
Ile Leu Asp Ile Asp Leu Lys Ile Pro Pro Arg Pro Pro Gly Tyr Ala
                             40
Phe Xaa
    50
 (2) INFORMATION FOR SEQ ID NO:2297:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 422 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..422
           (D) OTHER INFORMATION: / Ceres Seq. ID 1600660
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:
 gegtttgtte teetgtteat caecegtgeg tgetetetet etetetet eteteteteg
                                                                        120
 tgcggcaact gcgaggccgc cgacgcccga cggcaggggt gcccaggcct tcttcggtcc
 categogagg ccatagttgc atcattegec tgagacgact geccageace aggactgate
                                                                        180
 tecteactag gggegtagag gtgaagagaa gaaettgaca atgageagea taggeaeagg
                                                                        240
 ttacgatctg tctgtcacca ccttctcccc agatggtcgc gtcttccagg tcgaatatgc
                                                                        300
 taccaaggee gtegacaaca gegggactgt tnttgggate aagtgcaaag atggcattgt
                                                                        360
 ssctgggtgt tgagaagctg gtaacctcag agatgatgct ggargggtca raccggagat
                                                                        420
 CC
 (2) INFORMATION FOR SEQ ID NO:2298:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 50 amino acids
            (B) TYPE: amino acid
           (C) STRANDEDNESS:
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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..50
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600661
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298: Ala Phe Val Leu Leu Phe Ile Thr Arg Ala Cys Ser Leu Ser Leu Ser

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5
Leu Ser Leu Ser Cys Gly Asn Cys Glu Ala Ala Asp Ala Arg Arg Gln
                                            30
     20
                 25
Gly Cys Pro Gly Leu Leu Arg Ser His Arg Glu Ala Ile Val Ala Ser
                           40
Phe Ala
   50
(2) INFORMATION FOR SEQ ID NO:2299:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 71 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..71
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600662
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:
Val Cys Ser Pro Val His His Pro Cys Val Leu Ser Leu Ser Leu Ser
                                    10
            5
Leu Ser Leu Val Arg Gln Leu Arg Gly Arg Arg Pro Thr Ala Gly
                                25
Val Pro Arg Pro Ser Ser Val Pro Ser Arg Gly His Ser Cys Ile Ile
                                                45
                           40
Arg Leu Arg Arg Leu Pro Ser Thr Arg Thr Asp Leu Leu Thr Arg Gly
                        55
Val Glu Val Lys Arg Arg Thr
                    70
(2) INFORMATION FOR SEQ ID NO:2300:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 amino acids
          (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..50
           (D) OTHER INFORMATION: / Ceres Seq. ID 1600663
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:
 Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Val Thr Thr Phe Ser
                                    10
 Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Thr Lys Ala Val Asp
                                25
            20
 Asn Ser Gly Thr Val Xaa Gly Ile Lys Cys Lys Asp Gly Ile Xaa Xaa
                             40
 Gly Cys
 (2) INFORMATION FOR SEQ ID NO:2301:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 209 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..209
           (D) OTHER INFORMATION: / Ceres Seq. ID 1600688
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

agtttgccgc tetgtgacet getgeegtet tetteegeeg eegeegeegt egtegtette 60 gteegtagat cagagagegg ggaggaagaa aaagegateg atggegteea aetaegtgga 120 caegeeggge gaggagggae ggtteeaegg eeeteaeage eaeageaeea geaegaeeee 180 gaeggeggeg eggeggege ggeggeate

- (2) INFORMATION FOR SEQ ID NO:2302:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600689
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Ser Leu Pro Leu Cys Asp Leu Leu Pro Ser Ser Ala Ala Ala Ala 1 5 10 15

Val Val Phe Val Arg Arg Ser Glu Ser Gly Glu Glu Lys Ala
20 25 30

Ile Asp Gly Val Gln Leu Arg Gly His Ala Gly Arg Gly Gly Thr Val

Pro Arg Pro Ser Gln Pro Gln His Gln His Asp Pro Asp Gly Gly Ala 50 55 60

Ala Ala Ala Ala

65

- (2) INFORMATION FOR SEQ ID NO:2303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600690
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

Val Cys Arg Ser Val Thr Cys Cys Arg Leu Leu Pro Pro Pro Pro 1 5 10 15

Ser Ser Ser Ser Val Asp Gln Arg Ala Gly Arg Lys Lys Arg 20 25 30

Ser Met Ala Ser Asn Tyr Val Asp Thr Pro Gly Glu Glu Gly Arg Phe 35 40 45

His Gly Pro His Ser His Ser Thr Ser Thr Thr Pro Thr Ala Ala Arg 50 55 60

Arg Arg Arg His

- (2) INFORMATION FOR SEQ ID NO:2304:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..36
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600691
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:
- Met Ala Ser Asn Tyr Val Asp Thr Pro Gly Glu Glu Gly Arg Phe His

Client Docket No. 80146.003 10 Gly Pro His Ser His Ser Thr Ser Thr Thr Pro Thr Ala Ala Arg Arg 25 20 Arg Arg Arg His 35 (2) INFORMATION FOR SEQ ID NO:2305: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..399 (D) OTHER INFORMATION: / Ceres Seq. ID 1600707 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305: aaaatcatac aatccgaggt ctcaaagtcg aagagggtta atcccctccc gttccactgt tgcccaagtc caaccaccag cgagatggcg gggaccgtga ccgcgaccgc aaccacggcn 120 accaccgagg kcgggaccac agtgaccgca gccacctccg agatsgaggc caccgcgacc 180 240 gcagccacct ccgagctgga ggccaccgcg accgcagccg ccatcgggcc gccttcagcc 300 atccccgata aatatatgca taaraaccgg ttgcagtcat ttgctgaacg aacatataag 360 aagaacgcca atctacaagg ttgagtctcc aaggccantc tcatcagcct aagttcacat sgcacagtgg aagtgggtga tcaacanttc tcatcaact (2) INFORMATION FOR SEQ ID NO:2306: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..107 (D) OTHER INFORMATION: / Ceres Seq. ID 1600708 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306: Lys Ile Ile Gln Ser Glu Val Ser Lys Ser Lys Arg Val Asn Pro Leu 1.0 5 Pro Phe His Cys Cys Pro Ser Pro Thr Thr Ser Glu Met Ala Gly Thr 25 20 Val Thr Ala Thr Ala Thr Thr Xaa Thr Thr Glu Xaa Gly Thr Thr Val 40 45 Thr Ala Ala Thr Ser Glu Xaa Glu Ala Thr Ala Thr Ala Ala Thr Ser 60 55 Glu Leu Glu Ala Thr Ala Thr Ala Ala Ala Ile Gly Pro Pro Ser Ala 75 70 Ile Pro Asp Lys Tyr Met His Xaa Asn Arg Leu Gln Ser Phe Ala Glu 90 Arg Thr Tyr Lys Lys Asn Ala Asn Leu Gln Gly 100 (2) INFORMATION FOR SEQ ID NO:2307: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..79
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307: Met Ala Gly Thr Val Thr Ala Thr Ala Thr Thr Xaa Thr Thr Glu Xaa 10 5 Gly Thr Thr Val Thr Ala Ala Thr Ser Glu Xaa Glu Ala Thr Ala Thr 25 20 Ala Ala Thr Ser Glu Leu Glu Ala Thr Ala Thr Ala Ala Ala Ile Gly 40 Pro Pro Ser Ala Ile Pro Asp Lys Tyr Met His Xaa Asn Arg Leu Gln 55 Ser Phe Ala Glu Arg Thr Tyr Lys Lys Asn Ala Asn Leu Gln Gly 75 70 (2) INFORMATION FOR SEQ ID NO:2308: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..132 (D) OTHER INFORMATION: / Ceres Seq. ID 1600721 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308: atccacaget egeateegat ttccaatttc aaatcetteg ategegenve geeegeeete 60 tegergetet etcegatgge cegeacgaag cagacggega ggaantcaae tggeggeaag 120 gcgccgcgga as (2) INFORMATION FOR SEQ ID NO:2309: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1600722 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309: Ile His Ser Ser His Pro Ile Ser Asn Phe Lys Ser Phe Asp Arg Xaa 1.0 5 1 Xaa Pro Ala Leu Ser Xaa Leu Ser Pro Met Ala Arg Thr Lys Gln Thr 25 Ala Arg Xaa Ser Thr Gly Gly Lys Ala Pro Arg 35 (2) INFORMATION FOR SEQ ID NO:2310: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1600723 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310: Ser Thr Ala Arg Ile Arg Phe Pro Ile Ser Asn Pro Ser Ile Ala Xaa 10 Arg Pro Pro Ser Arg Xaa Ser Leu Arg Trp Pro Ala Arg Ser Arg Arg

Arg Gly Xaa Gln Leu Ala Ala Arg Arg Arg Gly

35 40 (2) INFORMATION FOR SEQ ID NO:2311: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1600724 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311: Pro Gln Leu Ala Ser Asp Phe Gln Phe Gln Ile Leu Arg Ser Arg Xaa 10 5 Ala Arg Pro Leu Xaa Ala Leu Ser Asp Gly Pro His Glu Ala Asp Gly 20 25 Glu Glu Xaa Asn Trp Arg Gln Gly Ala Ala Glu 35 40 (2) INFORMATION FOR SEQ ID NO:2312: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..153 (D) OTHER INFORMATION: / Ceres Seq. ID 1600739 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312: awaatctcca ccaccacca caccaccaaa ccctagccgc bwcccttcgc cgcckngctg ateggecatg tetteetega ceteegatge ggecagggae gaegtegtet cateteeega cetgeecece etgteegege aegtegeege gge (2) INFORMATION FOR SEQ ID NO:2313: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..50 (D) OTHER INFORMATION: / Ceres Seq. ID 1600740 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313: Asn Leu His His His His His Gln Thr Leu Ala Xaa Xaa Leu Arg 5 10 Arg Xaa Ala Asp Arg Pro Cys Leu Pro Arg Pro Pro Met Arg Pro Gly 25 Thr Thr Ser Ser His Leu Pro Thr Cys Pro Pro Cys Pro Arg Thr Ser 40 Pro Arg (2) INFORMATION FOR SEQ ID NO:2314: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 421 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..421
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600744
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:

 cecetegtee aaaaccetag cectegegee geegeegeeg tgeecagege tegagekeet 60
 cgeetgeege gagetegege egeaaegeea ceatgaagtt caacategeg aaccegteta 120
 cegggtgeea gaagaagetg gaaategatg acgaccagaa actacgtgee ttttkatgae 180
 cgaagatete ecaggaggte agtggtgatg etetgggtga ggagtttaag ggttatgtet 240
 teaagateat gggtggatgt gacaaacaag getteecaat gaageaagga gttetgaett 300
 ctggtegtgt ecgeettetg etecacagag geaeteeetg etteegeggt tatngeagge 360
 gtaategteg agegeaggag gaantetete egtggttetg attetgagee aagacctate 420
- (2) INFORMATION FOR SEQ ID NO:2315:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..49
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600745
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

Pro Ser Ser Lys Thr Leu Ala Leu Ala Pro Pro Pro Pro Cys Pro Ala 1 5 10

Leu Glu Xaa Leu Ala Cys Arg Glu Leu Ala Pro Gln Arg His His Glu 20 25 30

Val Gln His Arg Glu Pro Val Tyr Arg Val Pro Glu Glu Ala Gly Asn 35 40 45

Arg

- (2) INFORMATION FOR SEQ ID NO:2316:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..44
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600746
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Met Thr Thr Arg Asn Tyr Val Pro Phe Xaa Asp Arg Arg Ser Pro Arg

Arg Ser Val Val Met Leu Trp Val Arg Ser Leu Arg Val Met Ser Ser 20 25 30

Arg Ser Trp Val Asp Val Thr Asn Lys Ala Ser Gln 35

- (2) INFORMATION FOR SEQ ID NO:2317:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1600747 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317: Met Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys Gln Gly Val Leu 10 5 Thr Ser Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro Cys Phe 30 25 20 Arg Gly Tyr Xaa Arg Arg Asn Arg Arg Ala Gln Glu Glu Xaa Ser Pro 40 Trp Phe 50 (2) INFORMATION FOR SEQ ID NO:2318: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 516 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..516 (D) OTHER INFORMATION: / Ceres Seq. ID 1600768 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318: cacateteet teetttete ggeategteg acaceteate ggeeteegat eteteeacga 60 gecteegete caateegagg ateegeggeg gegggeagtg gteggeegge gatggegeae 120 cqaqtqqaca acqaqtacqa ctacctcttc aagatcqtqc tcatcqqcqa ctccqqcqtc 180 ggcaagtcca acatecttte eeggtteace egcaacgagt tetgeetega gtecaagtee 240 accatcggcg tcgagttcgc cacccgcacc ctccagatcg aagggaaaac catcaaagct 300 caaatatggg atactgcggg gcaagagagg taccgtgcaa tcacaagtgc ttactacaga 360 ggagccgtgg gtgcacttct agtctatgac atcacgaaga agcagacatt tgaaaacata 420 cagaggtggc tcccgcgagc tcgtgaccac gcggactcca acatcgtgat catgatggtc 480 ggcmacaagt ccgacctgaa accacctgag gtcggt (2) INFORMATION FOR SEQ ID NO:2319: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 172 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..172 (D) OTHER INFORMATION: / Ceres Seq. ID 1600769 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319: His Ile Ser Phe Leu Phe Ser Ala Ser Ser Thr Pro His Arg Pro Pro 10 Ile Ser Pro Arg Ala Ser Ala Pro Ile Arg Gly Ser Ala Ala Ala Gly 30 25 20 Ser Gly Arg Pro Ala Met Ala His Arg Val Asp Asn Glu Tyr Asp Tyr 40 Leu Phe Lys Ile Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Asn 55 Ile Leu Ser Arg Phe Thr Arg Asn Glu Phe Cys Leu Glu Ser Lys Ser 75 70 Thr Ile Gly Val Glu Phe Ala Thr Arg Thr Leu Gln Ile Glu Gly Lys 90 Thr Ile Lys Ala Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg 105 Ala Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val

120 Tyr Asp Ile Thr Lys Lys Gln Thr Phe Glu Asn Ile Gln Arg Trp Leu

135

125

Pro Arg Ala Arg Asp His Ala Asp Ser Asn Ile Val Ile Met Met Val 150 155

Gly Xaa Lys Ser Asp Leu Lys Pro Pro Glu Val Gly 165

- (2) INFORMATION FOR SEQ ID NO:2320:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

His Leu Leu Pro Phe Leu Gly Ile Val Asp Thr Ser Ser Ala Ser Asp 10 5

Leu Ser Thr Ser Leu Arg Ser Asn Pro Arg Ile Arg Gly Gly Gln 25 20

Trp Ser Ala Gly Asp Gly Ala Pro Ser Gly Gln Arg Val Arg Leu Pro 45 4Ω

Leu Gln Asp Arg Ala His Arg Arg Leu Arg Arg Arg Gln Val Gln His 60 55

Pro Phe Pro Val His Pro Gln Arg Val Leu Pro Arg Val Gln Val His 75 70

His Arg Arg Arg Val Arg His Pro His Pro Pro Asp Arg Arg Glu Asn 90 85

His Gln Ser Ser Asn Met Gly Tyr Cys Gly Ala Arg Glu Val Pro Cys 105 110

Asn His Lys Cys Leu Leu Gln Arg Ser Arg Gly Cys Thr Ser Ser Leu 125 115 120

- (2) INFORMATION FOR SEQ ID NO:2321:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600771
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

Met Ala His Arg Val Asp Asn Glu Tyr Asp Tyr Leu Phe Lys Ile Val 10 5

Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Asn Ile Leu Ser Arg Phe 25 20

Thr Arg Asn Glu Phe Cys Leu Glu Ser Lys Ser Thr Ile Gly Val Glu 40

Phe Ala Thr Arg Thr Leu Gln Ile Glu Gly Lys Thr Ile Lys Ala Gln 55

Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg Ala Ile Thr Ser Ala 75 70

Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val Tyr Asp Ile Thr Lys 85

Lys Gln Thr Phe Glu Asn Ile Gln Arg Trp Leu Pro Arg Ala Arg Asp 105 100 His Ala Asp Ser Asn Ile Val Ile Met Met Val Gly Xaa Lys Ser Asp

240

300

420

480

125 120 115 Leu Lys Pro Pro Glu Val Gly 135 130 (2) INFORMATION FOR SEQ ID NO:2322: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..484 (D) OTHER INFORMATION: / Ceres Seq. ID 1600772 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322: atcctgaacc cgaaagctga actaccacac acaacaaata actgacgcag gcgatccatc actccacagt gtccacacac cggtcggaac cgaggccaac cgccgccgcc gccgccaatg tegtecectg cagegeeggt geageegeeg gegeegege eggtgegett eggegteetg ggatgcgctg acatcgcgcg taagatctcg cgcgcaatgc tgatgctccc tccgggcgcc gccaccatcg ccgccgtagg cagtcgctcc gatgacaagg cccgccgctt catctccgaa ateggettee eegeggegeg egteeaeggg teetaegagt eteteetaga ggaceeggae gtggaggccg tgtacctccc gctcccact agtctccacg tgccctgggc cacagccgtc getgegegtg geaageacet geteetegag aageeeaceg egetetgeae tgesgaacte gacg (2) INFORMATION FOR SEQ ID NO:2323: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..122 (D) OTHER INFORMATION: / Ceres Seq. ID 1600773 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323: Met Ser Ser Pro Ala Ala Pro Val Gln Pro Pro Ala Pro Arg Ala Val 1.0 5 1 Arg Phe Gly Val Leu Gly Cys Ala Asp Ile Ala Arg Lys Ile Ser Arg 30 25 Ala Met Leu Met Leu Pro Pro Gly Ala Ala Thr Ile Ala Ala Val Gly 45 40 Ser Arg Ser Asp Asp Lys Ala Arg Arg Phe Ile Ser Glu Ile Gly Phe 60 55 Pro Ala Ala Arg Val His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro 75 Asp Val Glu Ala Val Tyr Leu Pro Leu Pro Thr Ser Leu His Val Pro 90 8.5 Trp Ala Thr Ala Val Ala Ala Arg Gly Lys His Leu Leu Leu Glu Lys 110 105 100 Pro Thr Ala Leu Cys Thr Xaa Glu Leu Asp 115 (2) INFORMATION FOR SEQ ID NO:2324: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 amino acids (B) TYPE: amino acid

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(ix) FEATURE:

- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600774
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

Met Leu Met Leu Pro Pro Gly Ala Ala Thr Ile Ala Ala Val Gly Ser 1 5 10 15

Arg Ser Asp Asp Lys Ala Arg Arg Phe Ile Ser Glu Ile Gly Phe Pro 20 25 30

Ala Ala Arg Val His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro Asp 35 40 45

Val Glu Ala Val Tyr Leu Pro Leu Pro Thr Ser Leu His Val Pro Trp 50 55 60

Ala Thr Ala Val Ala Ala Arg Gly Lys His Leu Leu Leu Glu Lys Pro 65 70 75 80

Thr Ala Leu Cys Thr Xaa Glu Leu Asp 85

- (2) INFORMATION FOR SEQ ID NO:2325:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600775
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

Met Leu Pro Pro Gly Ala Ala Thr Ile Ala Ala Val Gly Ser Arg Ser 1 5 10 15

Asp Asp Lys Ala Arg Arg Phe Ile Ser Glu Ile Gly Phe Pro Ala Ala 20 25 30

Arg Val His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro Asp Val Glu

Ala Val Tyr Leu Pro Leu Pro Thr Ser Leu His Val Pro Trp Ala Thr 50 55 60

Ala Val Ala Ala Arg Gly Lys His Leu Leu Leu Glu Lys Pro Thr Ala 65 70 75 80

Leu Cys Thr Xaa Glu Leu Asp 85

- (2) INFORMATION FOR SEQ ID NO:2326:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..382
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600776
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

ccattagggt tcacttccaa actcggcacc tataaacact tctctcacgc cccacggtcg cccaccgctc cgctcgcac catcgtgtag gttaggctag gttcgaccag ctagcggaaa 120 tggtgggctt caggttccat cagtaccagg tggtggggcg cgcgctgccg acgcccggcg 180 atgagcacc caagatctac cgcatgaagc tctgggccac caacgaggtc cgcgccaaga 240 gcaagttctg gtacttcttg aggaagttga agaaggctaa gaagagcaac ggccaggtcc tggccatcaa cgagatcttt gagcgtaacc cgacgacaat caagaactac ggcatctggc 300 tgcgctacca gagcagaacc gg

- (2) INFORMATION FOR SEQ ID NO:2327:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600777
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

Met Val Ala Phe Arg Phe His Gln Tyr Gln Val Val Gly Arg Ala Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Pro Thr Pro Gly Asp Glu His Pro Lys Ile Tyr Arg Met Lys Leu Trp 20 25 30

Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp Tyr Phe Leu Arg 35 40 45

Lys Leu Lys Lys Ala Lys Lys Ser Asn Gly Gln Val Leu Ala Ile Asn 50 55 60

Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn Tyr Gly Ile Trp 65 70 75 80

Leu Arg Tyr Gln Ser Arg Thr 85

- (2) INFORMATION FOR SEQ ID NO:2328:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600778
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

Met Lys Leu Trp Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp

1 10 15

Tyr Phe Leu Arg Lys Leu Lys Lys Ala Lys Lys Ser Asn Gly Gln Val
20 25 30

Leu Ala Ile Asn Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn 35 40 45

Tyr Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr
50 55

- (2) INFORMATION FOR SEQ ID NO:2329:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..483
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600782
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

gtetttetet geetttettt ecetagegee gegeeggege egeeattega teaggeeget 60 tcgccggcga cagcatattc caggtcggtt ggttttggca cttcggaccg gcggccatgg 120 cttccgacgg catcggcccc agagatgtat gtgttgttgg ggttgcacgc accccaatgg 180 geggttteet tggtgeettg tetecettge etgetaegaa aettggetet atagtaatte 240 aagctgctct ggaaagagca aacgtggatc cagccctcgt gcaggaggtc tactttggaa 300 acgtcttgag tgctaatttg gggcaagctc ctgcaaggca agctgctctg ggtgccggga 360 taccaaactc tgttgtttgc accactgtta acaaagtctg tgcatctggc atgaaagcta 420 ctatgtttgc agcacagtca attcaattgg gtatcaatga tattgttgtg gctggtggca 480 tgg (2) INFORMATION FOR SEQ ID NO:2330: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..104 (D) OTHER INFORMATION: / Ceres Seq. ID 1600783 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330: Ser Phe Ser Ala Phe Leu Ser Leu Ala Pro Arg Arg Arg His Ser 10 5 Ile Arg Pro Leu Arg Arg Gln His Ile Pro Gly Arg Leu Val Leu 25 Ala Leu Arg Thr Gly Gly His Gly Phe Arg Arg His Arg Pro Gln Arg 40 Cys Met Cys Cys Trp Gly Cys Thr His Pro Asn Gly Arg Phe Pro Trp 55 60 Cys Leu Val Ser Leu Ala Cys Tyr Glu Thr Trp Leu Tyr Ser Asn Ser 75 70 Ser Cys Ser Gly Lys Ser Lys Arg Gly Ser Ser Pro Arg Ala Gly Gly 90 85 Leu Leu Trp Lys Arg Leu Glu Cys 100 (2) INFORMATION FOR SEQ ID NO:2331: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..122 (D) OTHER INFORMATION: / Ceres Seq. ID 1600784 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331: Met Ala Ser Asp Gly Ile Gly Pro Arg Asp Val Cys Val Val Gly Val 10 Ala Arg Thr Pro Met Gly Gly Phe Leu Gly Ala Leu Ser Pro Leu Pro 25 30 20 Ala Thr Lys Leu Gly Ser Ile Val Ile Gln Ala Ala Leu Glu Arg Ala 35 40 Asn Val Asp Pro Ala Leu Val Gln Glu Val Tyr Phe Gly Asn Val Leu 55 Ser Ala Asn Leu Gly Gln Ala Pro Ala Arg Gln Ala Ala Leu Gly Ala 75 70 Gly Ile Pro Asn Ser Val Val Cys Thr Thr Val Asn Lys Val Cys Ala 90 85 Ser Gly Met Lys Ala Thr Met Phe Ala Ala Gln Ser Ile Gln Leu Gly 105 100 Ile Asn Asp Ile Val Val Ala Gly Gly Met 120 115 (2) INFORMATION FOR SEQ ID NO:2332: (i) SEQUENCE CHARACTERISTICS:

- - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..102 (D) OTHER INFORMATION: / Ceres Seq. ID 1600785 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332: Met Gly Gly Phe Leu Gly Ala Leu Ser Pro Leu Pro Ala Thr Lys Leu 10 Gly Ser Ile Val Ile Gln Ala Ala Leu Glu Arg Ala Asn Val Asp Pro 30 25 20 Ala Leu Val Gln Glu Val Tyr Phe Gly Asn Val Leu Ser Ala Asn Leu 40 45 Gly Gln Ala Pro Ala Arg Gln Ala Ala Leu Gly Ala Gly Ile Pro Asn 55 Ser Val Val Cys Thr Thr Val Asn Lys Val Cys Ala Ser Gly Met Lys 75 70 Ala Thr Met Phe Ala Ala Gln Ser Ile Gln Leu Gly Ile Asn Asp Ile 85 Val Val Ala Gly Gly Met 100 (2) INFORMATION FOR SEQ ID NO:2333: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 520 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..520 (D) OTHER INFORMATION: / Ceres Seq. ID 1600786 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333: cagaaggaga gcaccctcca cctggtgctc cgcctcaggg gtggcatgca gatttttgtg aagacattga ctggcaagac catcaccttg gaggtggaga gctctgacac cattgacaat 120 gtgaaggcca agatccagga caaggaggc attcccccag accagcagcg tetgatettt 180 gctggcaagc agctggagga tggtcgcacc ctcgcggact acaacatcca gaaggagagt 240 accettcace ttgttctccg cetcaggggt ggtatgcaga tetttgtgaa gaccetgact 300 ggaaaaacca taaccctgga ggttgagagc tcggacacca tcgacaatgt gaaggcgaag 360 atccaggaca aggagggcat ccccccggac cagcagcgtc tgatcttcgc cggcaaacag 420 ctggaggatg gccgcacctt agcagactac aacatccaaa aggagagcac cctccacttg 480 tgctcrgtct ccgtggtggt cagtaagtca tgggtcgttt (2) INFORMATION FOR SEQ ID NO:2334: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 173 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..173 (D) OTHER INFORMATION: / Ceres Seq. ID 1600787 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334: Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met 10 Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val 25 20 Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys 45

Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln

55

180

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Client Docket No. 80146.003
Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser
                                       75
                   70
Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val
                                  90
              8.5
Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp
                                                  110
                               105
           100
Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro
                                              125
                          120
Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly
                      135
                                          140
Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu
                  150
                                      155
Cys Xaa Val Ser Val Val Ser Lys Ser Trp Val Val
               165
                                   170
(2) INFORMATION FOR SEQ ID NO:2335:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 158 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
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- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..158
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600788
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335: Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu

10 5 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp 25

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys 45 40

Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu 60 55

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe 75 70 Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser

90 Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile

105 100 Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp 1.25

120 115 Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His 135 140

Leu Cys Xaa Val Ser Val Val Ser Lys Ser Trp Val Val 150 145

- (2) INFORMATION FOR SEQ ID NO:2336:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..500
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600790
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336: cccccgaagt ctgaacatac tagaagcgta accctaagtc tcggacccca accctcgagg aaggcgaccg gagatggcgg cgtcgtcggc agtggagaag ctcaaggtcc tctgggactc gcaggtcaac gacgaggagc agtgggcgct caattataag ctgctgaagg ccgctggtct

gtttgcggga tccatcttcc tgatgcggaa cttcggtgat ctgatggcca tttagtaggc 240 ttatcagcag cattacccat cgctcgcaa cgtgcagact aaggaagcac tgaccggccg 300 gtcatggcga ggatccacct ctacgtcgtc gccgcggcct gcgccgtcgc cetcgcgctc 360 gccggcgacc cggacatgct ccaggacgtc tgcgtggctg actacgcttc cccggtcaag ctgaacgggt tcccgtgcaa ggcgaacatc tcggcggacg acttcttctt cgacgggctg 480 aggagccggg caacaccaac

- (2) INFORMATION FOR SEQ ID NO:2337:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..52
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600791
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

Pro Pro Lys Ser Glu His Thr Arg Ser Val Thr Leu Ser Leu Gly Pro

1 10 15

Gln Pro Ser Arg Lys Ala Thr Gly Asp Gly Gly Val Val Gly Ser Gly 20 25 30

Glu Ala Gln Gly Pro Leu Gly Leu Ala Gly Gln Arg Arg Gly Ala Val 35 40 45

Gly Ala Gln Leu

50

- (2) INFORMATION FOR SEQ ID NO:2338:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..53
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600792
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

Met Ala Ala Ser Ser Ala Val Glu Lys Leu Lys Val Leu Trp Asp Ser 1 5 10 15

Gln Val Asn Asp Glu Glu Gln Trp Ala Leu Asn Tyr Lys Leu Leu Lys 20 25 30

Ala Ala Gly Leu Phe Ala Gly Ser Ile Phe Leu Met Arg Asn Phe Gly 35 40 45

Asp Leu Met Ala Ile

50

- (2) INFORMATION FOR SEQ ID NO:2339:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..65
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

Met Ala Arg Ile His Leu Tyr Val Val Ala Ala Ala Cys Ala Val Ala 1 5 10 15
Leu Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp Val Cys Val Ala

20 25 Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Pro Cys Lys Ala Asn 4.5 40 Ile Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg Ser Arg Ala Thr 55 Pro 65 (2) INFORMATION FOR SEQ ID NO:2340: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 471 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..471 (D) OTHER INFORMATION: / Ceres Seq. ID 1600794 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340: gattetgaca ectectette ecaacaacte ectteetata gatetegeeg ecceetttet ccccatttcc gcaccacgcc cagtcgccca cgcagccggc ccaagcccaa aaacctttct 120 ccatcctcta ctctcatccc cacgatggcc gccgccgcca ccacgccgca ctccctcctc 180 ctccagcgcg ccgcgatccc ggccgcggct acgggggagg aggcgaccgt ggctacggcg 240 geggegaceg tggttaeggt ggaggtggeg accgeggeta eggeggegae egtggetaeg 300 ggggaggcgg cggctatggc ggtgggtacg gtggaggcgg cggtggaggc ggccgcggct 360 gcttcaagtg cggcgaggag ggccacatgg caagggactg ctcccagggc ggcggctacg 420 gagggggagg gcggcggcgg cgcggcagcg agtgctacaa ctgcggccag g (2) INFORMATION FOR SEQ ID NO:2341: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..157 (D) OTHER INFORMATION: / Ceres Seq. ID 1600795 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341: Asp Ser Asp Thr Ser Ser Ser Gln Gln Leu Pro Ser Tyr Arg Ser Arg 5 10 Arg Pro Leu Ser Pro His Phe Arg Thr Thr Pro Ser Arg Pro Arg Ser 25 30 20 Arg Pro Lys Pro Lys Asn Leu Ser Pro Ser Ser Thr Leu Ile Pro Thr 40 Met Ala Ala Ala Thr Thr Pro His Ser Leu Leu Gln Arg Ala 55 Ala Ile Pro Ala Ala Ala Thr Gly Glu Glu Ala Thr Val Ala Thr Ala 75 70 Ala Ala Thr Val Val Thr Val Glu Val Ala Thr Ala Ala Thr Ala Ala 90 85 Thr Val Ala Thr Gly Glu Ala Ala Ala Met Ala Val Gly Thr Val Glu 105 100 Ala Ala Val Glu Ala Ala Ala Ala Ser Ser Ala Ala Arg Arg Ala 120 Thr Trp Gln Gly Thr Ala Pro Arg Ala Ala Ala Thr Glu Gly Glu Gly 140 135

(2) INFORMATION FOR SEQ ID NO:2342:

(i) SEQUENCE CHARACTERISTICS:

150

Gly Gly Gly Ala Ala Ala Ser Ala Thr Thr Ala Ala Arg

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..156
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

Ile Leu Thr Pro Pro Leu Pro Asn Asn Ser Leu Pro Ile Asp Leu Ala 1 5 10 15

Ala Pro Phe Leu Pro Ile Ser Ala Pro Arg Pro Val Ala His Ala Ala 20 25 30

Gly Pro Ser Pro Lys Thr Phe Leu His Pro Leu Leu Ser Ser Pro Arg 35 40 45

Trp Pro Pro Pro Pro Pro Arg Arg Thr Pro Ser Ser Ser Ser Ala Pro 50 55 60

Arg Ser Arg Pro Arg Leu Arg Gly Arg Arg Pro Trp Leu Arg Arg 65 70 75 80

Arg Arg Pro Trp Leu Arg Trp Arg Trp Arg Pro Arg Leu Arg Arg Arg 85 90 95

Pro Trp Leu Arg Gly Arg Arg Arg Leu Trp Arg Trp Val Arg Trp Arg 100 105 110

Arg Arg Trp Arg Arg Pro Arg Leu Leu Gln Val Arg Arg Gly Gly Pro 115 120 125

His Gly Lys Gly Leu Leu Pro Gly Arg Arg Leu Arg Arg Gly Arg Ala 130 135 140

Ala Ala Arg Gln Arg Val Leu Gln Leu Arg Pro 145 150 155

- (2) INFORMATION FOR SEQ ID NO:2343:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600797
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

Met Ala Ala Ala Thr Thr Pro His Ser Leu Leu Leu Gln Arg Ala 1 5 10 15

Ala Ile Pro Ala Ala Ala Thr Gly Glu Glu Ala Thr Val Ala Thr Ala
20 25 30

Ala Ala Thr Val Val Thr Val Glu Val Ala Thr Ala Ala Thr Ala Ala 35 40 45

Thr Val Ala Thr Gly Glu Ala Ala Ala Met Ala Val Gly Thr Val Glu 50 55 60

Ala Ala Val Glu Ala Ala Ala Ala Ala Ser Ser Ala Ala Arg Arg Ala 65 70 75 80

Thr Trp Gln Gly Thr Ala Pro Arg Ala Ala Ala Thr Glu Gly Glu Gly 85 90 95

Gly Gly Gly Ala Ala Ala Ser Ala Thr Thr Ala Ala Arg 100 105

- (2) INFORMATION FOR SEQ ID NO:2344:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..326
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600812
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

 ccccaacete gtgttegtte ggagegeaca cacacacac cagatetece ecaaatkeea 60

 cccgteggea ccteegette aagatgeaga tetttgtgaa aaceetgace ggeaagaeta 120

 tcaccetega ggtggagteg tetgacacca ttgacaacgt taaggeeaag atecaggaea 240

 ggegeacget tgetgactac aacateeaga sggagngeac ectecacett gtgeteegee 300

 tcaggggagg catgeagate tttgtg
- (2) INFORMATION FOR SEQ ID NO:2345:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600813
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:
- Pro Thr Ser Cys Ser Phe Gly Ala His Thr His Thr Thr Arg Ser Pro
- Pro Asn Xaa Thr Arg Arg His Leu Arg Phe Lys Met Gln Ile Phe Val 20 25 30
- Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp 35 40 45
- Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro
 50 55 60
- Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly 65 70 75 80
- Arg Thr Leu Ala Asp Tyr Asn Ile Gln Xaa Glu Xaa Thr Leu His Leu 85 90 95
- Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val 100 105
- (2) INFORMATION FOR SEQ ID NO:2346:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600814
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:
- Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1 5 10 15
- Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp 20 25 30
- Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys 35 40 45
- Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Xaa Glu 50 55 60
- Xaa Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe 65 70 75 80

Val

- (2) INFORMATION FOR SEQ ID NO:2347:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..438
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600820
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347: 60 akgcatagta aagtkagcaa tgtcgatgga ttacttggct gctgctgtac ccgtgacctt 120 ggctctggga gtgggatcta tcttgttggt cttacgatgg acgtactgcc gccgccgaac aagegeegaa gaagtgagae tgeegeeggg gteaagggge eteetgttee tgggggagae 180 240 getecactae etggeagegt cetecacece gggggtattg ceaceattet tecagegaeg gttggagagg tatggcccca tcttccggac gaacctggtc ggggaggacc tcgtcgtgtc 300 360 gctggacgcg gactgaacgc gcacgtgctg aagcaggagg agcgcggctt ccagatctgg tacccgccct ccttcatgcg cgtcttcggc gccgacaaca tcaccgccaa gctcggcgtg 420 ctccaccact acatgagg
- (2) INFORMATION FOR SEQ ID NO:2348:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600821
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:
- Xaa His Ser Lys Xaa Ser Asn Val Asp Gly Leu Leu Gly Cys Cys Cys 1 5 10 15
 Thr Arg Asp Leu Gly Ser Gly Ser Gly Ile Tyr Leu Val Gly Leu Thr
- Mot Agn Val Low Pro Pro Pro Asn Lys Arg Arg Arg Ser Glu Thr Ale
- Met Asp Val Leu Pro Pro Pro Asn Lys Arg Arg Arg Ser Glu Thr Ala
 35 40 45
- Gly Ser Val Leu His Pro Gly Gly Ile Ala Thr Ile Leu Pro Ala Thr 65 70 75 80
 Val Gly Glu Val Trp Pro His Leu Pro Asp Glu Pro Gly Arg Gly Gly
- 85 90 95
 Pro Arg Arg Val Ala Gly Arg Gly Leu Asn Ala His Val Leu Lys Gln
- Glu Glu Arg Gly Phe Gln Ile Trp Tyr Pro Pro Ser Phe Met Arg Val
- Phe Gly Ala Asp Asn Ile Thr Ala Lys Leu Gly Val Leu His His Tyr 130 135 140

Met Arg

- (2) INFORMATION FOR SEQ ID NO:2349:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

Xaa Ile Val Lys Xaa Ala Met Ser Met Asp Tyr Leu Ala Ala Val 1 5 10 15

Pro Val Thr Leu Ala Leu Gly Val Gly Ser Ile Leu Leu Val Leu Arg 20 25 30

Trp Thr Tyr Cys Arg Arg Arg Thr Ser Ala Glu Glu Val Arg Leu Pro 35 40 45

Pro Gly Ser Arg Gly Leu Leu Phe Leu Gly Glu Thr Leu His Tyr Leu 50 55 60

Ala Ala Ser Ser Thr Pro Gly Val Leu Pro Pro Phe Phe Gln Arg Arg 65 70 75 80

Leu Glu Arg Tyr Gly Pro Ile Phe Arg Thr Asn Leu Val Gly Glu Asp 85 90 95

Leu Val Val Ser Leu Asp Ala Asp 100

- (2) INFORMATION FOR SEQ ID NO:2350:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

Met Asp Val Leu Pro Pro Pro Asn Lys Arg Arg Arg Ser Glu Thr Ala

5 10 15

15 10 Pro Pro Leu Pro

Ala Gly Val Lys Gly Pro Pro Val Pro Gly Gly Asp Ala Pro Leu Pro 20 25 30

Gly Ser Val Leu His Pro Gly Gly Ile Ala Thr Ile Leu Pro Ala Thr 35 40 45

Val Gly Glu Val Trp Pro His Leu Pro Asp Glu Pro Gly Arg Gly Gly 50 55 60

Pro Arg Arg Val Ala Gly Arg Gly Leu Asn Ala His Val Leu Lys Gln 65 70 75 80

Glu Glu Arg Gly Phe Gln Ile Trp Tyr Pro Pro Ser Phe Met Arg Val 85 90 95

Phe Gly Ala Asp Asn Ile Thr Ala Lys Leu Gly Val Leu His His Tyr 100 105 110

Met Arg

- (2) INFORMATION FOR SEQ ID NO:2351:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..314
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600835
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

agcacgtaca gagcaagcga agggagaact caagcgaggg aggcagaggg cgamgtaagc aagcagctag ctgctcactg cttgctctgt gctggtcgtt tgctctgtgc tggtcgcgtt

cettttgeag gaacteeteg eetggtgatg gacaggeaca eatgeagget etgetteegg 180 eggtteeaca aeggeegge getgggegge eacatgeget eccatgteat yggeeggete 240 gteggetgea gegeactege egetgeegg sageaattgn gettegetet eeetggegte 300 eacetegteg aegg

- (2) INFORMATION FOR SEQ ID NO:2352:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600836
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

Ser Thr Tyr Arg Ala Ser Glu Gly Arg Thr Gln Ala Arg Glu Ala Glu
1 10 15

Gly Xaa Val Ser Lys Gln Leu Ala Ala His Cys Leu Leu Cys Ala Gly
20 25 30

Arg Leu Leu Cys Ala Gly Arg Val Pro Phe Ala Gly Thr Pro Arg Leu

Val Met Asp Arg His Thr Cys Arg Leu Cys Phe Arg Arg Phe His Asn
50 60

Gly Arg Ala Leu Gly Gly His Met Arg Ser His Val Xaa Gly Arg Val 70 75 80

Val Gly Cys Ser Ala Leu Ala Ala Ala Ala Xaa Gln Leu Xaa Phe Ala 85 90 95

Leu Pro Gly Val His Leu Val Asp 100

- (2) INFORMATION FOR SEQ ID NO:2353:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

His Val Gln Ser Lys Arg Arg Glu Asn Ser Ser Glu Gly Gly Arg Gly
1 5 10 15

Arg Xaa Lys Gln Ala Ala Ser Cys Ser Leu Leu Ala Leu Cys Trp Ser 20 25 30

Phe Ala Leu Cys Trp Ser Arg Ser Phe Cys Arg Asn Ser Ser Pro Gly 35 40 45

Asp Gly Gln Ala His Met Gln Ala Leu Leu Pro Ala Val Pro Gln Arg 50 55 60

Pro Arg Ala Gly Arg Pro His Ala Leu Pro Cys His Xaa Pro Arg Arg 65 70 75 80

Arg Leu Gln Arg Thr Arg Arg Cys Arg Xaa Ala Ile Xaa Leu Arg Ser 85 90 95

Pro Trp Arg Pro Pro Arg Arg Arg 100

- (2) INFORMATION FOR SEQ ID NO:2354:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- Page 1192 Client Docket No. 80146.003 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..55 (D) OTHER INFORMATION: / Ceres Seq. ID 1600838 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354: Met Asp Arg His Thr Cys Arg Leu Cys Phe Arg Arg Phe His Asn Gly 10 Arg Ala Leu Gly Gly His Met Arg Ser His Val Xaa Gly Arg Val Val 25 30 20 Gly Cys Ser Ala Leu Ala Ala Ala Ala Xaa Gln Leu Xaa Phe Ala Leu 40 Pro Gly Val His Leu Val Asp 50 (2) INFORMATION FOR SEQ ID NO:2355: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 495 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..495 (D) OTHER INFORMATION: / Ceres Seq. ID 1600844 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355: ttttggagtt tggacgggct cgcctcggcc gctctggcgc ttgtgcggtg ggtgaagccg 60 120 ccgggtgctg gtgcgggaag cctcgccaga cctagcgctg ccgactgccg agctgggtgc qqqcqcqagq agtctacqgq aagacaagga attatgagtg aaacagggca cactgtacaa 180 gtcactaacc tctcgagcag agtatctgaa agtgatcttc atgagttctt ttcgttctct 240 ggtcctattc agcatataga acttatcaga tcagaaggat acggtgccac tgcttatgtg 300 acattcaagg aacgctttgc cttggaaact gcagtattgc tcagtggggc tactattgtg 360 420 gatcagccag tatgcataac ctattgggga caacctgagg gaacttttaa tttctgggac aggccaactt gggaggttga agagcaaatc gaatacagga actaccaaac atgccagtac 480 aacactactc cgcag (2) INFORMATION FOR SEQ ID NO:2356: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..165 (D) OTHER INFORMATION: / Ceres Seq. ID 1600845 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356: Phe Trp Ser Leu Asp Gly Leu Ala Ser Ala Ala Leu Ala Leu Val Arg 10 30
- Trp Val Lys Pro Pro Gly Ala Gly Ala Gly Ser Leu Ala Arg Pro Ser 25 Ala Ala Asp Cys Arg Ala Gly Cys Gly Arg Glu Glu Ser Thr Gly Arg 40 4.5 Gln Gly Ile Met Ser Glu Thr Gly His Thr Val Gln Val Thr Asn Leu 60 55 50 Ser Ser Arg Val Ser Glu Ser Asp Leu His Glu Phe Phe Ser Phe Ser 75 70
- Gly Pro Ile Gln His Ile Glu Leu Ile Arg Ser Glu Gly Tyr Gly Ala 90 Thr Ala Tyr Val Thr Phe Lys Glu Arg Phe Ala Leu Glu Thr Ala Val

- (2) INFORMATION FOR SEQ ID NO:2357:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600846
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

Met Ser Glu Thr Gly His Thr Val Gln Val Thr Asn Leu Ser Ser Arg

1 5 10 15

Val Ser Glu Ser Asp Leu His Glu Phe Phe Ser Phe Ser Gly Pro Ile
20 25 30

Gln His Ile Glu Leu Ile Arg Ser Glu Gly Tyr Gly Ala Thr Ala Tyr 35 40 45

Val Thr Phe Lys Glu Arg Phe Ala Leu Glu Thr Ala Val Leu Leu Ser 50 55 60

Gly Ala Thr Ile Val Asp Gln Pro Val Cys Ile Thr Tyr Trp Gly Gln 65 70 75 80

Pro Glu Gly Thr Phe Asn Phe Trp Asp Arg Pro Thr Trp Glu Val Glu
85 90 95

Glu Gln Ile Glu Tyr Arg Asn Tyr Gln Thr Cys Gln Tyr Asn Thr Thr

Pro Gln

- (2) INFORMATION FOR SEQ ID NO:2358:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..426
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600851
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

- (2) INFORMATION FOR SEQ ID NO:2359:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600852
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

Asn Arg Pro Pro Pro Phe Asn Ser Leu Ala Arg Ser Pro Ser Ile Phe 1 5 10 15

Leu Pro Leu Ser Ala Val Cys Ser Arg Pro Ala Pro Ser Arg Met Gln 20 25 30

Glu Ala Ser Ser Ala Ala Ala Arg Gly Arg Ala Arg Pro Ser Gly Gly

Ala Ala Ser Val Arg Arg Gly Pro Pro Ala Ala Gln Gly Val Arg

Ala Ala Gly Ala Gly Gly Glu Arg Gly Gly Pro Val Pro Ala Val Cys 65 70 75 80

Val Ala Gly His Gln Val Leu Leu Gln Gln Leu Gln His Leu Pro 85 90 95

Ala Ala Pro Leu Leu Gln Gly Leu Pro Pro Leu Leu Asp Gln Gly Arg
100 105 110

His Ala Ala Gln Arg Pro Arg Arg Xaa Ala Ala Pro Xaa Lys Lys Pro 115 120 125

Phe Leu Val Val Val Val Val Val Leu Arg Gly Arg Arg 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2360:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..141
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600853
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

Thr Ala Pro Leu Leu Ser Thr Arg Ser Leu Val Arg Leu Pro Ser Phe 1 5 10 15

Ser Leu Ser Arg Gln Ser Ala Ala Gly Gln Arg Arg Arg Ala Cys Arg 20 25 30

Arg Arg His Arg Arg Arg Gly Ala Glu Pro Gly Arg Arg Ala Ala 35 40 45

Gln His Gln Phe Ala Gly Val Asp Leu Arg Arg Pro Lys Gly Tyr Ala 50 55 60

Pro Pro Ala Pro Ala Val Ser Glu Gly Asp Pro Cys Pro Arg Cys Ala
65 70 75 80

Ser Arg Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Thr Ser Gln
85 90 95

Pro Arg His Phe Cys Lys Gly Cys Arg Arg Tyr Trp Thr Lys Gly Gly 100 105 110

Thr Leu Arg Asn Val Pro Val Gly Xaa Arg His Xaa Ala Arg Ser Pro 115 120 125

Ser Leu Ser Ser Ser Ser Ser Ser Tyr Ala Ala Ala 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2361:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600854
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:
- Met Gln Glu Ala Ser Ser Ala Ala Ala Arg Gly Arg Ala Arg Pro Ser 1 5 10 15
- Gly Gly Ala Ala Ser Val Arg Arg Gly Pro Pro Ala Ala Gln Gly 20 25 30
- Val Arg Ala Ala Gly Ala Gly Gly Glu Arg Gly Gly Pro Val Pro Ala 35 40 45
- Val Cys Val Ala Gly His Gln Val Leu Leu Gln Gln Leu Gln His 50 55 60
- Leu Pro Ala Ala Pro Leu Leu Gln Gly Leu Pro Pro Leu Leu Asp Gln 65 70 75 80
- Gly Arg His Ala Ala Gln Arg Pro Arg Arg Xaa Ala Ala Pro Xaa Lys 85 90 95
- Lys Pro Phe Leu Val Val Val Val Val Val Leu Arg Gly Arg Arg 100 105 110
- (2) INFORMATION FOR SEQ ID NO:2362:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..407
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

 acgaataaag catcgatcac gacaagatgg cgtacacaga caatgcgatg agagccttgt

 tgcgctcttc tacgtcgtgc atggtgagaa ggaagagtcc aagggcatcg atgcgaaagc

 gtccgggccc ggtggtcct tcgacatcac caagttgggc gcctccggca acggcaagac

 agacagcaca aaggcagtgc aggaggcatg ggcatcaacg tgtggcggca ctgggaagca

 gacaatcctt atacccaagg gcgacttcct tgtcggacaa ctcaacttca caggcccgtg

 caagggcgac gtgaccatct aggtggatgg caatctgcta gcgaccacat acctaagcca

 360
- gtacaaggaa catggtaatt ggatcgagat tctacgcgtg gataacc (2) INFORMATION FOR SEQ ID NO:2363:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600856
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:
- Arg Ile Lys His Arg Ser Arg Gln Asp Gly Val His Arg Gln Cys Asp
 1 5 10 15
- Glu Ser Leu Val Ala Leu Phe Tyr Val Val His Gly Glu Lys Glu Glu
 20 25 30
- Ser Lys Gly Ile Asp Ala Lys Ala Ser Gly Pro Gly Gly Ser Phe Asp 35 40 45
- Ile Thr Lys Leu Gly Ala Ser Gly Asn Gly Lys Thr Asp Ser Thr Lys

- (2) INFORMATION FOR SEQ ID NO:2364:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids

100 105

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600857
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364: Met Ala Tyr Thr Asp Asn Ala Met Arg Ala Leu Leu Arg Ser Ser Thr

1 5 10 15
Ser Cys Met Val Arg Arg Lys Ser Pro Arg Ala Ser Met Arg Lys Arg

20 25 30
Pro Gly Pro Val Gly Pro Ser Thr Ser Pro Ser Trp Ala Pro Pro Ala

35 40 45
Thr Ala Arg Gln Thr Ala Gln Arg Gln Cys Arg Arg His Gly His Gln

50 55 60 Arg Val Ala Ala Leu Gly Ser Arg Gln Ser Leu Tyr Pro Arg Ala Thr

65 70 75
Ser Leu Ser Asp Asn Ser Thr Ser Gln Ala Arg Ala Arg Ala Thr 85 90 95

- (2) INFORMATION FOR SEQ ID NO:2365:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600858
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met Arg Ala Leu Leu Arg Ser Ser Thr Ser Cys Met Val Arg Arg Lys 1 5 10 15

Ser Pro Arg Ala Ser Met Arg Lys Arg Pro Gly Pro Val Gly Pro Ser 20 25 30

Thr Ser Pro Ser Trp Ala Pro Pro Ala Thr Ala Arg Gln Thr Ala Gln
35 40 45

Arg Gln Cys Arg Arg His Gly His Gln Arg Val Ala Ala Leu Gly Ser 50 55

Arg Gln Ser Leu Tyr Pro Arg Ala Thr Ser Leu Ser Asp Asn Ser Thr 65 70 75 80

Ser Gln Ala Arg Ala Arg Ala Thr 85

- (2) INFORMATION FOR SEQ ID NO:2366:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- Client Docket No. 80146.003 (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..458 (D) OTHER INFORMATION: / Ceres Seq. ID 1600859 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366: atggtggtat ggcggcattc gtgcaggacc gacccccacc tccacctcgt atgctctctc 60 tetetetete teetteeeat ggetgatgee tgacaeggtg acaececeaa catteteeet cactagctag ctgtgtcctg cctacctagc ggtatcaata cccggctgca gctcaccacc accaccaacc aaccaaccca cagttcccat ataggcagcc atcggctaca cagcctcgcc tccgtaagca gagtgtgtcg ttggaagaga gacgacggcg gccatggcga cctccttcca ggggacgacc accaagtgca ccgcctgcga caagacggtg taccttgtgg acaagctcac 360 cgccgacaac cgcatctacc acaaggcctg cttccgctgc caccactgca agggcaccct 420 caageteges aactacaact cettegaggg agtgetet (2) INFORMATION FOR SEQ ID NO:2367: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..30 (D) OTHER INFORMATION: / Ceres Seq. ID 1600860 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367: Met Val Val Trp Arg His Ser Cys Arg Thr Asp Pro His Leu His Leu 10 5 Val Cys Ser Leu Ser Leu Ser Leu Leu Pro Met Ala Asp Ala 25 20 (2) INFORMATION FOR SEQ ID NO:2368: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..42 (D) OTHER INFORMATION: / Ceres Seq. ID 1600861
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

Trp Trp Tyr Gly Gly Ile Arg Ala Gly Pro Thr Pro Thr Ser Thr Ser 10 5

Tyr Ala Leu Ser Leu Ser Leu Ser Phe Pro Trp Leu Met Pro Asp Thr 25

Val Thr Pro Pro Thr Phe Ser Leu Thr Ser 35

- (2) INFORMATION FOR SEQ ID NO:2369:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..58
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600862
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

Met Ala Thr Ser Phe Gln Gly Thr Thr Thr Lys Cys Thr Ala Cys Asp

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                                    10
Lys Thr Val Tyr Leu Val Asp Lys Leu Thr Ala Asp Asn Arg Ile Tyr
                                25
            20
His Lys Ala Cys Phe Arg Cys His His Cys Lys Gly Thr Leu Lys Leu
Xaa Asn Tyr Asn Ser Phe Glu Gly Val Leu
   50
                      55
(2) INFORMATION FOR SEQ ID NO:2370:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 451 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..451
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600868
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:
gataaggcac ggagaacgag tgaccggcgc gtgaagcagc ggtggtggag tgggcctagg
                                                                        60
gcagggtagc cgtcaaggca gggcgttcgt aggcgctacg aaagctcgag gactgtactc
                                                                       120
gctcgcaaac cctagccgcc ggaccggccg gtgaccgtgc ggcgctgagg cgcgcgctat
                                                                       180
ataaacagag ccatccattc cgtctcttac cgttcagtcc cacctcgacc gcctcctctc
                                                                       240
ccctcccccg gctctgtctg ttgacttacc ccgtcgagct atctagtcag ctgctcccgt
                                                                       300
tgccatgggg aaggagaagg ttcacatcaa cattgtggtc attggccatg tcgactccgg
                                                                       360
caagtccacc accaccggcc acctcatcta caagcttgga ggcattgaca agcgtgtcat
                                                                       420
cgagaggttt gagaaggagg ctgccgagat g
(2) INFORMATION FOR SEQ ID NO:2371:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 49 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..49
           (D) OTHER INFORMATION: / Ceres Seq. ID 1600869
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:
Met Gly Lys Glu Lys Val His Ile Asn Ile Val Val Ile Gly His Val
                                     10
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
            20
                                 25
Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
Met
 (2) INFORMATION FOR SEQ ID NO:2372:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 34 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
```

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..34
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372: Met Ser Thr Pro Ala Ser Pro Pro Pro Pro Ala Thr Ser Ser Thr Ser 1

Leu Glu Ala Leu Thr Ser Val Ser Ser Arg Gly Leu Arg Arg Arg Leu 25

Pro Arg

- (2) INFORMATION FOR SEQ ID NO:2373:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..167
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373: ctecttitee ececttiqua tiqqqtiqee geaacactae agacacaaac acagtetagg
- (2) INFORMATION FOR SEQ ID NO:2374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (1x) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..47
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600886
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

Asn Arg Ala Arg Ala Pro Arg Glu Glu Gly Lys Pro Gly Glu Arg Glu 10 5

Arg Asp Thr Ser Ser Phe Ser Pro Leu Cys Ile Gly Leu Pro Gln His 30 25

Tyr Arg His Lys His Ser Leu Gly Gly Phe Phe Arg Ser Leu Arg 40

- (2) INFORMATION FOR SEQ ID NO:2375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..38
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600887
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

Ile Glu Pro Glu Arg Arg Gly Arg Arg Ala Asn Arg Glu Arg Glu Arg 1.0

Glu Thr Pro Pro Pro Phe Pro Pro Phe Ala Leu Gly Cys Arg Asn Thr 20 25 30

Thr Asp Thr Asn Thr Val 35

- (2) INFORMATION FOR SEQ ID NO:2376:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..527
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600896
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376: ttcctaatgg gacgacagga catgctcttg atattctttc acgagcacca ctctggagag 60 agggtcttga ctatcggcat ggtacaggcc atggaattgg atcttatttg aatgtccatg 120 aaggtootca totaattago ttoagacott otgotogaaa tgtacogotg caagcatcaa 180 tgactgtgac agatgagcct ggttattatg aagatggggc ctttggtata agattggaga 240 atgtacttat ttgcaaagac gccaatgcta agtttaattt tggagataaa ggttatttgg 300 catttgaaca tataawcatg ggctccatac cagaccaagc tgatagacac cgagcttctg 360 acccctgttg agatcgactg ggtgaacacg taccactcag actgccggaa gatcttggag 420 cctcatctga acgagcagga gaagcaatgg ctgatgaaag ctactgagcc cgtagctgca 480 agaggetgag cettttegte aaegttgeat gecaeegage geeagge
- (2) INFORMATION FOR SEQ ID NO:2377:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600897
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:
- Pro Asn Gly Thr Thr Gly His Ala Leu Asp Ile Leu Ser Arg Ala Pro 1 5 10 15
- Leu Trp Arg Glu Gly Leu Asp Tyr Arg His Gly Thr Gly His Gly Ile 20 25 30
- Gly Ser Tyr Leu Asn Val His Glu Gly Pro His Leu Ile Ser Phe Arg 35 40 45
- Pro Ser Ala Arg Asn Val Pro Leu Gln Ala Ser Met Thr Val Thr Asp 50 55 60
- Glu Pro Gly Tyr Tyr Glu Asp Gly Ala Phe Gly Ile Arg Leu Glu Asn 65 70 75 80
- Val Leu Ile Cys Lys Asp Ala Asn Ala Lys Phe Asn Phe Gly Asp Lys 85 90 95
- Gly Tyr Leu Ala Phe Glu His Ile Xaa Met Gly Ser Ile Pro Asp Gln 100 105 110
- Ala Asp Arg His Arg Ala Ser Asp Pro Cys 115 120
- (2) INFORMATION FOR SEQ ID NO:2378:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600898
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:
- Met Thr Val Thr Asp Glu Pro Gly Tyr Tyr Glu Asp Gly Ala Phe Gly 1 5 10 15
- Ile Arg Leu Glu Asn Val Leu Ile Cys Lys Asp Ala Asn Ala Lys Phe 20 25 30
- Asn Phe Gly Asp Lys Gly Tyr Leu Ala Phe Glu His Ile Xaa Met Gly 35 40 45

Ser Ile Pro Asp Gln Ala Asp Arg His Arg Ala Ser Asp Pro Cys 50 55

- (2) INFORMATION FOR SEQ ID NO:2379:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..526
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600899
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379: actetetect eteggegtee eegtteecea acetetegte tgetgeetge etgeetgeaa aaaggagttt gtcatggcgt ctaagcgcat cctcaaggag ctgaaggacc tgcagaaaga 120 180 ccccccaca tcatgcagtg caggtcctgc tggtgaggac atgtttcatt ggcaagcaac aattatggga ccacctgaca gtccctatgc tggcggtgtt ttcttagtga acattcattt 240 cccgccagat taccccttca aacctccaaa ggtttctttc aagacaaagg tcttccatcc taatatcaac agcaatggaa gtatatgcct tgacattctc aaagagcagt ggagccctgc tctgacaatt tctaaggtcc tgctctccat ctgctccctg ctgaccgact ccaacccgga 420 cgaccctctt gtcccggaga ttgcccacat gtacaagacg gaccggccga agtacgagtc 480 gacggcccgc agctggacgc agaagtacgc gatgggctga cgaacg
- (2) INFORMATION FOR SEQ ID NO:2380:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..172
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600900
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:
- Leu Ser Pro Leu Gly Val Pro Val Pro Gln Pro Leu Val Cys Cys Leu 1.0 Pro Ala Cys Lys Lys Glu Phe Val Met Ala Ser Lys Arg Ile Leu Lys
- 25 20
- Glu Leu Lys Asp Leu Gln Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly 45 4.0
- Pro Ala Gly Glu Asp Met Phe His Trp Gln Ala Thr Ile Met Gly Pro 60 55
- Pro Asp Ser Pro Tyr Ala Gly Gly Val Phe Leu Val Asn Ile His Phe 75 70
- Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe Lys Thr Lys 90 85
- Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile 110 105 100
- Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu 125 120 115
- Ser Ile Cys Ser Leu Leu Thr Asp Ser Asn Pro Asp Asp Pro Leu Val 135 140 130 Pro Glu Ile Ala His Met Tyr Lys Thr Asp Arg Pro Lys Tyr Glu Ser

- 150 Thr Ala Arg Ser Trp Thr Gln Lys Tyr Ala Met Gly 165
- (2) INFORMATION FOR SEQ ID NO:2381:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600901
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp 1 10 15

Pro Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Met Phe His

Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly
35 40 45

Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50 55 60

Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser

Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala 85 90 95

Ser Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys 115 120 125

Thr Asp Arg Pro Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys 130 135 140

Tyr Ala Met Gly

145

- (2) INFORMATION FOR SEQ ID NO:2382:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600902
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr 1 5 10 15

Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro
20 25 30

Phe Lys Pro Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn 35 40 45

Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp 50 55 60

Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu 65 70 75 80

Leu Thr Asp Ser Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His 85 90 95

Met Tyr Lys Thr Asp Arg Pro Lys Tyr Glu Ser Thr Ala Arg Ser Trp 100 105 110

Thr Gln Lys Tyr Ala Met Gly

- (2) INFORMATION FOR SEQ ID NO:2383:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..452
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383: attetgtege gttetttega egecaaceee gaceegegge eecaceacee agggecaaat 60 teccetgega tectetgtgt ceaectetee ttteteaeae etegaegeet etetetettt 120 ccccgagctc tcgaaaccct aggtgcgtgc cgaccggcgg cggcggcgag gtgatggcga 180 tggacccgga cgcggtggcg aaagccttcg tggagcacta ctaccggacg ttcgaccac 240 accgcgcggc gctggtgggg ctgtatcagg agacctccat gctcaccttc gagggccaga 300 agttccaggg cccatccgcc attgccggca agctcggatc tcttcccttc caggcctgcg 360 agcaccagat cgtcaccgtc gactgccagc cgtcggggcc ccagggaggc atgctcgtct 420 togtotocgg ttocatocgc accggcocga gg
- (2) INFORMATION FOR SEQ ID NO:2384:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..150
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:
- Ser Val Ala Phe Phe Arg Arg Gln Pro Arg Pro Ala Ala Pro Pro Pro 10 15
- Arg Ala Lys Phe Pro Cys Asp Pro Leu Cys Pro Pro Leu Leu Ser His 20 25 30
- Thr Ser Thr Pro Leu Ser Leu Ser Pro Ser Ser Arg Asn Pro Arg Cys 35 40 45
- Val Pro Thr Gly Gly Gly Glu Val Met Ala Met Asp Pro Asp Ala 50 55 60
- Val Ala Lys Ala Phe Val Glu His Tyr Tyr Arg Thr Phe Asp Thr Asn 65 70 75 80
- Arg Ala Ala Leu Val Gly Leu Tyr Gl
n Glu Thr Ser Met Leu Thr Phe $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95 \hspace{1.5cm}$
- Glu Gly Gln Lys Phe Gln Gly Pro Ser Ala Ile Ala Gly Lys Leu Gly
 100
 105
 110
- Ser Leu Pro Phe Gln Ala Cys Glu His Gln Ile Val Thr Val Asp Cys 115 120 125
- Gln Pro Ser Gly Pro Gln Gly Gly Met Leu Val Phe Val Ser Gly Ser 130 135 140
- Ile Arg Thr Gly Pro Arg
- 145 150
- (2) INFORMATION FOR SEQ ID NO:2385:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600905
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:
- Met Ala Met Asp Pro Asp Ala Val Ala Lys Ala Phe Val Glu His Tyr 1 5 10 15

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Tyr Arg Thr Phe Asp Thr Asn Arg Ala Ala Leu Val Gly Leu Tyr Gln
                                25
            20
Glu Thr Ser Met Leu Thr Phe Glu Gly Gln Lys Phe Gln Gly Pro Ser
                                                45
                            40
        35
Ala Ile Ala Gly Lys Leu Gly Ser Leu Pro Phe Gln Ala Cys Glu His
                        55
                                            60
Gln Ile Val Thr Val Asp Cys Gln Pro Ser Gly Pro Gln Gly Gly Met
                                        75
                    70
Leu Val Phe Val Ser Gly Ser Ile Arg Thr Gly Pro Arg
                                    90
                85
(2) INFORMATION FOR SEQ ID NO:2386:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600906
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

Met Asp Pro Asp Ala Val Ala Lys Ala Phe Val Glu His Tyr Tyr Arg 10

Thr Phe Asp Thr Asn Arg Ala Ala Leu Val Gly Leu Tyr Gln Glu Thr 25

Ser Met Leu Thr Phe Glu Gly Gln Lys Phe Gln Gly Pro Ser Ala Ile 45 40

Ala Gly Lys Leu Gly Ser Leu Pro Phe Gln Ala Cys Glu His Gln Ile 60 55

Val Thr Val Asp Cys Gln Pro Ser Gly Pro Gln Gly Gly Met Leu Val 7.5

Phe Val Ser Gly Ser Ile Arg Thr Gly Pro Arg 85

- (2) INFORMATION FOR SEQ ID NO:2387:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..377
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600932
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

ttctactgtt caccccgcgt gcgctcgctc actcgctctc tcccctctgg ctctgagtgg 60 120 cgctagtggg cgaccgcgcc gcgtccctcc gtcagtgccc aggtgtagcc tcgtcagccc ctccgtcagt cttcgtcggc cccctcgccg acgagcaccc accaggcatg agagcgcgct 180 tctagaataa tgtctgtgct tacctgcgtg attgaaagca tgggctcatc ctgtagcaga 240 teccattett tegaegagge tgaageaget gaaaatgeaa agtetgeaga cattgaeegg 300 agattttgca agadacaaaa gccgaacaac acatccacaa gctcttactt ctcggtgctg 360 gagaatcggg gaagtct

- (2) INFORMATION FOR SEQ ID NO:2388:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

Ser Thr Val His Pro Ala Cys Ala Arg Ser Leu Ala Leu Ser Pro Leu 1 5 10 15

Ala Leu Ser Gly Ala Ser Gly Arg Pro Arg Arg Val Pro Pro Ser Val 20 25 30

Pro Arg Cys Ser Leu Val Ser Pro Ser Val Ser Leu Arg Arg Pro Pro 35 40 45

Arg Arg Arg Ala Pro Thr Arg His Glu Ser Ala Leu Leu Glu 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2389:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

Met Ser Val Leu Thr Cys Val Ile Glu Ser Met Gly Ser Ser Cys Ser 1 10 15

Arg Ser His Ser Phe Asp Glu Ala Glu Ala Glu Asn Ala Lys Ser 20 25 30

Ala Asp Ile Asp Arg Arg Phe Cys Lys Xaa Gln Lys Pro Asn Asn Thr 35 40

Ser Thr Ser Ser Tyr Phe Ser Val Leu Glu Asn Arg Gly Ser 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2390:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..52
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

Met Gly Ser Ser Cys Ser Arg Ser His Ser Phe Asp Glu Ala Glu Ala 1 5 10 15

Ala Glu Asn Ala Lys Ser Ala Asp Ile Asp Arg Arg Phe Cys Lys Xaa 20 25 30

Gln Lys Pro Asn Asn Thr Ser Thr Ser Ser Tyr Phe Ser Val Leu Glu 35 40 45

Asn Arg Gly Ser 50

- (2) INFORMATION FOR SEQ ID NO:2391:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1600949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

ccattaaccc cggcccggc aactccccaa gtcgagcaac aggccaaacc cccagccgc 60
ggaagccgct accgctagca cctccgakcg agtcggcgc atggaagacg tcatcaccga 120
cgtgccgccg ccttcccgct tttcccctga cgacctcgac aacttcgccg ctccgccagc 180
gcagcccacc cccatcttcg tcgtttcccc gaaccctagc ccaccggccc cgcgcctcct 240
cgtcgtattc atctcccca cctccctcgc gctcctcgc tccccgccgc cgctcctcgc ctccctgctc ctcccggacc tgcccctact cccgcacgcg cccatgcgcg tgtactccac 360
ccctccggcg cgctcctcgc cgcggcgc

- (2) INFORMATION FOR SEQ ID NO:2392:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..128
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600950
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

Ile Asn Pro Gly Pro Gly Asn Ser Pro Ser Arg Ala Thr Gly Gln Thr 1 5 10 15

Pro Ser Arg Arg Lys Pro Leu Pro Leu Ala Pro Pro Xaa Glu Ser Ala 20 25 30

Pro Trp Lys Thr Ser Ser Pro Thr Cys Arg Arg Leu Pro Ala Phe Pro 35 40 45

Leu Thr Thr Ser Thr Thr Ser Pro Leu Arg Gln Arg Ser Pro Pro Pro 50 55 60

Ser Ser Ser Phe Pro Arg Thr Leu Ala His Arg Pro Arg Ala Ser Ser 65 70 75 80
Ser Tyr Ser Ser Pro Pro Pro Pro Ser Arg Ser Ser Pro Pro Arg Arg

85 90 95
Arg Ser Ser Pro Pro Cys Ser Ser Arg Thr Cys Pro Tyr Ser Arg Thr

100 105 110

Arg Pro Cys Ala Cys Thr Pro Pro Leu Arg Arg Ala Pro Arg Arg Gly
115 120 125

- (2) INFORMATION FOR SEQ ID NO:2393:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600951
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

Met Glu Asp Val Ile Thr Asp Val Pro Pro Pro Ser Arg Phe Ser Pro

Asp Asp Leu Asp Asn Phe Ala Ala Pro Pro Ala Gln Pro Thr Pro Ile
20 25 30

Phe Val Val Ser Pro Asn Pro Ser Pro Pro Ala Pro Arg Leu Leu Val

Val Phe Ile Ser Pro Thr Ser Leu Ala Leu Leu Ala Ser Pro Pro 50 55 60

Leu Leu Ala Ser Leu Leu Leu Pro Asp Leu Pro Leu Leu Pro His Ala

65 70 75 80
Pro Met Arg Val Tyr Ser Thr Pro Pro Ala Arg Ser Ser Pro Arg Arg
85 90 95

- (2) INFORMATION FOR SEQ ID NO:2394:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..511
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600952
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394: acacgaataa agcatcgatc acaataagat ggcgtgtata gacaatgcaa tgagagcctt 120 gttcctttta gcgctcttct gtgtcgtgca tggtgagaag gcaaagtcaa aggacaacga tgcaaaagcg tccgggcccg gtgggtcctt cgacatcacc aagttgggcg cctccggcaa 180 240 tggcaagacg gatagcacga aggctgtgca ggaggcgtgg gcatcagcgt gcggcggcac 300 cgggaagcag acgatectea tecceaaggg cgaetteete gteggaecae teaaetteae 360 aggcccatgc aagggcgacg tgaccatcca ggtgaatggc aatctgctgg cgaccacgga cctaagccag tacaaggatc atggtaattg gatcgagatt ctacgcgtgg acttcgtgaa 420 caacggggag gtgtccggga tcacgctgct caactccaag ttcttccaca tgaacatgta 480 caagtgcaag gacatgctga tcaaggacgt c
- (2) INFORMATION FOR SEQ ID NO:2395:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600953
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395: Met Ala Cys Ile Asp Asn Ala Met Arg Ala Leu Phe Leu Leu Ala Leu
- 1 5 10 15

 Phe Cys Val Val His Gly Glu Lys Ala Lys Ser Lys Asp Asn Asp Ala
 20 25 30
- Lys Ala Ser Gly Pro Gly Gly Ser Phe Asp Ile Thr Lys Leu Gly Ala
- Ser Gly Asn Gly Lys Thr Asp Ser Thr Lys Ala Val Gln Glu Ala Trp 50 55 60
- Ala Ser Ala Cys Gly Gly Thr Gly Lys Gln Thr Ile Leu Ile Pro Lys
 65 70 80
- Gly Asp Phe Leu Val Gly Pro Leu Asn Phe Thr Gly Pro Cys Lys Gly 85 90 95
- Asp Val Thr Ile Gln Val Asn Gly Asn Leu Leu Ala Thr Thr Asp Leu
 100 105 110
- Ser Gln Tyr Lys Asp His Gly Asn Trp Ile Glu Ile Leu Arg Val Asp 115 120 125
- Phe Val Asn Asn Gly Glu Val Ser Gly Ile Thr Leu Leu Asn Ser Lys
 130 140
- Phe Phe His Met Asn Met Tyr Lys Cys Lys Asp Met Leu Ile Lys Asp 145 150 155 160
- (2) INFORMATION FOR SEQ ID NO:2396:

360

420

- Page 1208 Client Docket No. 80146.003 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..154 (D) OTHER INFORMATION: / Ceres Seq. ID 1600954 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396: Met Arg Ala Leu Phe Leu Leu Ala Leu Phe Cys Val Val His Gly Glu 10 5 Lys Ala Lys Ser Lys Asp Asn Asp Ala Lys Ala Ser Gly Pro Gly Gly 25 20 Ser Phe Asp Ile Thr Lys Leu Gly Ala Ser Gly Asn Gly Lys Thr Asp 40 Ser Thr Lys Ala Val Gln Glu Ala Trp Ala Ser Ala Cys Gly Gly Thr 55 Gly Lys Gln Thr Ile Leu Ile Pro Lys Gly Asp Phe Leu Val Gly Pro 75 70 Leu Asn Phe Thr Gly Pro Cys Lys Gly Asp Val Thr Ile Gln Val Asn 90 85 Gly Asn Leu Leu Ala Thr Thr Asp Leu Ser Gln Tyr Lys Asp His Gly 105 Asn Trp Ile Glu Ile Leu Arg Val Asp Phe Val Asn Asn Gly Glu Val 120 Ser Gly Ile Thr Leu Leu Asn Ser Lys Phe Phe His Met Asn Met Tyr 130 135 Lys Cys Lys Asp Met Leu Ile Lys Asp Val 150 (2) INFORMATION FOR SEQ ID NO:2397: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..450 (D) OTHER INFORMATION: / Ceres Seq. ID 1600955 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397: agggtgtgca ctccgatcct gccctctaat aacagcagca gcagccgcca tggaaggcag cagcaagaag ctccagccgt tcctcctcac gctgctgctg gtgctctcca ccgccgtgac 120 gcccatcctc tcgctgtcag tgccagacga cgaggtagcc tgcgactgcg acaaacccaa 180 ggegeccaag eegtegeace egeccaagae caageeetee caecegtege egtegeegaa 240 qcccaagaac cccaagccac ccaggggcag caccgggtac ccagcgccgg ggcaccaacc 300
 - gcccaagage ecetectace eceeggtegt eggeeeteec aagggeeeeg teaegegeee gccagtcacg cgtccgccgg tcgtcggtcc tcccaagggc cccgtcacgc gcccgccggt cacgcgtccg cggttgtcgg accaccggtg (2) INFORMATION FOR SEQ ID NO:2398:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..150

```
(D) OTHER INFORMATION: / Ceres Seq. ID 1600956
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:
Arg Val Cys Thr Pro Ile Leu Pro Ser Asn Asn Ser Ser Ser Ser Arg
                                 10
              5
His Gly Arg Gln Gln Glu Ala Pro Ala Val Pro Pro His Ala Ala
                                                30
                             25
          20
Ala Gly Ala Leu His Arg Arg Asp Ala His Pro Leu Ala Val Ser Ala
                                           4.5
                         40
Arg Arg Arg Gly Ser Leu Arg Leu Arg Gln Thr Gln Gly Ala Gln Ala
                     55
                                        60
Val Ala Pro Ala Gln Asp Gln Ala Leu Pro Pro Val Ala Val Ala Glu
                 70
                                     75
Ala Gln Glu Pro Gln Ala Thr Gln Gly Gln His Arg Val Pro Ser Ala
                               90
             85
Gly Ala Pro Thr Ala Gln Glu Pro Leu Leu Pro Pro Gly Arg Arg Pro
          100 105
                                                110
Ser Gln Gly Pro Arg His Ala Pro Ala Ser His Ala Ser Ala Gly Arg
      115 120
                                            125
Arg Ser Ser Gln Gly Pro Arg His Ala Pro Ala Gly His Ala Ser Ala
  130 135
                                         140
Val Val Gly Pro Pro Val
      150
(2) INFORMATION FOR SEQ ID NO:2399:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 149 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..149
         (D) OTHER INFORMATION: / Ceres Seq. ID 1600957
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:
Gly Cys Ala Leu Arg Ser Cys Pro Leu Ile Thr Ala Ala Ala Ala Ala
                              10
            5
Met Glu Gly Ser Ser Lys Lys Leu Gln Pro Phe Leu Leu Thr Leu Leu
                                     30
                             25
           20
Leu Val Leu Ser Thr Ala Val Thr Pro Ile Leu Ser Leu Ser Val Pro
                                             45
                          40
Asp Asp Glu Val Ala Cys Asp Cys Asp Lys Pro Lys Ala Pro Lys Pro
                                        60
                      55
Ser His Pro Pro Lys Thr Lys Pro Ser His Pro Ser Pro Ser Pro Lys
                   70
                                     75
Pro Lys Asn Pro Lys Pro Pro Arg Gly Ser Thr Gly Tyr Pro Ala Pro
                                  90
               85
Gly His Gln Pro Pro Lys Ser Pro Ser Tyr Pro Pro Val Val Gly Pro
                              105
           100
Pro Lys Gly Pro Val Thr Arg Pro Pro Val Thr Arg Pro Pro Val Val
                          120 125
 Gly Pro Pro Lys Gly Pro Val Thr Arg Pro Pro Val Thr Arg Pro Arg
                                         1.40
    130
Leu Ser Asp His Arg
 145
 (2) INFORMATION FOR SEQ ID NO:2400:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 133 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
```

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600958
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400: Met Glu Gly Ser Ser Lys Lys Leu Gln Pro Phe Leu Leu Thr Leu Leu 10
- Leu Val Leu Ser Thr Ala Val Thr Pro Ile Leu Ser Leu Ser Val Pro 25
- Asp Asp Glu Val Ala Cys Asp Cys Asp Lys Pro Lys Ala Pro Lys Pro 40
- Ser His Pro Pro Lys Thr Lys Pro Ser His Pro Ser Pro Ser Pro Lys 55
- Pro Lys Asn Pro Lys Pro Pro Arg Gly Ser Thr Gly Tyr Pro Ala Pro 75 70
- Gly His Gln Pro Pro Lys Ser Pro Ser Tyr Pro Pro Val Val Gly Pro 90 85
- Pro Lys Gly Pro Val Thr Arg Pro Pro Val Thr Arg Pro Pro Val Val 105 100
- Gly Pro Pro Lys Gly Pro Val Thr Arg Pro Pro Val Thr Arg Pro Arg 125 120 115

Leu Ser Asp His Arg

130

- (2) INFORMATION FOR SEQ ID NO:2401:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..491
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600963
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401: attgggccaa aatgtaagag tagaaacaac cccagccgcc gccaacccca accccgttct 60 ceggecegee getetetete tectagtece ettetategt ggeaacgaeg agegaeagte 120 gctgccgccc tacggcaggt gcccaggtct tcttcggtcc cttcgccgtc gacgagcact 180 accaggaact tgatcttata atacaaactt caatatgttc tctgctccag gcaacaattc 240 300 tatggctctt gtagccccac ggccagggat ggagctggct aatattcaac atcatccaaa 360 tcaggctcct gggcctggag gaaaacaacg cacatctagc ctggaggcac caataatgct 420 acttacaggt caccagagtg ctatctactg catgaaattc aatcctgcgg gaactgtgat agcatcaggt tcccatgaca aggatatctt cttatggtat gttcatggtg aatgtaagaa 480 ctttatggta c
- (2) INFORMATION FOR SEQ ID NO:2402:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600964
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:
- Met Phe Ser Ala Pro Gly Asn Asn Ser Met Ala Leu Val Ala Pro Arg 10 5
- Pro Gly Met Glu Leu Ala Asn Ile Gln His His Pro Asn Gln Ala Pro 30 25
- Gly Pro Gly Gly Lys Gln Arg Thr Ser Ser Leu Glu Ala Pro Ile Met

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35

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Leu Leu Thr Gly His Gln Ser Ala Ile Tyr Cys Met Lys Phe Asn Pro
50

55

60

Ala Gly Thr Val Ile Ala Ser Gly Ser His Asp Lys Asp Ile Phe Leu
65

70

Trp Tyr Val His Gly Glu Cys Lys Asn Phe Met Val
85

90

(2) INFORMATION FOR SEQ ID NO:2403:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..83
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600965
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

Met Ala Leu Val Ala Pro Arg Pro Gly Met Glu Leu Ala Asn Ile Gln 1 5 10

His His Pro Asn Gln Ala Pro Gly Pro Gly Gly Lys Gln Arg Thr Ser 20 25 30

Ser Leu Glu Ala Pro Ile Met Leu Leu Thr Gly His Gln Ser Ala Ile 35 40 45

Tyr Cys Met Lys Phe Asn Pro Ala Gly Thr Val Ile Ala Ser Gly Ser 50 55

His Asp Lys Asp Ile Phe Leu Trp Tyr Val His Gly Glu Cys Lys Asn 65 70 75 80

Phe Met Val

- (2) INFORMATION FOR SEQ ID NO:2404:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..74
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600966
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

Met Glu Leu Ala Asn Ile Gln His His Pro Asn Gln Ala Pro Gly Pro 1 5 10 15

Gly Gly Lys Gln Arg Thr Ser Ser Leu Glu Ala Pro Ile Met Leu Leu 20 25 30

Thr Gly His Gln Ser Ala Ile Tyr Cys Met Lys Phe Asn Pro Ala Gly 35 40 45

Thr Val Ile Ala Ser Gly Ser His Asp Lys Asp Ile Phe Leu Trp Tyr 50 55 60

Val His Gly Glu Cys Lys Asn Phe Met Val 65

- (2) INFORMATION FOR SEQ ID NO:2405:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405: ctgtggtttg gacagctagc tacatggact cctgctttca cgttctcata caggcactcc 60 tgcactgtgc tccttcgtct cctcctcccc tgcctgccac caactgccaa ggtttatgtt 120 caggtggcac tgccagcaga agtgatccgt tgacttcagc tatgggcaac ctgtgctgct 180 gtgttcaagt cgaccagtcg actgtggcca tcagggagca gtttggcaag tttgacagcg 240 tgcttgagcc aggatgccac tgcatgcctt ggttcgccgg caagcgtgta gctgggcaac 300 tcacactcag gctgcagcaa ctggatgtgc gctgtgagac aaaaacaaag gacaatgttt 360 tcgtgaatgt ggtggcatct attcagtacc gcgctctggc tgacaaagca agtgacgctt 420 tctacaaact gagcaacaca aggtcccaga tcccaagcct acgtctttga cgtgatcaga 480 gcaagcgttc ccaagctcca tttggacgat qct

- (2) INFORMATION FOR SEQ ID NO:2406:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..155
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

Val Val Trp Thr Ala Ser Tyr Met Asp Ser Cys Phe His Val Leu Ile 10 Gln Ala Leu Leu His Cys Ala Pro Ser Ser Pro Pro Pro Leu Pro Ala 25 20

Thr Asn Cys Gln Gly Leu Cys Ser Gly Gly Thr Ala Ser Arg Ser Asp 40

Pro Leu Thr Ser Ala Met Gly Asn Leu Cys Cys Cys Val Gln Val Asp 55

Gln Ser Thr Val Ala Ile Arg Glu Gln Phe Gly Lys Phe Asp Ser Val 75 70

Leu Glu Pro Gly Cys His Cys Met Pro Trp Phe Ala Gly Lys Arg Val 90 85

Ala Gly Gln Leu Thr Leu Arg Leu Gln Gln Leu Asp Val Arg Cys Glu 105

Thr Lys Thr Lys Asp Asn Val Phe Val Asn Val Val Ala Ser Ile Gln 120 125

Tyr Arg Ala Leu Ala Asp Lys Ala Ser Asp Ala Phe Tyr Lys Leu Ser 135 Asn Thr Arg Ser Gln Ile Pro Ser Leu Arg Leu

150

- (2) INFORMATION FOR SEQ ID NO:2407:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

Met Asp Ser Cys Phe His Val Leu Ile Gln Ala Leu Leu His Cys Ala 5 10

Pro Ser Ser Pro Pro Pro Leu Pro Ala Thr Asn Cys Gln Gly Leu Cys 25

360 420

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Ser Gly Gly Thr Ala Ser Arg Ser Asp Pro Leu Thr Ser Ala Met Gly
                            40
Asn Leu Cys Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala Ile Arg
                        55
Glu Gln Phe Gly Lys Phe Asp Ser Val Leu Glu Pro Gly Cys His Cys
                    70
                                        75
Met Pro Trp Phe Ala Gly Lys Arg Val Ala Gly Gln Leu Thr Leu Arg
                85
                                    90
Leu Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp Asn Val
           100
                               105
Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala Asp Lys
                           120
                                               125
Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn Thr Arg Ser Gln Ile Pro
    130
                       135
                                           140
Ser Leu Arg Leu
145
(2) INFORMATION FOR SEQ ID NO:2408:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 102 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..102
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600978
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:
Met Gly Asn Leu Cys Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala
                                    10
Ile Arg Glu Gln Phe Gly Lys Phe Asp Ser Val Leu Glu Pro Gly Cys
            20
                                25
His Cys Met Pro Trp Phe Ala Gly Lys Arg Val Ala Gly Gln Leu Thr
                            4.0
Leu Arg Leu Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp
                        5.5
Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala
                    70
                                        75
Asp Lys Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn Thr Arg Ser Gln
                85
Ile Pro Ser Leu Arg Leu
            100
(2) INFORMATION FOR SEQ ID NO:2409:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 437 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..437
          (D) OTHER INFORMATION: / Ceres Seq. ID 1600993
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:
                                                                        60
gtgcctcttc ctaatccatc gcagagcgcc gccggcgggt agcgctactg ctagaggaga
                                                                       120
ggaageggaa agggeggegg eggegettgt ggteagteaa agateeaace teeggacteg
                                                                       180
cgatggggcg gcggatcctc aacgatgctc tgcgcacgat ggtcaacgca gaccggcggg
                                                                       240
ggaacgcgtc ggcgcttctc cgacccatct ccggcgtcat ggtctccttc ctcaacatca
tgaagtaccg agggtatatc aaaaaatttg aggtcattga tgagaataga gttgggaaaa
                                                                       300
```

ttagagtgga gcttgatgga cgtcttaaag attgcaaagc tctcacctac aggcaagacc

tcaaagctaa ggagatagat ccgctctgcc atggtgggcc tgctatcata cgttatttat

accagtgaaa attttcc

- (2) INFORMATION FOR SEQ ID NO:2410:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600994
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

Ala Arg Gly Glu Glu Ala Glu Arg Ala Ala Ala Leu Val Val Ser 20 25 30

Gln Arg Ser Asn Leu Arg Thr Arg Asp Gly Ala Ala Asp Pro Gln Arg 35 40 45

Cys Ser Ala His Asp Gly Gln Arg Pro Ala Gly Glu Arg Val Gly 50 60

Ala Ser Pro Thr His Leu Arg Arg His Gly Leu Leu Pro Gln His His 65 70 75 80

Glu Val Pro Arg Val Tyr Gln Lys Ile 85

- (2) INFORMATION FOR SEQ ID NO:2411:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1600995
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

Met Gly Arg Arg Ile Leu Asn Asp Ala Leu Arg Thr Met Val Asn Ala 1 5 10 15

Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg Pro Ile Ser Gly Val 20 25 30

Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg Gly Tyr Ile Lys Lys 35 40 45

Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys Ile Arg Val Glu Leu 50 60

Asp Gly Arg Leu Lys Asp Cys Lys Ala Leu Thr Tyr Arg Gln Asp Leu 65 70 75 80 Lys Ala Lys Glu Ile Asp Pro Leu Cys His Gly Gly Pro Ala Ile Ile

90

Arg Tyr Leu Tyr Gln

100

(2) INFORMATION FOR SEQ ID NO:2412:

85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89

```
(D) OTHER INFORMATION: / Ceres Seq. ID 1600996
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:
Met Val Asn Ala Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg Pro
                                    10
Ile Ser Gly Val Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg Gly
                                                     30
                               25
            20
Tyr Ile Lys Lys Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys Ile
                            40
Arg Val Glu Leu Asp Gly Arg Leu Lys Asp Cys Lys Ala Leu Thr Tyr
                                            60
                        55
Arg Gln Asp Leu Lys Ala Lys Glu Ile Asp Pro Leu Cys His Gly Gly
                                        75
                    70
Pro Ala Ile Ile Arg Tyr Leu Tyr Gln
                85
(2) INFORMATION FOR SEQ ID NO:2413:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 451 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..451
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601004
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:
                                                                        60
aacacrtaac cagcacacag ctctcgcctt ctctctccca tcggcacacc cgagctcgct
                                                                       120
coctcottcc acgtcgaggt ccgagtcctg ctttgatggc gaccgacgtg gctgagactc
ccgcgccgtt ggtggatgcg gccccagagg cgcccgccga cgccccggcg gcgcctgctg
                                                                       180
ccgacgcgaa gccggccaag gccaagaagg ccaccgcgcc gaagaagcgc gccagcccga
                                                                       240
cccacccgcc gtacgccgag atggtctcgg aggcgatcac gtcgctcaag gagaggacgg
                                                                       300
                                                                       360
ggtccagcag ctatgcgatt gccaaagttc gtggaggaca agcacaagga caagctcccg
cccaacttcc gcaagcttct gaacgttcag ctcaagaagc tcgtcgccgg cggcaagctg
                                                                       420
accaaggtga wgaactcgta caagctgtcg t
(2) INFORMATION FOR SEQ ID NO: 2414:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 149 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..149
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601005
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:
 His Xaa Thr Ser Thr Gln Leu Ser Pro Ser Leu Ser His Arg His Thr
                                     10
                5
 Arg Ala Arg Ser Leu Leu Pro Arg Arg Gly Pro Ser Pro Ala Leu Met
                                 25
 Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala Pro
                             40
 Glu Ala Pro Ala Asp Ala Pro Ala Ala Pro Ala Ala Asp Ala Lys Pro
                         55
 Ala Lys Ala Lys Lys Ala Thr Ala Pro Lys Lys Arg Ala Ser Pro Thr
                                         75
                     70
 His Pro Pro Tyr Ala Glu Met Val Ser Glu Ala Ile Thr Ser Leu Lys
                                     90
 Glu Arg Thr Gly Ser Ser Ser Tyr Ala Ile Ala Lys Val Arg Gly Gly
                                 105
```

Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg

Client Docket No. 80146.003 120 115 Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Xaa Glu 135 140 Leu Val Gln Ala Val 145 (2) INFORMATION FOR SEQ ID NO:2415: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..118 (D) OTHER INFORMATION: / Ceres Seq. ID 1601006 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415: Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala 10 5 Pro Glu Ala Pro Ala Asp Ala Pro Ala Ala Pro Ala Ala Asp Ala Lys 25 20 Pro Ala Lys Ala Lys Lys Ala Thr Ala Pro Lys Lys Arg Ala Ser Pro 40 Thr His Pro Pro Tyr Ala Glu Met Val Ser Glu Ala Ile Thr Ser Leu 55 60 Lys Glu Arg Thr Gly Ser Ser Tyr Ala Ile Ala Lys Val Arg Gly 70 75 Gly Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu 85 90 Arg Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Xaa 100 105 Glu Leu Val Gln Ala Val 115 (2) INFORMATION FOR SEQ ID NO:2416: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..105 (D) OTHER INFORMATION: / Ceres Seq. ID 1601007 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416: Met Arg Pro Gln Arg Arg Pro Pro Thr Pro Arg Arg Arg Leu Leu Pro 10 Thr Arg Ser Arg Pro Arg Pro Arg Pro Pro Arg Arg Arg Ser Ala 25 Pro Ala Arg Pro Thr Arg Arg Thr Pro Arg Trp Ser Arg Arg Arg Ser 40 Arg Arg Ser Arg Arg Gly Arg Gly Pro Ala Ala Met Arg Leu Pro Lys 55 60 Phe Val Glu Asp Lys His Lys Asp Lys Leu Pro Pro Asn Phe Arg Lys 70 75 Leu Leu Asn Val Gln Leu Lys Lys Leu Val Ala Gly Gly Lys Leu Thr 85 90

Lys Val Xaa Asn Ser Tyr Lys Leu Ser 100

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..460
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601012
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417: cggaacccca ttccccgccg cctcgcgcc ccgctcgctt cacttctcta ggtgcgcacc 60 120 gatcagaagg tgcctgcctc ctcctcgtcg gcgaaaagat ggcggtgccg ctgctgacga 180 agaagatcgt gaagaagcgg gtcaagcagt tcaagaggcc ccacctcgac cgctacaagt geettaagee aagetggege aggeeaaagg gtattgatte eegtgteagg aggaagttea 240 agggatgcac cttgatgccc aacattggtt atggttctga caagtcgacc aggcactacc 300 360 tocccagoaa gttcaagaag tttgtggtoo acaacgttto tgagotggag ttgctcatga 420 tgcacaacag gacctactgc gctgaaattg ctcacaacgt gtccaccaag aagcgcaagg agategtgga gegtgetgea cagetegaea ttgtggteae
- (2) INFORMATION FOR SEQ ID NO:2418:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601013
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:
- Glu Pro His Ser Pro Pro Pro Arg Ala Pro Ala Arg Phe Thr Ser Leu 5 10
- Gly Ala His Arg Ser Glu Gly Ala Cys Leu Leu Leu Val Gly Glu Lys 30 25 20
- Met Ala Val Pro Leu Leu Thr Lys Lys Ile Val Lys Lys Arg Val Lys 45 40 35
- Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys Cys Leu Lys Pro Ser 60
- Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys 75 70 65
- Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Ser Thr 90 85
- Arg His Tyr Leu Pro Ser Lys Phe Lys Lys Phe Val Val His Asn Val 110 105 100
- Ser Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu 125 120 115
- Ile Ala His Asn Val Ser Thr Lys Lys Arg Lys Glu Ile Val Glu Arg 140 135
- Ala Ala Gln Leu Asp Ile Val Val 150
- (2) INFORMATION FOR SEQ ID NO:2419:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..120
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601014

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:
Met Ala Val Pro Leu Leu Thr Lys Lys Ile Val Lys Lys Arg Val Lys
               5
                                   10
Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys Cys Leu Lys Pro Ser
                               25
                                                   30
Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys
Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Ser Thr
                       55
Arg His Tyr Leu Pro Ser Lys Phe Lys Lys Phe Val Val His Asn Val
                   70
                                        75
Ser Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu
               85
                                   90
Ile Ala His Asn Val Ser Thr Lys Lys Arg Lys Glu Ile Val Glu Arg
           100
                               105
Ala Ala Gln Leu Asp Ile Val Val
       115
(2) INFORMATION FOR SEQ ID NO:2420:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 496 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..496
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601015
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:
aacagtgtga agcccgctaa agagagtggt tgcaaaaatc tctactccga ccccaccta
aggcaccgac tcgccgggga cagagagaga ccgacgcgcc ggcagatccc aagctcaccg
                                                                      120
gagagggga agaggggac cgaaggcggc gatgggtttc atcatggact tcgcggagaa
tatgatecte egtetgatgg aggaeeegga caagegegae caggttegge gggageatgt
                                                                      240
ctacaagatg aaggagcggt gcgagcgcac taaggcggcg tggagcctcc ctctgcqccc
                                                                      300
ctacggette tggacetteg accgetteaa etegeagete teetgggate eccagateag
                                                                      360
ccaggeegee ggeegteggg acceetacga tgaeeteate geeegeeact etggetegee
                                                                      420
gccgtcttcc tgaacacccg ttccgatctt tgcccagaag gtctacttgg gcatcaataa
                                                                      480
gaaactcttt cccctc
(2) INFORMATION FOR SEQ ID NO:2421:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 90 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..90
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601016
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:
Asn Ser Val Lys Pro Ala Lys Glu Ser Gly Cys Lys Asn Leu Tyr Ser
                                    10
Asp Pro His Leu Arg His Arg Leu Ala Gly Asp Arg Glu Arg Pro Thr
            20
                                25
Arg Arg Gln Ile Pro Ser Ser Pro Glu Arg Gly Lys Arg Ala Thr Glu
                            40
Gly Gly Asp Gly Phe His His Gly Leu Arg Gly Glu Tyr Asp Pro Pro
                        55
Ser Asp Gly Gly Pro Gly Gln Ala Arg Pro Gly Ser Ala Gly Ala Cys
```

65 70 Leu Gln Asp Glu Gly Ala Val Arg Ala His

85 (2) INFORMATION FOR SEQ ID NO:2422: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1601017 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422: Met Gly Phe Ile Met Asp Phe Ala Glu Asn Met Ile Leu Arg Leu Met 10 Glu Asp Pro Asp Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr Lys 20 25 Met Lys Glu Arg Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro Leu 40 Arg Pro Tyr Gly Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser 50 55 Trp Asp Pro Gln Ile Ser Gln Ala Ala Gly Arg Arg Asp Pro Tyr Asp 65 70 75 Asp Leu Ile Ala Arg His Ser Gly Ser Pro Pro Ser Ser 85 90 (2) INFORMATION FOR SEQ ID NO:2423: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..89 (D) OTHER INFORMATION: / Ceres Seq. ID 1601018 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423: Met Asp Phe Ala Glu Asn Met Ile Leu Arg Leu Met Glu Asp Pro Asp 10 Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr Lys Met Lys Glu Arg 25 20 Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro Leu Arg Pro Tyr Gly 40 Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser Trp Asp Pro Gln 55 Ile Ser Gln Ala Ala Gly Arg Arg Asp Pro Tyr Asp Asp Leu Ile Ala 65 70 75 80 Arg His Ser Gly Ser Pro Pro Ser Ser 85 (2) INFORMATION FOR SEQ ID NO: 2424: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1601029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

(A) NAME/KEY: -(B) LOCATION: 1..436 tetttetega geetgaceet taegeetteg etegegeege egegeegeeg eegetaegee 60 cegeaceteg etteattteg tgtegeeaag atgacgaage geactaagaa ggeaggaatt 120 gttggeaaat atggaaceag gtatggteet agettgegta ageaaateaa gaagatggag 180 gtateteage tteeaagtae ttttgegagt tetgtgggaa gtttgetgtg aagagggaaag 240 cagttggaat ttgggggte aaggactgtg ggaaggtgaa ggetggtggt gettaeacea tgaacaetge tagtgeggte accgteagga geacgateeg eegeeteeag acgaggeaac 360 aatggegeta ggegge

- (2) INFORMATION FOR SEQ ID NO:2425:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..76
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601030
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

Ser Phe Ser Ser Leu Thr Leu Thr Pro Ser Leu Ala Pro Pro Arg Arg
1 10 15

Arg Arg Tyr Ala Pro His Leu Ala Ser Phe Arg Val Ala Lys Met Thr 20 25 30

Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr 35 40 45

Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser Gln Leu 50 55 60

Pro Ser Thr Phe Ala Ser Ser Val Gly Ser Leu Leu 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2426:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..60
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601031
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

Met Glu Pro Gly Met Val Leu Ala Cys Val Ser Lys Ser Arg Arg Trp

1 10 15

Arg Tyr Leu Ser Phe Gln Val Leu Leu Arg Val Leu Trp Glu Val Cys 25 30

Cys Glu Glu Glu Ser Ser Trp Asn Leu Gly Val Gln Gly Leu Trp Glu 35 40 45

Gly Glu Gly Trp Trp Cys Leu His His Glu His Cys 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601032

60

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:
Met Val Leu Ala Cys Val Ser Lys Ser Arg Arg Trp Arg Tyr Leu Ser
                                    10
Phe Gln Val Leu Leu Arg Val Leu Trp Glu Val Cys Cys Glu Glu
                                25
Ser Ser Trp Asn Leu Gly Val Gln Gly Leu Trp Glu Gly Glu Gly Trp
                            40
Trp Cys Leu His His Glu His Cys
    50
(2) INFORMATION FOR SEQ ID NO:2428:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 497 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
           (B) LOCATION: 1..497
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601040
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:
aatttccgtt tccatacttc cggcgcggcg gagatcgaat cgagcgcccg ccacggcgat
                                                                        120
ggcgactaga gtcctgccgc cggctctgct ctctttcata ctcctcctgc tgctctcgct
                                                                        180
ctcagcccgc gacaccgtcg ccgcgggcga ggatttccca cgcgacgggc gggtgatcga
cctcgacgac agcaatttcg aggcggcgct gggcgccatc gactttctct tcgtcgactt
                                                                        240
ctacgcccct tggtgcggcc actgcaagag acttgcgccc gagttagatg aagctgcacc
                                                                        300
ggtgttgtca gggttgagtg agcctattgt tgttgccaaa gtcaacgctg ataaatacag
                                                                        360
aaaactcgga tcaaaatatg gagtggatgg gttccctacc ctcatgctct ttatccatgg
                                                                        420
tgttccaatt gaatacactg gttcgaggaa agctgaccag cttgtccgca atctgaagaa
                                                                        480
gttcgtttcg ccagatg
(2) INFORMATION FOR SEQ ID NO:2429:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 165 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..165
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601041
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:
 Ile Ser Val Ser Ile Leu Pro Ala Arg Arg Arg Ser Asn Arg Ala Pro
                                     1.0
                 5
 Ala Thr Ala Met Ala Thr Arg Val Leu Pro Pro Ala Leu Leu Ser Phe
                                                      30
                                 25
             20
 Ile Leu Leu Leu Leu Ser Leu Ser Ala Arg Asp Thr Val Ala Ala
                              40
                                                  45
 Gly Glu Asp Phe Pro Arg Asp Gly Arg Val Ile Asp Leu Asp Asp Ser
                                              60
                         55
     50
 Asn Phe Glu Ala Ala Leu Gly Ala Ile Asp Phe Leu Phe Val Asp Phe
                                          75
                     70
 Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Glu Leu Asp
                                                          95
                  85
                                      90
 Glu Ala Ala Pro Val Leu Ser Gly Leu Ser Glu Pro Ile Val Val Ala
                                                      11.0
                                  105
              100
 Lys Val Asn Ala Asp Lys Tyr Arg Lys Leu Gly Ser Lys Tyr Gly Val
                                                  125
                              120
 Asp Gly Phe Pro Thr Leu Met Leu Phe Ile His Gly Val Pro Ile Glu
                                              140
                          135
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Tyr Thr Gly Ser Arg Lys Ala Asp Gln Leu Val Arg Asn Leu Lys Lys

155 160 150 145 Phe Val Ser Pro Asp 165 (2) INFORMATION FOR SEQ ID NO:2430: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..146 (D) OTHER INFORMATION: / Ceres Seq. ID 1601042 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430: Met Ala Thr Arg Val Leu Pro Pro Ala Leu Leu Ser Phe Ile Leu Leu 10 5 Leu Leu Ser Leu Ser Ala Arg Asp Thr Val Ala Ala Gly Glu Asp 25 Phe Pro Arg Asp Gly Arg Val Ile Asp Leu Asp Asp Ser Asn Phe Glu 40 Ala Ala Leu Gly Ala Ile Asp Phe Leu Phe Val Asp Phe Tyr Ala Pro 55 Trp Cys Gly His Cys Lys Arg Leu Ala Pro Glu Leu Asp Glu Ala Ala 75 70 Pro Val Leu Ser Gly Leu Ser Glu Pro Ile Val Val Ala Lys Val Asn 90 8.5 Ala Asp Lys Tyr Arg Lys Leu Gly Ser Lys Tyr Gly Val Asp Gly Phe 110 105 100 Pro Thr Leu Met Leu Phe Ile His Gly Val Pro Ile Glu Tyr Thr Gly 125 120 Ser Arg Lys Ala Asp Gln Leu Val Arg Asn Leu Lys Lys Phe Val Ser 135 130 Pro Asp 145 (2) INFORMATION FOR SEQ ID NO:2431: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 388 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..388 (D) OTHER INFORMATION: / Ceres Seq. ID 1601051 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431: caaaaaatca aaacaactca gcgattcgat tcgcggcgag tcaagcggga tgccgccgcg caeggeteeg geggegaeet caaeceegee geggaaggtg ceceteegga agetgetgeg tgcggcgtcg gtcgcctgcg gggtgcagtt cggctgggcg ctgcagctgt cgttgctgac cccgtacgtg caggagctgg gcatcccgca cgcctttgcc agtctcgtct ggctgtgcgg 300 tecgetgtee ggeetecteg tecageceet egteggeeae etetecgace geateggeee cgccgcttcg ccgctcgggc gccgcagg (2) INFORMATION FOR SEQ ID NO:2432: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601052
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

Arg Ser Leu Ala Leu Leu Ser Pro Ser Pro Leu Leu Ser Gly Val 1 5 10 15

Leu Asn Ser Asn Gln Lys Ile Lys Thr Thr Gln Arg Phe Asp Ser Arg 20 25 30

Arg Val Lys Arg Asp Ala Ala Ala His Gly Ser Gly Asp Leu Asn 35 40 45

Pro Ala Ala Glu Gly Ala Pro Pro Glu Ala Ala Ala Cys Gly Val Gly 50 55 60

Arg Leu Arg Gly Ala Val Arg Leu Gly Ala Ala Ala Val Val Ala Asp
65 70 75 80

Pro Val Arg Ala Gly Ala Gly His Pro Ala Arg Leu Cys Gln Ser Arg 85 90 95

Leu Ala Val Arg Ser Ala Val Arg Pro Pro Arg Pro Ala Pro Arg Arg
100 105 110

Pro Pro Leu Arg Pro His Arg Pro Arg Arg Phe Ala Ala Arg Ala Pro 115 120 125

Gln

- (2) INFORMATION FOR SEQ ID NO:2433:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601053
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Val Ser Ser Ser Thr Pro Leu Pro Glu Ser Ser Pro Leu Arg Gly Ile 1 $$ 5 $$ 10 $$ 15

Ser Gln Ala Gly Cys Arg Arg Ala Arg Leu Arg Arg Arg Pro Gln Pro 35 40 45

Arg Arg Gly Arg Cys Pro Ser Gly Ser Cys Cys Val Arg Arg Arg Ser 50 55 60

Pro Ala Gly Cys Ser Ser Ala Gly Arg Cys Ser Cys Arg Cys 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..93
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601054
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

Met Pro Pro Arg Thr Ala Pro Ala Ala Thr Ser Thr Pro Pro Arg Lys $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Val Pro Leu Arg Lys Leu Leu Arg Ala Ala Ser Val Ala Cys Gly Val 20 25 30

```
Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln
                            40
Glu Leu Gly Ile Pro His Ala Phe Ala Ser Leu Val Trp Leu Cys Gly
                        55
Pro Leu Ser Gly Leu Leu Val Gln Pro Leu Val Gly His Leu Ser Asp
                    70
                                        75
Arg Ile Gly Pro Ala Ala Ser Pro Leu Gly Arg Arg Arg
(2) INFORMATION FOR SEQ ID NO:2435:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 509 base pairs
```

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..509
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601061

atcqqcctaq cagcqatqqq caatcqaqct atcqcaqaaa tccaqtttqc qgactacatc

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435: 60 gagcagagca gcagtgacca gtgagctgct tgtccaagaa tcgctcccac tcccggctgt cgggagagcg cagcccagct agccgcctcc gcttcttgga ggtcgatggc cgcgaagggg 120 ttgagggagg tggggaggag gagggcggcg gaggtcgggc ggcgctgctt gtctggcggg 180 agcgctgggc cgccggcgcc ggcggcgaag cggaaggagg gagggaaggc ggtgaacctg 240 300 ttcacggccg tcaaccaggc gctccacatc gccctcgaca ccgacccccg cgcctacgtc ttcggagagg acgtcgggtt cggcggcgtc ttccgctgca cgacaggcct cgccgatcgg 360 ttcggcaaga gcagagtgtt caacacgccg ctgtgtgagc agggtattgc tggatttgcc 420
- tttccaqcct ttgaatcaga ttgtccaat (2) INFORMATION FOR SEQ ID NO:2436:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601062
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:
- Met Ala Ala Lys Gly Leu Arg Glu Val Gly Arg Arg Ala Ala Glu 10
- Val Gly Arg Arg Cys Leu Ser Gly Gly Ser Ala Gly Pro Pro Ala Pro 2.5 30 2.0
- Ala Ala Lys Arg Lys Glu Gly Gly Lys Ala Val Asn Leu Phe Thr Ala 4.0
- Val Asn Gln Ala Leu His Ile Ala Leu Asp Thr Asp Pro Arg Ala Tyr 55
- Val Phe Gly Glu Asp Val Gly Phe Gly Gly Val Phe Arg Cys Thr Thr 70 Gly Leu Ala Asp Arg Phe Gly Lys Ser Arg Val Phe Asn Thr Pro Leu
- 90 Cys Glu Gln Gly Ile Ala Gly Phe Ala Ile Gly Leu Ala Ala Met Gly
- 105 Asn Arg Ala Ile Ala Glu Ile Gln Phe Ala Asp Tyr Ile Phe Pro Ala 120 125 115
- Phe Glu Ser Asp Cys Pro
- (2) INFORMATION FOR SEQ ID NO:2437:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..404
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601064
- (2) INFORMATION FOR SEQ ID NO:2438:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601065
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

Lys Asp Val His Arg Glu Thr Leu Val Arg Thr Arg Arg His His Arg

10
15
15

Arg Leu Ser Leu Val Pro Ser Arg Ser Pro Leu Val Ser Thr Pro Thr 20 25 30

Asp Arg Ser Glu Ser Arg Gly Val Ser Ala Val Lys Ala Thr Ala Ser 35 40 45

Ala Met Ala Asp Glu Glu His Ser Glu Arg Arg Glu Glu Ala Ser Glu 50 55 60

Leu Ala Pro Phe Asp Pro Thr Lys Lys Lys Lys Lys Lys Lys Val Val 65 70 70 70 75 80 11e Gln Glu Pro Ser Asp Glu Val Asp Lys Lys Leu Ala Glu Lys Thr Glu

85 90 95

Thr Leu Ala Val Ala Glu Pro Ala Glu Leu Asn Phe Thr Gly Met Lys

100 105 110

Lys Xaa Lys Lys Lys Pro Val Asp Leu Asp Ser Thr Leu Asp Glu Leu
115 120 125

115 Gly Asp Gly Glu Asp Thr

130

- (2) INFORMATION FOR SEQ ID NO:2439:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601066
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:
 Met Ala Asp Glu Glu His Ser Glu Arg Arg Glu Glu Ala Ser Glu Leu
 10 10 15

- (2) INFORMATION FOR SEQ ID NO:2440:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..496
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601078
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

- (2) INFORMATION FOR SEQ ID NO:2441:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601079
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

Met Asp Glu Ala Ala Val Asp Asp Leu Ile Arg Arg Leu Leu Glu Ala 1 5 10 15

Arg Gly Gly Arg Thr Pro Arg Asn Ala Gln Val Thr Asp Ala Glu Ile $20 \hspace{1cm} 25 \hspace{1cm} 30$

Arg Arg Leu Cys Ala Ala Ala Lys Asp Val Phe Leu Ser Gln Pro Asn 35 40 45

Leu Leu Glu Leu Glu Ala Pro Ile Lys Ile Cys Gly Asp Val His Gly 50 55 60

Gln Tyr Ser Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly Tyr Pro Pro 65 70 75 80

Asp Ala Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Lys Gln 85 90 95

Ser Ile Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile Lys Tyr Pro $100 \ \ 105 \ \ 110$

Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala Ser Ile Asn 115 120 125

Arg Ile Tyr Gly

130

(2) INFORMATION FOR SEQ ID NO:2442: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..69 (D) OTHER INFORMATION: / Ceres Seq. ID 1601080 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442: Met Leu Arg Ser Gly Ala Ser Ala Pro Pro Pro Arg Met Cys Ser Ser 10 5 Pro Ser Pro Thr Ser Trp Ser Ser Arg Pro Pro Ser Arg Tyr Ala Gly 30 25 2.0 Met Ser Met Val Ser Ile Gln Thr Phe Phe Asp Tyr Leu Ser Met Val 45 40 Ala Ile His Gln Met Gln Ile Ile Cys Ser Ser Val Thr Met Leu Ile 60 55 Gly Gly Asn Arg Ala (2) INFORMATION FOR SEQ ID NO:2443: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..472 (D) OTHER INFORMATION: / Ceres Seq. ID 1601089 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443: gagcaacaag agagagaga catagccgca caaagggaag gagaccctcg ccaacctcga 60 agctagtcca aactagtggg aggttgagtg cagggatcga tcgaggaaga cgagacaagc 120 ttcttcttct gctgccgccg ccgccagctc tagctcacca cgagttacta gccaatctga 180 caccgaccgt ccatggcgcg gggcaaggtg caacttcggc gcgtcgagaa cccggtgcac 240 cggcaggtga cattetgcaa gegeegegeg gggetgetea agaaggeeeg ggagetetee 300 gteetetgeg aegecagegt eggeateate gtetteteeg egeaeggeaa getetaegae 360 420 ctcgccacca ccgggaccat ggaggagctg atcgagaggt acaaggctgc cagcgccgga gaagcgacga ccgacggctg cggcaggcac aacaggatgg accccaaaca tg (2) INFORMATION FOR SEQ ID NO:2444: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 156 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..156 (D) OTHER INFORMATION: / Ceres Seq. ID 1601090 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444: Ala Thr Arg Glu Arg Gly His Ser Arg Thr Lys Gly Arg Arg Pro Ser 10 Pro Thr Ser Lys Leu Val Gln Thr Ser Gly Arg Leu Ser Ala Gly Ile 30 20 Asp Arg Gly Arg Arg Asp Lys Leu Leu Leu Leu Pro Pro Pro Pro 40 Ala Leu Ala His His Glu Leu Leu Ala Asn Leu Thr Pro Thr Val His

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55
    50
Gly Ala Gly Gln Gly Ala Thr Ser Ala Arg Arg Glu Pro Gly Ala Pro
                                        75
                    70
Ala Gly Asp Ile Leu Gln Ala Pro Arg Gly Ala Ala Gln Glu Gly Pro
                                    90
               85
Gly Ala Leu Arg Pro Leu Arg Arg Gln Arg Arg His His Arg Leu Leu
                                                   110
           100
                               105
Arg Ala Arg Gln Ala Leu Arg Pro Arg His His Arg Asp His Gly Gly
                                               125
                           120
       115
Ala Asp Arg Glu Val Gln Gly Cys Gln Arg Arg Arg Ser Asp Asp Arg
                    135
                                           140
Arg Leu Arg Gln Ala Gln Gln Asp Gly Pro Gln Thr
                   150
(2) INFORMATION FOR SEQ ID NO:2445:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 93 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..93
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601091
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:
Met Ala Arg Gly Lys Val Gln Leu Arg Arg Val Glu Asn Pro Val His
                                    10
                5
Arg Gln Val Thr Phe Cys Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala
                                25
Arg Glu Leu Ser Val Leu Cys Asp Ala Ser Val Gly Ile Ile Val Phe
                            40
Ser Ala His Gly Lys Leu Tyr Asp Leu Ala Thr Thr Gly Thr Met Glu
                                            60
                        55
Glu Leu Ile Glu Arg Tyr Lys Ala Ala Ser Ala Gly Glu Ala Thr Thr
                                        75
                    70
 Asp Gly Cys Gly Arg His Asn Arg Met Asp Pro Lys His
                 85
 (2) INFORMATION FOR SEQ ID NO: 2446:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 481 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..481
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601092
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:
 aaaaaaactc gctctcactt tactcctatc cactgcggcc tggacgcgtg cgagagactt
 gacaaagcag cagcagggat ggcgcctctg aagctgtacg ggatgccgct gtcccccaac
                                                                       120
 gtggtgcgcg tggccaccgg tgctcaacga gaagggcctc gacttcgaga tcgtccccgt
                                                                       180
 cgacctcacc accggcgccc acaagcagcc cgacttcctc accetcaacc ctttcggcca
                                                                       240
 gatcccggct ctcgtcgacg gagacgaagt cctcttcgag tcccgcgcga tcaaccggta
                                                                       300
 categocage aagtaegegt eggagggeae ggaeetgete eeegegaegg egteggegge
 gaagctggag gtgttggcct gggaggtgga gtcgcaccac ttccacccga acgcgtcgcc
                                                                       420
 gctggtgttc cagctgctcg tgaggccgct cctgggcggc gccccgacgc ggcggtggtg
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(2) INFORMATION FOR SEQ ID NO:2447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601093
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

Lys Lys Thr Arg Ser His Phe Thr Pro Ile His Cys Gly Leu Asp Ala $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Cys Glu Arg Leu Asp Lys Ala Ala Ala Gly Met Ala Pro Leu Lys Leu 20 25 30

Tyr Gly Met Pro Leu Ser Pro Asn Val Val Arg Val Ala Thr Gly Ala 35 40 45

Gln Arg Glu Gly Pro Arg Leu Arg Asp Arg Pro Arg Pro His His 50 55 60

Arg Arg Pro Gln Ala Ala Arg Leu Pro His Pro Gln Pro Phe Arg Pro 65 70 75 80

Asp Pro Gly Ser Arg Arg Arg Arg Ser Pro Leu Arg Val Pro Arg 85 90 95

Asp Gln Pro Val His Arg Gln Gln Val Arg Val Gly Gly His Gly Pro
100 105 110

Ala Pro Arg Asp Gly Val Gly Gly Glu Ala Gly Gly Val Gly Leu Gly
115 120 125

Gly Gly Val Ala Pro Leu Pro Pro Glu Arg Val Ala Ala Gly Val Pro 130 135 140

(2) INFORMATION FOR SEQ ID NO:2448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601094
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

Met Ala Pro Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val 1 5 10 15

Arg Val Ala Thr Gly Ala Gln Arg Glu Gly Pro Arg Leu Arg Asp Arg 20 25 30

Pro Arg Arg Pro His His Arg Arg Pro Gln Ala Ala Arg Leu Pro His 35 40 45

Pro Gln Pro Phe Arg Pro Asp Pro Gly Ser Arg Arg Arg Arg Ser 50 55 60

Pro Leu Arg Val Pro Arg Asp Gln Pro Val His Arg Gln Gln Val Arg 65 70 75 80

Val Gly Gly His Gly Pro Ala Pro Arg Asp Gly Val Gly Glu Ala 85 90 95

Gly Gly Val Gly Leu Gly Gly Gly Val Ala Pro Leu Pro Pro Glu Arg 100 105 110

Val Ala Ala Gly Val Pro Ala Ala Arg Glu Ala Ala Pro Gly Arg Arg 115 120 125

Pro Asp Ala Ala Val Val

- (2) INFORMATION FOR SEQ ID NO:2449:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..126
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601095
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

Met Pro Leu Ser Pro Asn Val Val Arg Val Ala Thr Gly Ala Gln Arg 1 5 10 15

Glu Gly Pro Arg Leu Arg Asp Arg Pro Arg Arg Pro His His Arg Arg 20 25 30

Pro Gln Ala Ala Arg Leu Pro His Pro Gln Pro Phe Arg Pro Asp Pro 35 40 45

Gly Ser Arg Arg Arg Arg Ser Pro Leu Arg Val Pro Arg Asp Gln 50

Pro Val His Arg Gln Gln Val Arg Val Gly Gly His Gly Pro Ala Pro 65 70 75 80

Arg Asp Gly Val Gly Gly Glu Ala Gly Gly Val Gly Leu Gly Gly Gly

85

90

95

Val Ala Pro Leu Pro Pro Glu Arg Val Ala Ala Gly Val Pro Ala Ala
100 105 110

Arg Glu Ala Ala Pro Gly Arg Arg Pro Asp Ala Ala Val Val 115 120 125

- (2) INFORMATION FOR SEQ ID NO:2450:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..519
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601118
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

60 cagtgagcta gcctcccgag ccctatctat ccttttctcg gcacctcgcg ggtctcccgt cogcoccgtc cogcattogt atoctotect cactetegec geogeogett cocctgegec 120 180 ccgagccaag atgaatgttg aaaagctcaa gaagatggca ggtgctgtgc gcactggggg 240 qaaqqqtaqc atqcqcaqqa agaaqaaqqc aqtccacaag actacqacca caqatqataa aaqqcttcaq aqcaccctga aaagaatagg agtgaacacc attcctggta ttgaagaggt 300 360 caacatettt aaggatgatg ttgttattea gtttgtgaat eetaaagtge aagetteaat tggtgctaat acatgggtgg tcagtggaac tccacagaca aagaagctgc aagatctgct 420 tecqtecatt ateaaceage tesqeeetga caacetagae aacetgegga ggettgegga 480 gcaattccag aagcaggccc ctggtgcttc aaggtgcag

- (2) INFORMATION FOR SEQ ID NO:2451:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..172
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601119
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

Ser Glu Leu Ala Ser Arg Ala Leu Ser Ile Leu Phe Ser Ala Pro Arg 10 Gly Ser Pro Val Arg Pro Val Pro His Ser Tyr Pro Leu Leu Thr Leu 20 25 Ala Ala Ala Ala Ser Pro Ala Pro Arg Ala Lys Met Asn Val Glu Lys 35 40 Leu Lys Lys Met Ala Gly Ala Val Arg Thr Gly Gly Lys Gly Ser Met 50 55 Arg Arg Lys Lys Lys Ala Val His Lys Thr Thr Thr Asp Asp Lys 75 70 Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val Asn Thr Ile Pro Gly 90 85 Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Val

100 105 110

Asn Pro Lys Val Gln Ala Ser Ile Gly Ala Asn Thr Trp Val Val Ser 115 120 125

Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Leu Leu Pro Ser Ile Ile 130 135 140 Asn Gln Leu Xaa Pro Asp Asn Leu Asp Asn Leu Arg Arg Leu Ala Glu

145 150 155 Gln Phe Gln Lys Gln Ala Pro Gly Ala Ser Arg Cys

- (2) INFORMATION FOR SEQ ID NO:2452:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids

165 170

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

Met Asn Val Glu Lys Leu Lys Lys Met Ala Gly Ala Val Arg Thr Gly 10 5

Gly Lys Gly Ser Met Arg Arg Lys Lys Ala Val His Lys Thr Thr 20 25

Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val 40

Asn Thr Ile Pro Gly Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val 50 55

Val Ile Gln Phe Val Asn Pro Lys Val Gln Ala Ser Ile Gly Ala Asn 70 75 80

Thr Trp Val Val Ser Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Leu 90 Leu Pro Ser Ile Ile Asn Gln Leu Xaa Pro Asp Asn Leu Asp Asn Leu

100 105 110 Arg Arg Leu Ala Glu Gln Phe Gln Lys Gln Ala Pro Gly Ala Ser Arg 115 120

Cys

- (2) INFORMATION FOR SEQ ID NO:2453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601121
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:
 Met Ala Gly Ala Val Arg Thr Gly Gly Lys Gly Ser Met Arg Arg Lys

1 5 10 15

Lys Lys Ala Val His Lys Thr Thr Thr Thr Asp Asp Lys Arg Leu Gln

20 25 30
Ser Thr Leu Lys Arg Ile Gly Val Asn Thr Ile Pro Gly Ile Glu Glu

35 40 45 Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Val Asn Pro Lys

50 55 60

Val Gln Ala Ser Ile Gly Ala Asn Thr Trp Val Val Ser Gly Thr Pro
65 70 75 80

Gln Thr Lys Lys Leu Gln Asp Leu Leu Pro Ser Ile Ile Asn Gln Leu 85 90 95

Xaa Pro Asp Asn Leu Asp Asn Leu Arg Arg Leu Ala Glu Gln Phe Gln 100 105 110

Lys Gln Ala Pro Gly Ala Ser Arg Cys 115 120

- (2) INFORMATION FOR SEQ ID NO:2454:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..514
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454: 60 gaggctgagg gttgcatatt tcattgcgca agctctcgac cattgcaatg ctgagaacag gaaaatctat catgatttga atgcttatag ggtacttttt gatgaggaag gtgatccccg 120 cttgtcaagt tttggattaa tgaagaacag ccgtgatggg aaaagttata gcactaacct 180 ggcttacact ccaccagagt ttctacgaac tggcagagta attccggaga gtgtgatcta 240 tagctatgga actgtcctgt tggatctttt gagcggaaaa cacattcctc ctagtcatgc 300 cctagattta ataaggggaa agaatatact gttgctgatg gattcctcct tagaagggca 360 gtatgctaat gaagatgctt cgaaattggt tgatcttgca tcaaagtgtc tgcaatttga 420 atctagggat agaccgaaca taaagtatct tctgtcttct gttggtcctc ttcagaatca 480 aaaggaggtt gcatcacatg tgttcatggg tatt
- (2) INFORMATION FOR SEQ ID NO:2455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..171
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601123
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

Arg Leu Arg Val Ala Tyr Phe Ile Ala Gln Ala Leu Asp His Cys Asn 1 5 10 15

Ala Glu Asn Arg Lys Ile Tyr His Asp Leu Asn Ala Tyr Arg Val Leu

Phe Asp Glu Gly Asp Pro Arg Leu Ser Ser Phe Gly Leu Met Lys

Asn Ser Arg Asp Gly Lys Ser Tyr Ser Thr Asn Leu Ala Tyr Thr Pro 50 55 60

Pro Glu Phe Leu Arg Thr Gly Arg Val Ile Pro Glu Ser Val Ile Tyr

420

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65
                    70
                                        75
Ser Tyr Gly Thr Val Leu Leu Asp Leu Leu Ser Gly Lys His Ile Pro
                                    90
Pro Ser His Ala Leu Asp Leu Ile Arg Gly Lys Asn Ile Leu Leu Leu
                                105
Met Asp Ser Ser Leu Glu Gly Gln Tyr Ala Asn Glu Asp Ala Ser Lys
                            120
Leu Val Asp Leu Ala Ser Lys Cys Leu Gln Phe Glu Ser Arg Asp Arg
                       135
                                           140
Pro Asn Ile Lys Tyr Leu Leu Ser Ser Val Gly Pro Leu Gln Asn Gln
                   150
                                       155
Lys Glu Val Ala Ser His Val Phe Met Gly Ile
               165
(2) INFORMATION FOR SEQ ID NO: 2456:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 125 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..125
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601124
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:
Met Lys Asn Ser Arg Asp Gly Lys Ser Tyr Ser Thr Asn Leu Ala Tyr
               5
                                   10
Thr Pro Pro Glu Phe Leu Arg Thr Gly Arg Val Ile Pro Glu Ser Val
                                2.5
                                                    30
Ile Tyr Ser Tyr Gly Thr Val Leu Leu Asp Leu Leu Ser Gly Lys His
                            40
Ile Pro Pro Ser His Ala Leu Asp Leu Ile Arg Gly Lys Asn Ile Leu
                       55
                                            60
Leu Leu Met Asp Ser Ser Leu Glu Gly Gln Tyr Ala Asn Glu Asp Ala
                    70
                                        75
Ser Lys Leu Val Asp Leu Ala Ser Lys Cys Leu Gln Phe Glu Ser Arg
               85
                                   90
Asp Arg Pro Asn Ile Lys Tyr Leu Leu Ser Ser Val Gly Pro Leu Gln
                              105
           100
Asn Gln Lys Glu Val Ala Ser His Val Phe Met Gly Ile
        115
                           120
(2) INFORMATION FOR SEQ ID NO:2457:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 474 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..474
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601125
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:
aggaaagggg aggaccggag cgagagcgag atggtagtgg tggccgccgc ggccgcacgc
ggeogegetg taaageeest gtteetegte etegteeace acageegeee egegeeeege
                                                                      120
cteccegee gaacegeeg egeceggeeg etgegettee teteetgete gaeeteageg
                                                                      180
cogcogctgt togcagccgt cgcatccatg gactogccgc cccagggtta ccgcaccaac
                                                                      240
qtcqqcatct qcctcqccqa cccatccctc accaagattt tctcgqcttc taggatcgac
                                                                      300
attoctagog ogtggcagat gootcagggt ggtatagatg caggggaaga accaagggcg
                                                                      360
```

gctgctttca gggaattgag agaagagact ggtgtcacat ccgcagagat cgtggctgag

gctccgtctq gttaacatat gatttcccgc cagatgtcag aaccaaactg aatg

- (2) INFORMATION FOR SEQ ID NO:2458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..144
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601126
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:
- Arg Lys Gly Glu Asp Arg Ser Glu Ser Glu Met Val Val Val Ala Ala 1 5 10 15
- Ala Ala Arg Gly Arg Ala Val Lys Pro Leu Phe Leu Val Leu Val 20 25 30
- His His Ser Arg Pro Ala Pro Arg Leu Pro Arg Arg Thr Ala Arg Ala 35 40 45
- Arg Pro Leu Arg Phe Leu Ser Cys Ser Thr Ser Ala Pro Pro Leu Phe 50 55 60
- Ala Ala Val Ala Ser Met Asp Ser Pro Pro Gln Gly Tyr Arg Thr Asn 65 70 75 80
- Val Gly Ile Cys Leu Ala Asp Pro Ser Leu Thr Lys Ile Phe Ser Ala 85 90 95
- Ser Arg Ile Asp Ile Pro Ser Ala Trp Gln Met Pro Gln Gly Gly Ile 100 105 110
- Asp Ala Gly Glu Glu Pro Arg Ala Ala Phe Arg Glu Leu Arg Glu 115 120 125
- Glu Thr Gly Val Thr Ser Ala Glu Ile Val Ala Glu Ala Pro Ser Gly 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2459:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..96
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601127
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:
- Glu Arg Gly Gly Pro Glu Arg Glu Arg Asp Gly Ser Gly Gly Arg Arg
- Gly Arg Thr Arg Pro Arg Cys Lys Ala Pro Val Pro Arg Pro Arg Pro 20 25 30
- Pro Gln Pro Pro Arg Ala Pro Pro Pro Pro Pro Asn Arg Pro Arg Pro 35 40 45
- Ala Ala Leu Pro Leu Leu Leu Asp Leu Ser Ala Ala Ala Val Arg
- Ser Arg Arg Ile His Gly Leu Ala Ala Pro Gly Leu Pro His Gln Arg 65 70 75 80
- Arg His Leu Pro Arg Arg Pro Ile Pro His Gln Asp Phe Leu Gly Phe
 85 90 95
- (2) INFORMATION FOR SEQ ID NO:2460:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

Met Val Val Ala Ala Ala Ala Ala Arg Gly Arg Ala Val Lys Pro 1 5 10 15

Leu Phe Leu Val Leu Val His His Ser Arg Pro Ala Pro Arg Leu Pro $20 \\ 25 \\ 30$

Arg Arg Thr Ala Arg Ala Arg Pro Leu Arg Phe Leu Ser Cys Ser Thr 35 40 45

Ser Ala Pro Pro Leu Phe Ala Ala Val Ala Ser Met Asp Ser Pro Pro 50 55 60

Gln Gly Tyr Arg Thr Asn Val Gly Ile Cys Leu Ala Asp Pro Ser Leu 65 70 75 80

Thr Lys Ile Phe Ser Ala Ser Arg Ile Asp Ile Pro Ser Ala Trp Gln 85 90 95

Met Pro Gln Gly Gly Ile Asp Ala Gly Glu Glu Pro Arg Ala Ala Ala 100 105 110

Phe Arg Glu Leu Arg Glu Glu Thr Gly Val Thr Ser Ala Glu Ile Val 115 120 125

Ala Glu Ala Pro Ser Gly

130

- (2) INFORMATION FOR SEQ ID NO:2461:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..483
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601141
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

ctatctccct gtttaatcaa tccttcaagc gcaagctgcc tcctcctcgt cgtccggtcg tqaqaaqqqa tqqcqqqccq tqqcaaqqct atcqqcqctq qcqccqcgaa gaaggcaacg 120 togaggaget ccaaggeegg actecagtte ccegteggea ggattgeeag gtteeteaag 180 gegggeaagt aegeggageg egteggegee ggegeeeeeg tgtacetege egeegteete 240 gagtacctcg cggctgaggt tctcgaactt gccgggaacg ccgcgaggga caacaagaag 300 acceptatty tycegegeca catecagett getytgegea acgaegagga getyaccaaa 360 ctgttgggtg gtgccaccat cgcgagcgga ggtgttatgc ctaacatcca tcagcatctg 420 ctccccaaga aggctgcctc ctcgtcgacg atctcgtagc ggcggcgcac atggcgagcg 480 acq

- (2) INFORMATION FOR SEQ ID NO:2462:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601142
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:
- Ile Ser Leu Phe Asn Gln Ser Phe Lys Arg Lys Leu Pro Pro Pro Arg

- (2) INFORMATION FOR SEQ ID NO:2463:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601143
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

Met Ala Gly Arg Gly Lys Ala Ile Gly Ala Gly Ala Ala Lys Lys Ala 1 5 10 15

Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile 20 25 30

Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly Ala Gly 35 40 45

Ala Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val 50 55 60

Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile
65 70 75 80

Val Pro Arg His Ile Gln Leu Ala Val Arg Asn Asp Glu Glu Leu Thr 85 90 95

Lys Leu Leu Gly Gly Ala Thr Ile Ala Ser Gly Gly Val Met Pro Asn 100 105 110

The His Gln His Leu Leu Pro Lys Lys Ala Ala Ser Ser Ser Thr Ile
115 120 125

Ser

- (2) INFORMATION FOR SEQ ID NO:2464:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..471
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601144
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

(XI) SECONNOL PROCEEDINGS SEE					C 0
ctcctcgact gctcccctc	c ttccagagtc	acggtgcctc	gccgtccttc	cctgatctga	60
caacccgttt accttgccc	a accaatecae	tecgaegget	aacccaccct	tctttaaccc	120
daadddgiil acciegeed	g geeggeeeue	00094095		as as at agas	180
cgccaccccg atccagccc	a gccgcactcc	aacacggtag	cagcagtcaa	dagadeceda	100
ccgcaatggc cgcggcgct	c ctcttactac	teataceace	catcaaccta	ctcqccqcqc	240
degeaatgge tgtggtgt	c ccccegacga			~+ ~++ ~>+ ~>	300
tegeattect caegeggee	c cgcgcccgga	tegegeteaa	agacagccac	gidildatda	000
cgggcgggtc cagcggcat	c gaactcacca	tggccacggc	cgctgcgcgg	gagggcgcgc	360
cdddcdddc cadodda.	- 999.		aaaaaaaaaa	accatecade	420
gggtctccat cctggcccg	c aaccttgccc	gcctcgagga	ggegegegee	gccatccage	120
gegacteggg cegegacga	c atcaacatco	acqcqqccga	cgtgcgggac	g	
gogaccoggg cogoga-s-	- 5 55 5				

- (2) INFORMATION FOR SEQ ID NO:2465:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..156
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601145
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

Pro Arg Leu Leu Pro Ser Phe Gln Ser His Gly Ala Ser Pro Ser Phe 1 5 10 15

Pro Asp Leu Thr Thr Arg Leu Pro Cys Pro Ala Gly Pro Leu Arg Arg 20 25 30

Leu Ala Arg Pro Ser Leu Thr Pro Pro Pro Arg Ser Ser Pro Ala Ala 35 40 45

Leu Gln His Gly Ser Ser Ser Gln Gln Thr Pro Thr Ala Met Ala Ala 50 60

Ala Leu Leu Leu Leu Val Pro Pro Val Gly Leu Leu Ala Ala Leu 65 70 75 80

Ala Phe Leu Thr Arg Pro Arg Ala Arg Ile Ala Leu Lys Asp Ser His
85 90 95

Val Phe Ile Thr Gly Gly Ser Ser Gly Ile Gly Leu Ala Met Ala Thr 100 105 110

Ala Ala Arg Glu Gly Ala Arg Val Ser Ile Leu Ala Arg As
n Leu 115 120 125

Ala Arg Leu Glu Glu Ala Arg Ala Ile Gln Arg Asp Ser Gly Arg
130 135 140

Asp Asp Val Gly Val His Ala Ala Asp Val Arg Asp 145 150 155

- (2) INFORMATION FOR SEQ ID NO:2466:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601146
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

Met Ala Ala Leu Leu Leu Leu Val Pro Pro Val Gly Leu Leu 1 5 10 15

Ala Ala Leu Ala Phe Leu Thr Arg Pro Arg Ala Arg Ile Ala Leu Lys 20 25 30

Asp Ser His Val Phe Ile Thr Gly Gly Ser Ser Gly Ile Gly Leu Ala $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Met Ala Thr Ala Ala Ala Arg Glu Gly Ala Arg Val Ser Ile Leu Ala 50 55 60

Arg Asn Leu Ala Arg Leu Glu Glu Ala Arg Ala Ile Gln Arg Asp 65 70 75 80

Ser Gly Arg Asp Asp Val Gly Val His Ala Ala Asp Val Arg Asp 85 90 95

- (2) INFORMATION FOR SEQ ID NO:2467:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..403
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601155
- (2) INFORMATION FOR SEQ ID NO:2468:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601156
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:
- Phe Phe Leu Ser Cys Pro Val Ser Arg Ser His Ser Thr Ala Ser Ile 1 5 10 15
- Ser Gln Ser Arg Arg Arg Arg Arg Val Pro Pro Ala Ala Pro Met 20 25 30
- Arg Ala Ile Ser Thr Ala Ala Gly Gly Met Leu Arg Ala Arg Leu Arg 35 40 45
- Ser Ser Ser Arg Val Arg Gly Gly Gly Asp Gly Ala Gly Arg Trp Thr 50 60
- Thr Pro Gly His Glu Glu Arg Pro Lys Gly Tyr Leu Phe Asn Arg Pro 65 70 75 80
- Pro Pro Pro Gly Glu Thr Arg Lys Trp Glu Asp Trp Glu Leu Pro
 85 90 95
- Asn Ala Lys Pro Asp Leu Thr Ile Glu Thr Trp Ala His Glu Lys Ala 115 120 125
- Leu Glu Arg Leu Lys Gln 130
- (2) INFORMATION FOR SEQ ID NO:2469:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..134
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601157
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:
- Phe Ser Ser Pro Ala Pro Ser Pro Val Pro Thr Ala Gln Pro Pro Ser
- Pro Asn Leu Ala Gly Asp Ala Asp Ala Phe His Arg Arg His Arg Cys
 20 25 30
- Gly Arg Ser Arg Arg Pro Arg Gly Ala Cys Cys Ala Arg Gly Ser Ala

Client Docket No. 80146.003 40 35 Pro Arg Pro Ala Cys Ala Ala Ala Met Ala Arg Gly Asp Gly Arg 55 60 Arg Arg Gly Thr Arg Lys Gly Pro Arg Gly Thr Ser Ser Thr Ala Arg 70 75 Arg Arg Arg Gly Arg Gly Ser Gly Arg Thr Gly Ser Cys Pro 85 90 95 Val Thr Ser Pro Pro Ser Ser Pro Ser Ser Ser Ala Ser Ala Ser 100 105 110 Thr Pro Ser Pro Thr Ser Arg Ser Arg Pro Gly Arg Thr Arg Arg Arg 115 120 Trp Asn Ala Ser Ser Ser 130 (2) INFORMATION FOR SEQ ID NO: 2470: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..133 (D) OTHER INFORMATION: / Ceres Seq. ID 1601158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470: Phe Pro Leu Leu Pro Arg Leu Pro Phe Pro Gln His Ser Leu His Leu 10 Pro Ile Ser Gln Ala Thr Pro Thr Arg Ser Thr Gly Gly Thr Asp Ala 20 25 Gly Asp Leu Asp Gly Arg Gly Gly His Ala Ala Arg Ala Ala Pro Leu Leu Val Pro Arg Ala Arg Arg Arg Trp Arg Gly Ala Met Asp Asp Ala Gly Ala Arg Gly Lys Ala Gln Gly Val Pro Leu Gln Pro Pro Ala 70 Ala Ala Gly Gly Asp Ala Glu Val Gly Gly Leu Gly Ala Ala Leu 90 Leu His His Leu Leu Pro His Arg Arg His Pro Arg Arg Pro Gln 100 105 Arg Gln Ala Arg Pro His Asp Arg Asp Leu Gly Ala Arg Glu Gly Ala 115 120 Gly Thr Pro Gln Ala 130 (2) INFORMATION FOR SEQ ID NO:2471: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 515 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..515
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

ccacgaagta gcgttggctg ttgcaaaagc aaccgtttca agtttcctcc ctagtgcacc caggaaatcg ccagcacctc ccctgttccc tctctgtctc tggctctctc tcctctccgc 120 ccctttttat cgcccgatct cacacatttt ggaaagagga gagagagag gagagattag agggagcgcc ctgcccaagc aaagagaaac cgcggcgcga gaagagggag gaagggcaga cgggcgagca ggatgagaga gatcatcagc atccacatcg gccaggccgg gatccaggtc ggcaacgcct gctgggagct ctactgcctc gagcacggca tcgagcccga tggcaccatg

cccagtgata ccacggttgg cgtcgcacat gatgccttca acacgttcnt tcagcgagac 420 cggttctggc aagcatgtgc cgagggccat cttcgtcgac cttgagccca ctgtcattga 480 tgaggttcgc actggctcgt accgccaact cttcc

- (2) INFORMATION FOR SEQ ID NO:2472:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601163
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

His Glu Val Ala Leu Ala Val Ala Lys Ala Thr Val Ser Ser Phe Leu

1 10 15

Pro Ser Ala Pro Arg Lys Ser Pro Ala Pro Pro Leu Phe Pro Leu Cys 20 25 30

Leu Trp Leu Ser Leu Leu Ser Ala Pro Phe Tyr Arg Pro Ile Ser His $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Ile Leu Glu Arg Gly Glu Arg Gly Glu Ile Arg Gly Ser Ala Leu 50 55 60

Pro Lys Gln Arg Glu Thr Ala Ala Arg Glu Glu Gly Gly Arg Ala Asp 65 70 75 80

Gly Arg Ala Gly

- (2) INFORMATION FOR SEQ ID NO:2473:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601164
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Arg Glu Ile Ile Ser Ile His Ile Gly Gln Ala Gly Ile Gln Val 1 5 10 15

Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Glu Pro 20 25 30

Asp Gly Thr Met Pro Ser Asp Thr Thr Val Gly Val Ala His Asp Ala 35 40 45

Phe Asn Thr Phe Xaa Gln Arg Asp Arg Phe Trp Gln Ala Cys Ala Glu 50 60

Gly His Leu Arg Arg Pro 65 70

- (2) INFORMATION FOR SEQ ID NO: 2474:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..55
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601165
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

Met Ala Pro Cys Pro Val Ile Pro Arg Leu Ala Ser His Met Met Pro 10 Ser Thr Arg Xaa Phe Ser Glu Thr Gly Ser Gly Lys His Val Pro Arg 25 20 Ala Ile Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Val Arg Thr 35 40 Gly Ser Tyr Arg Gln Leu Phe

- 50 55
- (2) INFORMATION FOR SEQ ID NO:2475: (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 508 base pairs (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..508
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601168
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

ggcaaaacca acagaacagg cctatgttcc catcgagtcg agtcgagacg agaccgtcct cogcccgagt ctcgctcgct agctagggtt tccaccaatg gcggcgccca ccacctcccg ccgcqqcccc qqcqqcqcg qcaacatgga cgacgagaac ctaaccttcg agacctcccc qqqqqtcqaq qtcqtcaqca gcttcqacca qatqqqcatc aaqqacqacc tcctccqcgg 240 catetacgge tacggtttcg agaageette cgccatecag cagegegecg tgctccccat 300 catcaacqqc cqcqacqtca tcqcqcaqqc ccaqtccqqt accqqcaaqa cqtccatqat 360 ctccctcacc gtctgccaga tcgtcgacac cgccgtgcgc gaggtgcagg ctttgattct 420 ctcgcctact agggagettg cttcccaaac agagagagtt atgctggcta ttggggacca cctcaacgtc caagtgcacg cttgcatt

- (2) INFORMATION FOR SEQ ID NO:2476:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601169
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:
- Gly Lys Thr Asn Arg Thr Gly Leu Cys Ser His Arg Val Glu Ser Arg 10
- Arg Asp Arg Pro Pro Pro Glu Ser Arg Ser Leu Ala Arg Val Ser Thr 25
- Asn Gly Gly Ala His His Leu Pro Pro Arg Pro Arg Arg Arg Ala Gln 40
- His Gly Arg Arg Glu Pro Asn Leu Arg Asp Leu Pro Gly Gly Arg Gly 55
- Arg Gln Gln Leu Arg Pro Asp Gly His Gln Gly Arg Pro Pro Pro Arg His Leu Arg Leu Arg Phe Arg Glu Ala Leu Arg His Pro Ala Ala Arg
- 90 Arg Ala Pro His His Gln Arg Pro Arg Arg His Arg Ala Gly Pro Val
- 100 105 110 Arg Tyr Arg Gln Asp Val His Asp Leu Pro His Arg Leu Pro Asp Arg 120 125 115
- Arg His Arg Arg Ala Arg Gly Ala Gly Phe Asp Ser Leu Ala Tyr 135
- (2) INFORMATION FOR SEQ ID NO:2477:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

Met Ala Ala Pro Thr Thr Ser Arg Arg Gly Pro Gly Gly Ala Arg Asn 1 5 10 15

Met Asp Asp Glu Asn Leu Thr Phe Glu Thr Ser Pro Gly Val Glu Val 20 25 30

Val Ser Ser Phe Asp Gln Met Gly Ile Lys Asp Asp Leu Leu Arg Gly 35 40 45

Ile Tyr Gly Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Ala

Val Leu Pro Ile Ile Asn Gly Arg Asp Val Ile Ala Gln Ala Gln Ser
70 75 80

Gly Thr Gly Lys Thr Ser Met Ile Ser Leu Thr Val Cys Gln Ile Val 85 90 95

Asp Thr Ala Val Arg Glu Val Gln Ala Leu Ile Leu Ser Pro Thr Arg 100 105 110

 $G_{\perp}u$ Leu Ala Ser Gln Thr Glu Arg Val Met Leu Ala Ile Gly Asp His 115 120 125

Leu Asn Val Gln Val His Ala Cys Ile 130 135

- (2) INFORMATION FOR SEQ ID NO:2478:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..121
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:

Met Asp Asp Glu Asn Leu Thr Phe Glu Thr Ser Pro Gly Val Glu Val

5 10 15

10 15

Val Ser Ser Phe Asp Gln Met Gly Ile Lys Asp Asp Leu Leu Arg Gly
20
25
30

Ile Tyr Gly Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln Gln Arg Ala 35 40

Val Leu Pro Ile Ile Asn Gly Arg Asp Val Ile Ala Gln Ala Gln Ser 50 55 60

Gly Thr Gly Lys Thr Ser Met Ile Ser Leu Thr Val Cys Gln Ile Val 65 70 75 80

Asp Thr Ala Val Arg Glu Val Gln Ala Leu Ile Leu Ser Pro Thr Arg

Glu Leu Ala Ser Gln Thr Glu Arg Val Met Leu Ala Ile Gly Asp His 100 105 110

Leu Asn Val Gln Val His Ala Cys Ile

- (2) INFORMATION FOR SEQ ID NO:2479:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

120

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..179
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

atoteaatte teecaceegg eegeeggeae cacaeggege eteegggage cacaaegaee gatggcgagg gcgcgcttcc ctctcctcst cctcctcctc gtggcgttnc tcgccrncac aggetecaeg geggeeegae aegeegegee egeaeeegeg teegegeeee gggegtege

(2) INFORMATION FOR SEQ ID NO:2480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601184
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:

Ile Ser Ile Leu Pro Pro Gly Arg Arg His His Thr Arg Ala Pro Gly 10 5

Ala Thr Thr Thr Asp Gly Glu Gly Ala Leu Pro Ser Pro Xaa Pro Pro 20 25 30

Pro Arg Gly Val Xaa Arg Xaa His Arg Leu His Gly Gly Pro Thr Arg 35 40

Arg Ala Arg Thr Arg Val Arg Ala Pro Gly Val 50 55

- (2) INFORMATION FOR SEQ ID NO:2481:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid

 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601185
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

Ser Gln Phe Ser His Pro Ala Ala Gly Thr Thr Arg Ala Leu Arg Glu 5 10

Pro Gln Arg Pro Met Ala Arg Ala Arg Phe Pro Leu Leu Xaa Leu Leu 20 25 Leu Val Ala Xaa Leu Ala Xaa Thr Gly Ser Thr Ala Ala Arg His Ala

40 Ala Pro Ala Pro Ala Ser Ala Pro Arg Ala Ser 55

- (2) INFORMATION FOR SEQ ID NO:2482:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601186

- Client Docket No. 80146.003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482: Leu Asn Ser Pro Thr Arg Pro Pro Ala Pro His Ala Arg Ser Gly Ser 10 His Asn Asp Arg Trp Arg Gly Arg Ala Ser Leu Ser Xaa Ser Ser Ser 2.0 25 Ser Trp Arg Xaa Ser Xaa Xaa Gln Ala Pro Arg Arg Pro Asp Thr Pro 40 Arg Pro His Pro Arg Pro Arg Pro Gly Arg Arg 50 55 (2) INFORMATION FOR SEQ ID NO:2483: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -

 - (B) LOCATION: 1..494
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601191
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

aggatgaatc ggaagagaa atcctaccaa acctagctac caactcgatc gtcgtcatca 60 cgctcgaccg cacaactcca ccgatgccgg cgcccctgct gccgccgcca ccgcggtacc 120 ggcggggaac gggcagaccg tgtgcgtgac cggcgcggcc gggtacatcg cctcgtggtt 180 ggtgaagctg ctgctcgaga agggatacac tgtgaagggc accgtcagga acccagatga 240 cccgaagaac gcgcacctca aggcgctgga cggcgccgcc gagcggctga tcctctgcaa 300 ggeogatetg etggaetacg acgecatetg eegegeegtg eagggetgee agggegtett 360 ccacaccgcc tececegtea ecgacgacce ggageaaatg gtggageegg eggtgegegg 420 caccgagtac gtgatcaacg cggcggcgga ggccggcacg gtgcggcggg tggtgttcac gtcgtccatc ggcg

- (2) INFORMATION FOR SEQ ID NO:2484:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..48
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601192
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

Asp Glu Ser Glu Glu Arg Ile Leu Pro Asn Leu Ala Thr Asn Ser Ile 10

Val Val Ile Thr Leu Asp Arg Thr Thr Pro Pro Met Pro Ala Pro Leu 25

Leu Pro Pro Pro Pro Arg Tyr Arg Arg Gly Thr Gly Arg Pro Cys Ala 40

- (2) INFORMATION FOR SEQ ID NO:2485:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..32
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601193

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

 Met Val Glu Pro Ala Val Arg Gly Thr Glu Tyr Val Ile Asn Ala Ala

 1 5 10 15

 Ala Glu Ala Gly Thr Val Arg Arg Val Val Phe Thr Ser Ser Ile Gly

 20 25 30
- (2) INFORMATION FOR SEQ ID NO:2486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..423
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

 ctatctccct gtttaatcaa tccttcaage gcaasstgce tcctcctcgt egtceggteg tggaaaggce tggegaagget ateggegetg gegeogaaga aggcaacgte gaggagetce aaggceggae tccagttcce egtcggeags acttgctagg ttcctcaagg tcgaggaagta eggegaagta eggegeege tggaceceeg tgtacctcge egcegtcctg egagtaccte geggetgagg tttgtgeece gettegttt ettteecete tccttgttge gattegette gggteeget egetgegte teggatetgg ttgtttgee gtggaegatt gtecttggat eygaaatga tegeggeatt gtacttcata aaaaggtete aatacattte 420
- (2) INFORMATION FOR SEQ ID NO:2487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601208
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:
- Ile Ser Leu Phe Asn Gln Ser Phe Lys Arg Xaa Xaa Pro Pro Pro Arg 1 5 10

Arg Pro Val Val Arg Arg Asp Gly Gly Pro Trp Gln Gly Tyr Arg Arg 20 25 30

Trp Arg Arg Arg Gln Arg Gly Ala Pro Arg Pro Asp Ser Ser 35 40 45

Ser Pro Ser Ala Xaa Leu Ala Arg Phe Leu Lys Ala Gly Lys Tyr Arg 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2488:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601209
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

120

180

240

300

360

420

480

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Met Ala Gly Arg Gly Lys Ala Ile Gly Ala Gly Ala Glu Glu Gly Asn
                                    10
Val Glu Glu Leu Gln Gly Arg Thr Pro Val Pro Arg Arg Gln Xaa Leu
                                25
            20
Leu Gly Ser Ser Arg Arg Ala Ser Thr Ala Glu Arg Val Gly Xaa Gly
                            40
Ala Pro Val Tyr Leu Ala Ala Val Leu Arg Val Pro Arg Gly
                        55
(2) INFORMATION FOR SEQ ID NO:2489:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 539 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..539
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601210
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:
acagtegeet cetteetgeg eegeegegem geegeegeta ceaeegeete geggeegeyt
gcggctccgc gtttccgcac ggaagttggt gaaggtttct tgaggctgag aacatggtgc
tgaagacgga actttgccgc ttcagcggcc agaagattta tcctgggaaa ggcattagat
ttatccgtgc tgattctcag gtcttccttt ttgccaactc gaaatgcaag cgctacttcc
acaaccgcct gaagcctgca aagcttacct ggacagcaat gtacaggaag cagcacaaga
aggatatcca tgctgaagcg gtaaagaaga ggcgccgcgc caccaagaag ccatactcca
ggtcaattgt gggtgcttcc ttggaagtaa tccagaagaa gagagctgag aagccagagg
tccgcgatgc tgctagagaa gctgctcttc gtgagatcaa ggagcgcatc aagaagacca
aggatgagaa gaaagcgaag aaggcggagg tgagcaagtc ccaggaagac gcagacaag
(2) INFORMATION FOR SEQ ID NO:2490:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 142 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..142
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601211
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:
Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
                                     10
 Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu
                                                     30
             20
                                 25
 Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Pro
                             40
 Ala Lys Leu Thr Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
                         55
 Ile His Ala Glu Ala Val Lys Lys Arg Arg Arg Ala Thr Lys Lys Pro
                                         75
                     70
 Tyr Ser Arg Ser Ile Val Gly Ala Ser Leu Glu Val Ile Gln Lys Lys
                                                          95
                                      90
 Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
                                 105
             100
```

Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala

120 Lys Lys Ala Glu Val Ser Lys Ser Gln Glu Asp Ala Asp Lys 135

125

(2) INFORMATION FOR SEQ ID NO:2491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..87 (D) OTHER INFORMATION: / Ceres Seq. ID 1601212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491: Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys 10 5 Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly 30 25 Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val 45 40 Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile 60 55 Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Ala Glu Val Ser Lys 75 70 Ser Gln Glu Asp Ala Asp Lys 85 (2) INFORMATION FOR SEQ ID NO:2492: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 483 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..483 (D) OTHER INFORMATION: / Ceres Seq. ID 1601224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492: agcatttcct caaacaattc gcgcgccgcc gccgccgctc tccggcgtct gctactcggc teegtgeeca ecaggeagea ggeeaceace ecaatecete tetteettea gagatgeaga 120 180 aggtgcggct caaatgggtg aagaaccggg gcctggatca cctgatcgag cgcaccacct caatcogogo gtootgootg otgotogaco acctotogog cotocotggt acctococog 240 tgccggcgcg ctccctcgca cgcctccaaa agccgcttgg cctgacggtg cctgtgcttc 300 getteetteg eegecateee aegetettet eegageaace geaceetegg tteeceaege 360 tgctctcctt ttccctcacg gctgcgtcac acaccctcct gtcccgcctt gccgatgcct 420 480 atgcgcacga cgcgcacctc cgcctcgcgc gcctcctcct cctcacccgc tccaaggtcg (2) INFORMATION FOR SEQ ID NO:2493: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1601225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

Ala Phe Pro Gln Thr Ile Arg Ala Pro Pro Pro Pro Leu Ser Gly Val

Cys Tyr Ser Ala Pro Cys Pro Pro Gly Ser Arg Pro Pro Pro Gln Ser 25

Leu Ser Ser Phe Arg Asp Ala Glu Gly Ala Ala Gln Met Gly Glu Glu 40

5

20

35

Pro Gly Pro Gly Ser Pro Asp Arg Ala His His Leu Asn Pro Arg Val Leu Pro Ala Ala Arg Pro Pro Leu Ala Pro Pro Trp Tyr Leu Pro Arg 75 70 Ala Gly Ala Leu Pro Arg Thr Pro Pro Lys Ala Ala Trp Pro Asp Gly 85 90 Ala Cys Ala Ser Leu Pro Ser Pro Pro Ser His Ala Leu Leu Arg Ala 100 105 110 Thr Ala Pro Ser Val Pro His Ala Ala Leu Leu Phe Pro His Gly Cys 115 120 125 Val Thr His Pro Pro Val Pro Pro Cys Arg Cys Leu Cys Ala Arg Arg 130 135 140 Ala Pro Pro Pro Arg Ala Pro Pro Pro Pro His Pro Leu Gln Gly Arg 155 145 150

(2) INFORMATION FOR SEQ ID NO:2494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601226
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:

His Phe Leu Lys Gln Phe Ala Arg Arg Arg Arg Arg Ser Pro Ala Ser 1 $$ 5 $$ 10 $$ 15 Ala Thr Arg Leu Arg Ala His Gln Ala Ala Gly His His Pro Asn Pro

20 20 30 Sor Leu Pro Ser Clu Met Cln Lys Val Arg Leu Lys Trp Val Lys Asn

Ser Leu Pro Ser Glu Met Gln Lys Val Arg Leu Lys Trp Val Lys Asn 35 40 45

Arg Gly Leu Asp His Leu Ile Glu Arg Thr Thr Ser Ile Arg Ala Ser 50 55 60

Cys Leu Leu Leu Asp His Leu Ser Arg Leu Pro Gly Thr Ser Pro Val 65 70 75 80 Pro Ala Arg Ser Leu Ala Arg Leu Gln Lys Pro Leu Gly Leu Thr Val

85 90 95
Pro Val Leu Arg Phe Leu Arg Arg His Pro Thr Leu Phe Ser Glu Gln

100 105 110
Pro His Pro Arg Phe Pro Thr Leu Leu Ser Phe Ser Leu Thr Ala Ala
115 120 125

Ser His Thr Leu Leu Ser Arg Leu Ala Asp Ala Tyr Ala His Asp Ala
130 135 140

His Leu Arg Leu Ala Arg Leu Leu Leu Leu Thr Arg Ser Lys Val Ala 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:2495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601227

Met Gln Lys Val Arg Leu Lys Trp Val Lys Asn Arg Gly Leu Asp His 1	Client	Docke	et No	· 80	146.	.003									Page	1249
Mot Gin Lys Val Arg Leu Lys Trp Val Lys Asn Arg Giy Leu Asp His 1	(21	\ QF(אוזייאור	יר חד	'SCRI	ር ውጥ ፐ <i>ር</i>)NI • (1)	SEO T	ID NO	7.249	95:					
Leu Ile Glu Arg Thr Thr Ser Ile Arg Ala Ser Cys Leu Leu Leu Asp 20 25 30 His Leu Ser Arg Leu Pro Gly Thr Ser Pro Val Pro Ala Arg Ser Leu 35 40 45 Ala Arg Leu Gln Lys Pro Leu Gly Leu Thr Val Pro Val Leu Arg Phe 50 50 55 Eau Arg Arg His Pro Thr Leu Phe Ser Glu Gln Pro His Pro Arg Phe 65 70 75 Pro Thr Leu Leu Ser Phe Ser Leu Thr Ala Ala Ser His Thr Leu Leu 85 90 Pro Thr Leu Leu Ser Phe Ser Leu Thr Ala Ala Ser His Thr Leu Leu 85 90 Arg Leu Ala Asp Ala Tyr Ala His Asp Ala His Leu Arg Leu Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 110 Arg Leu Lys Lys Val Ala 110 Arg Leu Lys Val Ala 110 Arg Asn Leu Ile Cys Gly Ala Lys Thr Gln Ser Asn Po Glu Asn Thr	Met Gln	Lys	Val	Arg	Leu	Lys	Trp	Val	Lys	Asn	Arg	Gly	Leu		His	
35		Glu			Thr	Ser	Ile		Ala	Ser	Cys	Leu		Leu	Asp	
Ala Arg Leu Gln Lys Pro Leu Gly Leu Thr Val Pro Val Leu Arg Phe 50 50 55 55 Leu Arg Arg His Pro Thr Leu Phe Ser Glu Gln Pro His Pro Arg Phe 75 75 80 Pro Thr Leu Leu Ser Phe Ser Leu Thr Ala Ala Ser His Thr Leu Leu Ser Arg Leu Ala Asp Ala Tyr Ala His Asp Ala His Leu Arg Leu Ala 100 105 110 Arg Leu Leu Leu Ueu Thr Arg Ser Lys Val Ala 115 120 (2) INFORMATION FOR SEQ ID NO:2496: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAMM/KEY: - (B) LOCATION: 1549 (D) OTHER INFORMATION: / Ceres Seq. ID 1601232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496: gtgatacaca tecgtecett etagteteet satasactagt treatette etagegeaaac actgaceaca agacaatteg gaacagteca cegegegeg cataggtet gaggeaacaga traatetegaa agacagtea accegegege cataggtet accegegeged accagate agacagtea accegegage accagate agacagate accegegede accagate accegegede accegeded accegede	His Leu			Leu	Pro	Gly		Ser	Pro	Val	Pro		Arg	Ser	Leu	
Leu Arg Arg His Pro Thr Leu Phe Ser Glu Gln Pro His Pro Arg Phe 80 70 70 75 80 80 95 95 80 90 95 95 90 95 95 96 96 96 96 96 96 96 96 96 96 96 96 96			Gln	Lys	Pro		Gly	Leu	Thr	Val		Val	Leu	Arg	Phe	
Pro Thr Leu Leu Ser Phe Ser Leu Thr Ala Ala Ser His Thr Leu Leu 85 Ser Arg Leu Ala Asp Ala Tyr Ala His Asp Ala His Leu Arg Leu Ala 100 Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 115 115 120 (2) INFORMATION FOR SEQ ID NO:2496: (i) SEQUENCE CHARACTERISTICS: (a) LENGTH: 549 base pairs (b) TYPE: nucleic acid (c) STRANDEDNESS: single (d) TOFOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 1549 (D) OTHER INFORMATION: / Ceres Seq. ID 1601232 (xi) SEQUENCE DESCRIFTION: SEQ ID NO:2496: gtgatacaca tecgtcctt ctagtctcct aataactagt ttctatcttg ctcccaaac cagcgcaaac catgccatgat gaattgage gaatggage ctaggtctc gaggacaacg tgattgat agacattcg gaatggage gaaggggged ctacgctcg tcggggacaacg tgattgatgaa agacgataga acacggtaga gaggtgtteg ggggattgag agacacgtca aacccgagaa acacggtaga gagattctc gcctgtatga agaggacaacg agaagattatct gccctgtatga agaggagaact tggtgcgga aatacggtt ctctaaagca tcgccagaac aagagagaaga cattgggga gaagattct gcccagattg cctctaaagca agagagaaca cattgggaa gaagattatct gcccagttg ctctaaagca tcgccagaac aagagagaagaa cattgggaa gaagattatct gccctgtatga acttgcagaac acattgggaa gaagattatct gccctgtatga acttgcagaac acttgggaa gaagattatct gcccagattg cctctaaagaa aattttggaa acttggaaa gaagatgaa aagaagaagaa tattggaaa tattgacttt cattggaaga cctctgaaacagaa aatttggaaa (C) SEQUENCE CHARACTERISTICS: (i) SEQUENCE CHARACTERISTICS: (i) SEQUENCE CHARACTERISTICS: (ii) MOLECULE TYPE: peptide (ix) FEATURE: (ia) NAME/KEY: peptide (ib) OTHER INFORMATION: / Ceres Seq. ID 1601233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497: Met Val Leu Glu Ala Thr Met Ile Cys Ile Asp Asn Ser Glu Trp Met 1 5 10 Arg Asn Gly Asp Tyr Ala Pro Ser Arg Phe Gln Ala Gln Ala Asp Ala 20 Val Asn Leu Ile Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn Thr	Leu Arg	Arg	His	Pro		Leu	Phe	Ser	Glu		Pro	His	Pro	Arg		
Arg Leu Leu Leu Thr Arg Ser Lys Val Ala 115 120 (2) INFORMATION FOR SEQ ID NO:2496: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 1549 (D) OTHER INFORMATION: / Ceres Seq. ID 1601232 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496: gtgatacaca tccgtccctt ctagtctct ataactagt ttctatcttg etcccaaac cagcgcaaca cctgccctga caccggcagc gacacgtca ccggcggcg catggtgct gaggcaacqat tagtctgcat agaccattca gaatgatgg ggaatggag ctacgctca gaggcaacqat cagcagtca acaccgatca acaccgatca acaccgatca acaccgatca acaccgatca caccgatca acaccgatca acaccgatca gaatgatgct gaggacact taggtgctc gaggcacact taggtgctc gaggcacact taggtgctc gaggcacact taggtgcgc gaaggatct gaggatgatca acaccagtt gaggacaact taggtgcgca gaagatct gaccagtca gaccagtca acaccgatca acaccgatca gaccagtca acaccgatca gaccagtca acaccgatca gaccagtca acaccgatca gaccagtca acaccgatca gaccagtca caccgatca acaccagtt gcctaagat gccagacac taggccgca acaccgatca acaccagtt gccagatt gccagatt gccagacac taggccgca acaccgatca acaccagtt gccagatt gccagattaga acttggcgc acaccgatca acacagtt gccagatt gccagattaga acttggcgc acaccgatca acacgatt gccagatt gccagattaga acttggcacagac acacgatca acacgatt gccagatt gccagatt gccagacac acaccagac acaccagac acacagat tagccagaca acacagat tagccagaca acacagat ttgccagatt gccagacaca ttgccagacac acaccagatt gccagatt gccagatt gccagacaca acaccagacacacac tagccagacacacacacacacacacacacacacacacaca		Leu	Leu		Phe	Ser	Leu	Thr		Ala	Ser	His	Thr		Leu	
(2) INFORMATION FOR SEQ ID NO:2496: (i) SEQUENCE CHARACTERISTICS: (i) A LENGTH: 549 base pairs (ii) MOLECULE TYPE: nucleic acid (c) STRANDEDNESS: single (d) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 1549 (D) OTHER INFORMATION: / Ceres Seq. ID 1601232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496: gtgatacaca tccqtccctt ctaqtctct aataactagt ttctatcttg ctcccaaac cagcgcaaca cctqccctga caccqgacga gacaqctca ccggcggcg catggtgctc gaggcaacqat taqaccattcg gagtacqaca cacggcaga cacacqtca aacccgagaga acacqgtaga cqtaqccqtc aacccgagaga acaccgagaa acccagaga acccag	Ser Arg	Leu		Asp	Ala	Tyr	Ala		Asp	Ala	His	Leu		Leu	Ala	
(2) INFORMATION FOR SEQ ID NO:2496: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 1549 (D) OTHER INFORMATION: / Ceres Seq. ID 1601232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496: gtgatacaca tccgtccctt ctagtctcct aataactagt ttctatcttg ctcccaaac cagcgcaaac cctgccctga caccggacg gacacgtcca ccggcggcg catggtgctc gaggcgcaacac tcggcctga caccggcagac gacacgtca acctcatct gcgcgcacaa gaccacgtca aacccggaga tgatctgca aagacatcg gaatgatcg gaatgatgc gagggttcc aaccccaca gcgacctcg gaagatctc gccgggttc aaccccaca gcgacctcg gaagatctc gccgggttc aaccccaca gcgacctcg gaagattct gccagcttg cctcaaagca agacagaca agacagata tatagcttt cattggaag cctggaaga agttttggac aagggacaact tggctgcgca aaccagtt gccagcttg cctcaaagca tcgccagaac agattttggaa acattggaag acaattggaagaacatttt cattggaagt cctgtgaagt acgacaagaa agtttttgga acgactgaa aagactgaaa aagactgaaa aagactgaaa aagactgaaa cattggtgaat (2) INFORMATION FOR SEQ ID NO:2497: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1146 (D) OTHER INFORMATION: / Ceres Seq. ID 1601233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497: Met Val Leu Glu Ala Thr Met Ile Cys Ile Asp Asn Ser Glu Trp Met 1 5 10 Arg Asn Gly Asp Tyr Ala Pro Ser Arg Phe Gln Ala Gln Ala Asp Ala 20 25 30 Val Asn Leu Ile Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn Thr	Arg Leu		Leu	Leu	Thr	Arg		Lys	Val	Ala						
Val Gly Val Met Thr Met Ala Gly Lys Gly Val Arg Val Leu Val Thr 50 55 60 Pro Thr Ser Asp Leu Gly Lys Ile Leu Ala Cys Met His Gly Leu Glu																

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Client Docket No. 80146.003
Val Gly Ala Glu Ala Asn Leu Ala Ala Ala Ile Gln Val Ala Gln Leu
                                 90
              85
Ala Leu Lys His Arg Gln Asn Lys Arg Gln Gln Arg Ile Ile Ala
                            105
                                               110
          100
Phe His Trp Lys Ser Cys Glu Val Arg Gln Glu Ser Phe Gly Asp Ile
                                           125
              120
Gly Lys Lys Leu Lys Lys Asn Asn Val Ala Leu Asp Ile Val Asp Leu
            135
Val Asn
145
(2) INFORMATION FOR SEQ ID NO:2498:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 140 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..140
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601234
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:
Met Ile Cys Ile Asp Asn Ser Glu Trp Met Arg Asn Gly Asp Tyr Ala
                                10
           5
Pro Ser Arg Phe Gln Ala Gln Ala Asp Ala Val Asn Leu Ile Cys Gly
                25
          2.0
Ala Lys Thr Gln Ser Asn Pro Glu Asn Thr Val Gly Val Met Thr Met
                                            45
                         40
Ala Gly Lys Gly Val Arg Val Leu Val Thr Pro Thr Ser Asp Leu Gly
                                        60
                      5.5
Lys Ile Leu Ala Cys Met His Gly Leu Glu Val Gly Ala Glu Ala Asn
                                     75
                 70
Leu Ala Ala Ile Gln Val Ala Gln Leu Ala Leu Lys His Arg Gln
                                 90
              85
Asn Lys Arg Gln Gln Gln Arg Ile Ile Ala Phe His Trp Lys Ser Cys
         100 105 110
Glu Val Arg Gln Glu Ser Phe Gly Asp Ile Gly Lys Lys Leu Lys Lys
      115 120
Asn Asn Val Ala Leu Asp Ile Val Asp Leu Val Asn
        135
(2) INFORMATION FOR SEQ ID NO:2499:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 131 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
          (B) LOCATION: 1..131
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601235
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:
Met Arg Asn Gly Asp Tyr Ala Pro Ser Arg Phe Gln Ala Gln Ala Asp
     5
                                 1.0
Ala Val Asn Leu Ile Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn
                              25
                                               30
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Thr Val Gly Val Met Thr Met Ala Gly Lys Gly Val Arg Val Leu Val

Thr Pro Thr Ser Asp Leu Gly Lys Ile Leu Ala Cys Met His Gly Leu

Glu Val Gly Ala Glu Ala Asn Leu Ala Ala Ala Ile Gln Val Ala Gln

55

7.5 65 Leu Ala Leu Lys His Arg Gln Asn Lys Arg Gln Gln Gln Arg Ile Ile 90 85 Ala Phe His Trp Lys Ser Cys Glu Val Arg Gln Glu Ser Phe Gly Asp 105 100 Ile Gly Lys Lys Leu Lys Lys Asn Asn Val Ala Leu Asp Ile Val Asp 120 115 Leu Val Asn 130 (2) INFORMATION FOR SEQ ID NO:2500: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 388 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..388 (D) OTHER INFORMATION: / Ceres Seq. ID 1601272 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500: 60 aagtaaaaaa aagttetege geatggtegg tetgegaetg cetetgaeeg eactgetete 120 ttctcctgtt ctctccccc acttcgagac ttcctccatt cgcggtttgc ctctctgcct ccctccctca gatcctccct aagattgcca tggcggacca gctcaccgac gaccagatcg 180 ccgagttcaa ggaagcattc agcctcttcg acaaggacgg cgacggctgc atcaccacca 240 aggaacttgg aactgtgatg cgctcgttgg ggcagaaccc tactgaggct gagcttcagg 300 acatgatcaa cgaggttgat gctgatggca atggaaccat cgacttccct gagtttctca 360 acctgatggc acgcaagatg aaggacac (2) INFORMATION FOR SEQ ID NO:2501: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..46 (D) OTHER INFORMATION: / Ceres Seq. ID 1601273 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501: Ser Lys Lys Lys Phe Ser Arg Met Val Gly Leu Arg Leu Pro Leu Thr 10 5 Ala Leu Leu Ser Ser Pro Val Leu Ser Pro His Phe Glu Thr Ser Ser 25 Ile Arg Gly Leu Pro Leu Cys Leu Pro Pro Ser Asp Pro Pro 40 (2) INFORMATION FOR SEQ ID NO:2502: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..79 (D) OTHER INFORMATION: / Ceres Seq. ID 1601274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502: Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala

10

Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu

25 20 Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu 45 40 Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile 55 Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp 70 (2) INFORMATION FOR SEQ ID NO:2503: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..43 (D) OTHER INFORMATION: / Ceres Seq. ID 1601275 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503: Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met 10 5 Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu 25 20 Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp 40 35 (2) INFORMATION FOR SEQ ID NO:2504: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..481 (D) OTHER INFORMATION: / Ceres Seq. ID 1601276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504: ckaaaagcac caccgccgcg ccgcccaaat cacagccacc gccgccatgg ccgcctccag 60 ccgccctctn gtctccgtga aagccctgga gggcgancat ggtcacggac gcccccggca 120 tegeettgee geeegtette ggtgegeega teegeeegga egtggteege tteacecaea 180 agctgctgtc ctgcaacaag cgccassctt acgcatctcc cgccgcgctg gccaccagac 240 300 gteggeegag teetggggta egggeegege tgtgteeegt ateeeeegeg teeeeggegg 360 cggcacccac cgcgccggcc agggagcatt cggcaacatg tgccgcggcg gacgcatgtt cgcgcccacc aagatctggc gcaagtggca ccgcgcgtca acgtcaacct ccgccgcgtc 420 geogtegeet eggssetege gecaeegeeg teeeggeeet egteeaggeg egeggeeaee 480 (2) INFORMATION FOR SEQ ID NO:2505: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1601277 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505: Xaa Lys Ala Pro Pro Pro Arg Arg Pro Asn His Ser His Arg Arg His

10

Gly Arg Leu Gln Pro Pro Ser Xaa Leu Arg Glu Ser Pro Gly Gly Arg

20 25 Xaa Trp Ser Arg Thr Pro Pro Ala Ser Pro Cys Arg Pro Ser Ser Val 40 45 Arg Arg Ser Ala Arg Thr Trp Ser Ala Ser Pro Thr Ser Cys Cys Pro 55 Ala Thr Ser Ala Xaa Leu Thr His Leu Pro Pro Arg Trp Pro Pro Asp 70 Val Gly Arg Val Leu Gly Tyr Gly Pro Arg Cys Val Pro Tyr Pro Pro 85 Arg Pro Arg Arg Arg His Pro Pro Arg Arg Pro Gly Ser Ile Arg Gln 100 105 110 His Val Pro Arg Arg Thr His Val Arg Ala His Gln Asp Leu Ala Gln 115 120 125 Val Ala Pro Arg Val Asn Val Asn Leu Arg Arg Val Ala Val Ala Ser 135 140 Xaa Leu Ala Pro Pro Pro Ser Arg Pro Ser Ser Arg Arg Ala Ala Thr 150 155

- (2) INFORMATION FOR SEQ ID NO:2506:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:

Xaa Lys His His Arg Arg Ala Ala Gln Ile Thr Ala Thr Ala Met 1 5 5 10 10 15 Ala Ala Ser Ser Arg Pro Xaa Val Ser Val Lys Ala Leu Glu Gly Xaa

Ala Ala Ser Ser Arg Pro Xaa vai Ser vai Lys Ala Leu Git Giy Ada 20 25 30

His Gly His Gly Arg Pro Arg His Arg Leu Ala Ala Arg Leu Arg Cys
40
45

Ala Asp Pro Pro Gly Arg Gly Pro Leu His Pro Gln Ala Ala Val Leu 50 55 60

Gln Gln Ala Pro Xaa Leu Arg Ile Ser Arg Arg Ala Gly His Gln Thr 65 70 75 80
Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val Ser Arg Ile Pro Arg

85 90 95

Val Pro Gly Gly Gly Thr His Arg Ala Gly Gln Gly Ala Phe Gly Asn
100 105 110

Met Cys Arg Gly Gly Arg Met Phe Ala Pro Thr Lys Ile Trp Arg Lys
115 120 125

Trp His Arg Ala Ser Thr Ser Thr Ser Ala Ala Ser Pro Ser Pro Arg 130 135 140

Xaa Ser Arg His Arg Arg Pro Gly Pro Arg Pro Gly Ala Arg Pro Pro 145 150 155 160

- (2) INFORMATION FOR SEQ ID NO:2507:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide (B) LOCATION: 1..145 (D) OTHER INFORMATION: / Ceres Seq. ID 1601279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507: Met Ala Ala Ser Ser Arg Pro Xaa Val Ser Val Lys Ala Leu Glu Gly 10 Xaa His Gly His Gly Arg Pro Arg His Arg Leu Ala Ala Arg Leu Arg 25 20 Cys Ala Asp Pro Pro Gly Arg Gly Pro Leu His Pro Gln Ala Ala Val
- 40 35 Leu Gln Gln Ala Pro Xaa Leu Arg Ile Ser Arg Arg Ala Gly His Gln 55

Thr Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val Ser Arg Ile Pro 75 70

Arg Val Pro Gly Gly Gly Thr His Arg Ala Gly Gln Gly Ala Phe Gly 90 85

Asn Met Cys Arg Gly Gly Arg Met Phe Ala Pro Thr Lys Ile Trp Arg 110 105 100

Lys Trp His Arg Ala Ser Thr Ser Thr Ser Ala Ala Ser Pro Ser Pro 125 120

Arg Xaa Ser Arg His Arg Arg Pro Gly Pro Arg Pro Gly Ala Arg Pro 135 130

Pro 145

- (2) INFORMATION FOR SEQ ID NO:2508:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..502
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601280
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508: gttcccctcc gctgtctcgc ctctcccttg gttcctcgcg gcgacgactg ggcgagcgcc 60 tecteceete ecteaetece teegtgaget ectegeegge ggegegegee geegeeegte 120 gccacgtctt ctccgctgac gtgggctcac cagatccaat gaaggctgcc aacttgacgc 180 aaggggaata aagatccaaa taagtttttg acattgatct gtagccagta ctgcaatggc 240 tatgaagett gtggtteteg gtateceetg ggatgttgae actgaagggt taegagagta 300 catggccaag tttggacccc tagacgattg tgtcgtcatg aaggagcggt cttctgggcg 360 atctcgcggg tttggctatg taacattcgc ctcagctgac gatgcaaaga atgttcttga 420 ttgcgagcat gttcttggga gccgtacatt agaagtgaag gtagctactc caaaggaaga 480 aatgaaatca caaggatcaa ag
- (2) INFORMATION FOR SEQ ID NO:2509:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601281
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509: Met Ala Met Lys Leu Val Val Leu Gly Ile Pro Trp Asp Val Asp Thr 10 5

Glu Gly Leu Arg Glu Tyr Met Ala Lys Phe Gly Pro Leu Asp Asp Cys 25

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Client Docket No. 80146.003
Val Val Met Lys Glu Arg Ser Ser Gly Arg Ser Arg Gly Phe Gly Tyr
                         40
Val Thr Phe Ala Ser Ala Asp Asp Ala Lys Asn Val Leu Asp Cys Glu
                    55
                             60
His Val Leu Gly Ser Arg Thr Leu Glu Val Lys Val Ala Thr Pro Lys
                 70
                                    75
Glu Glu Met Lys Ser Gln Gly Ser Lys
(2) INFORMATION FOR SEQ ID NO:2510:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 87 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..87
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601282
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:
Met Lys Leu Val Val Leu Gly Ile Pro Trp Asp Val Asp Thr Glu Gly
    5
                              10
Leu Arg Glu Tyr Met Ala Lys Phe Gly Pro Leu Asp Asp Cys Val Val
                      25
                                              3.0
       20
Met Lys Glu Arg Ser Ser Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr
                        40
Phe Ala Ser Ala Asp Asp Ala Lys Asn Val Leu Asp Cys Glu His Val
50 55
                          60
Leu Gly Ser Arg Thr Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu
70 75
Met Lys Ser Gln Gly Ser Lys
        85
(2) INFORMATION FOR SEQ ID NO:2511:
   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 67 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..67
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601283
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:
Met Ala Lys Phe Gly Pro Leu Asp Asp Cys Val Val Met Lys Glu Arg
                                10
Ser Ser Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr Phe Ala Ser Ala
          20
                       25
Asp Asp Ala Lys Asn Val Leu Asp Cys Glu His Val Leu Gly Ser Arg
                         40
Thr Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu Met Lys Ser Gln
  50
Gly Ser Lys
65
(2) INFORMATION FOR SEQ ID NO:2512:
    (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..496
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

 ageggtegaa gaaagaatt aatgaaacgg cagtcgcaac tcgcaagcaa atcgaacgaa 60
 cccagccgaa gcgcgagctg agcaaggcgg aggcggcggg accggcgatg gagcggctgc 120
 ageggatett tggcgcctcc ggcatggggc agccgccgac ggactcgccg ctgctcgact 180
 cctccgagca ggtctacatc tcctccctcg cgcttctcaa gatgctcaag cacgggaggg 240
 ccggcgtgcc catggaggtc atgggtctca tgctcggcga gttcgtcgat gactacaccg 300
 tcagggtcgt cgacgtcttc gccatgccgc agagcgggac tggggtcagc gtcgaggccg 360
 tcgaccacgt cttccagaca aacatgcttg acatgctcaa gcagaccggc aggccagaaa 420
 tggttgtagg ctggtatcac tcacatcctg gcttcggttg ctggctatca ggcgttgata 480
- (2) INFORMATION FOR SEQ ID NO:2513:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

tcaatactca gcagag

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601289
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:
- Ile Glu Arg Thr Gln Pro Lys Arg Glu Leu Ser Lys Ala Glu Ala Ala 20 25 30
- Gly Pro Ala Met Glu Arg Leu Gln Arg Ile Phe Gly Ala Ser Gly Met $35 \ \ 40 \ \ 45$
- Gly Gln Pro Pro Thr Asp Ser Pro Leu Leu Asp Ser Ser Glu Gln Val 50 55 60
- Tyr Ile Ser Ser Leu Ala Leu Leu Lys Met Leu Lys His Gly Arg Ala 65 70 75 80
- Gly Val Pro Met Glu Val Met Gly Leu Met Leu Gly Glu Phe Val Asp 85 90 95
- Asp Tyr Thr Val Arg Val Val Asp Val Phe Ala Met Pro Gln Ser Gly
 100
 105
 110
- Thr Gly Val Ser Val Glu Ala Val Asp His Val Phe Gln Thr Asn Met 115 120 125
- Leu Asp Met Leu Lys Gln Thr Gly Arg Pro Glu Met Val Val Gly Trp 130 135 140
- Tyr His Ser His Pro Gly Phe Gly Cys Trp Leu Ser Gly Val Asp Ile 145 150 155 160
- Asn Thr Gln Gln
- (2) INFORMATION FOR SEQ ID NO:2514:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601290
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:
- Met Glu Arg Leu Gln Arg Ile Phe Gly Ala Ser Gly Met Gly Gln Pro

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Pro Thr Asp Ser Pro Leu Leu Asp Ser Ser Glu Gln Val Tyr Ile Ser
                          25
Ser Leu Ala Leu Lys Met Leu Lys His Gly Arg Ala Gly Val Pro
                        40
Met Glu Val Met Gly Leu Met Leu Gly Glu Phe Val Asp Asp Tyr Thr
                     55
Val Arg Val Val Asp Val Phe Ala Met Pro Gln Ser Gly Thr Gly Val
                 70
                                   75
Ser Val Glu Ala Val Asp His Val Phe Gln Thr Asn Met Leu Asp Met
             85
                               90
Leu Lys Gln Thr Gly Arg Pro Glu Met Val Val Gly Trp Tyr His Ser
          100 105 110
His Pro Gly Phe Gly Cys Trp Leu Ser Gly Val Asp Ile Asn Thr Gln
                               125
                       120
Gln
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(2) INFORMATION FOR SEQ ID NO:2515:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..117
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

Met Gly Gln Pro Pro Thr Asp Ser Pro Leu Leu Asp Ser Ser Glu Gln 1 $$ 5 $$ 10 $$ 15

Val Tyr Ile Ser Ser Leu Ala Leu Leu Lys Met Leu Lys His Gly Arg 20 25 30

Ala Gly Val Pro Met Glu Val Met Gly Leu Met Leu Gly Glu Phe Val 35 40 45

Asp Asp Tyr Thr Val Arg Val Val Asp Val Phe Ala Met Pro Gln Ser 50 55 60

Gly Thr Gly Val Ser Val Glu Ala Val Asp His Val Phe Gln Thr Asn 65 70 75 80

Met Leu Asp Met Leu Lys Gln Thr Gly Arg Pro Glu Met Val Val Gly 85 90 95

Trp Tyr His Ser His Pro Gly Phe Gly Cys Trp Leu Ser Gly Val Asp
100 105 110

Ile Asn Thr Gln Gln

115

- (2) INFORMATION FOR SEQ ID NO:2516:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601294
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

ateggeteac geactgacge acatecatta cettetataa taegtetgeg gtgteaaaat teectetea geegtgttge tegeogeege eeeggegtgt tgetegeega caeeggeege eeggeageea aaatgeegtt caagaggtte gtggagateg ggegagtgge eettgtaaac taeageaagg agtatggeeg eetegtegte ategtegaeg tegtegaeea gaacaggget

cttgttgatgccccegacatggttcgttgccaaatgaacttcaageggettteectgactgacatcaagattgacattaaacgtgtcccaaagaagactacactgatcaaggcaatggaggaagetgatgtgaaaagcaagtgggagaatagetcatggggcaagaagetgattgttcagaagaggagagcatcactcaatgactttgacaggttcaaggtcatgttggcgaagatcaag

- (2) INFORMATION FOR SEQ ID NO:2517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601295
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:
- Ile Gly Ser Arg Thr Asp Ala His Pro Leu Pro Ser Ile Ile Arg Leu
 1 5 10 15
- Arg Cys Gln Asn Phe Pro Leu Ser Arg Val Ala Arg Arg Pro Ala 20 25 30
- Val Leu Leu Ala Asp Thr Ala Pro Pro Ala Ala Lys Met Pro Phe Lys 35 40 45
- Arg Phe Val Glu Ile Gly Arg Val Ala Leu Val Asn Tyr Ser Lys Glu 50 55 60
- Tyr Gly Arg Leu Val Val Ile Val Asp Val Val Asp Gln Asn Arg Ala 65 70 75 80
- Leu Val Asp Ala Pro Asp Met Val Arg Cys Gln Met Asn Phe Lys Arg $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$
- Leu Ser Leu Thr Asp Ile Lys Ile Asp Ile Lys Arg Val Pro Lys Lys 100 105 110
- Thr Thr Leu Ile Lys Ala Met Glu Glu Ala Asp Val Lys Ser Lys Trp 115 120 125
- Glu Asn Ser Ser Trp Gly Lys Lys Leu Ile Val Gln Lys Arg Arg Ala 130 135 140
- Ser Leu Asn Asp Phe Asp Arg Phe Lys Val Met Leu Ala Lys Ile Lys 145 150 150 160 Arg
- (2) INFORMATION FOR SEQ ID NO:2518:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..117
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601296
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:
- Met Pro Phe Lys Arg Phe Val Glu Ile Gly Arg Val Ala Leu Val Asn 1 $$ 5 $$ 10 $$ 15
- Tyr Ser Lys Glu Tyr Gly Arg Leu Val Val Ile Val Asp Val Val Asp 20 25 30
- Gln Asn Arg Ala Leu Val Asp Ala Pro Asp Met Val Arg Cys Gln Met
- Asn Phe Lys Arg Leu Ser Leu Thr Asp Ile Lys Ile Asp Ile Lys Arg
 50 60
- Val Pro Lys Lys Thr Thr Leu Ile Lys Ala Met Glu Glu Ala Asp Val 65 70 75 80

Lys Ser Lys Trp Glu Asn Ser Ser Trp Gly Lys Lys Leu Ile Val Gln 85 y 90 y 95 Lys Arg Arg Ala Ser Leu Asn Asp Phe Asp Arg Phe Lys Val Met Leu 100 y 100 y

Ala Lys Ile Lys Arg

115

- (2) INFORMATION FOR SEQ ID NO:2519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..471
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601303
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

aacccctcgg acagaccage cttcaaacta gggtttacte etecegetee gagaaageaa 60 acaagegtea geteegegg eggeetegeg eteteteeee egeegeacet tetetacgee 120 aggactgeea agatgaaget egteagatte ettatgaage taaacaatga gaeggteace 180 ategagetea agaacggeae ggttgteeae ggeaceatea eeggtgttga eataageatg 240 aacacteate tgaagacagt gaagettaca etgaaaggga agaaceetgt aacgetggae 300 caceteageg tgegaggaaa caacateege tattacatte tteetgacag ettaaacttg 360 gagactttge tggtagagga aacceetagg gttaageeta agaageegae tacaggaaag 420 eetttgggge gtgggeggg eegtggtegt ggaegtggte ggggaegggg g

- (2) INFORMATION FOR SEQ ID NO:2520:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..157
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601304
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Asn Pro Ser Asp Arg Pro Ala Phe Lys Leu Gly Phe Thr Pro Pro Ala $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Pro Arg Lys Gln Thr Ser Val Ser Ser Ala Gly Gly Leu Ala Leu Ser 20 25 30

Pro Pro Pro His Leu Leu Tyr Ala Arg Thr Ala Lys Met Lys Leu Val 35 40 45

Arg Phe Leu Met Lys Leu Asn Asn Glu Thr Val Thr Ile Glu Leu Lys 50 55 60

Asn Gly Thr Val Val His Gly Thr Ile Thr Gly Val Asp Ile Ser Met 65 70 75 80 Asn Thr His Leu Lys Thr Val Lys Leu Thr Leu Lys Gly Lys Asn Pro

85 90 95

Val Thr Leu Asp His Leu Ser Val Arg Gly Asn Asn Ile Arg Tyr Tyr

100 105 110

Ile Leu Pro Asp Ser Leu Asn Leu Glu Thr Leu Leu Val Glu Glu Thr

Pro Arg Val Lys Pro Lys Lys Pro Thr Thr Gly Lys Pro Leu Gly Arg
130 135 140

- Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly 145 150 155
- (2) INFORMATION FOR SEQ ID NO:2521:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601305
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:
- Ile Glu Leu Lys Asn Gly Thr Val Val His Gly Thr Ile Thr Gly Val 20 25 30
- Asp Ile Ser Met Asn Thr His Leu Lys Thr Val Lys Leu Thr Leu Lys 35 40 45
- Gly Lys Asn Pro Val Thr Leu Asp His Leu Ser Val Arg Gly Asn Asn 50 60
- Ile Arg Tyr Tyr Ile Leu Pro Asp Ser Leu Asn Leu Glu Thr Leu Leu 65 70 75 80
- Val Glu Glu Thr Pro Arg Val Lys Pro Lys Lys Pro Thr Thr Gly Lys 85 90 95
- Pro Leu Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg 100 105 110

Gly

- (2) INFORMATION FOR SEQ ID NO:2522:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:
- Met Lys Leu Asn Asn Glu Thr Val Thr Ile Glu Leu Lys Asn Gly Thr 1 5 10 15
- Val Val His Gly Thr Ile Thr Gly Val Asp Ile Ser Met Asn Thr His $20 \\ 25 \\ 30$
- Leu Lys Thr Val Lys Leu Thr Leu Lys Gly Lys Asn Pro Val Thr Leu 35 40 45
- Asp His Leu Ser Val Arg Gly Asn Asn Ile Arg Tyr Tyr Ile Leu Pro 50 60
- Asp Ser Leu Asn Leu Glu Thr Leu Leu Val Glu Glu Thr Pro Arg Val 65 70 75 80
- Lys Pro Lys Lys Pro Thr Thr Gly Lys Pro Leu Gly Arg Gly Arg Gly 85 90 95
- Arg Gly Arg Gly Arg Gly Arg Gly 100 105
- (2) INFORMATION FOR SEQ ID NO:2523:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..389

- (D) OTHER INFORMATION: / Ceres Seq. ID 1601317
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

 agaacttttg teccectece tectecaeae etetegttet etececetee geetgeteee 60
 teteaggage gegegegege gegeecagat etagggttte gteegeggea agatgageag 120
 cecgeatgge ggtetegaeg accagatega geggeteatg eagtgeaage egetegetga 180
 geetgaggtt agagetettt gtgagaagge aaaggagatt etgatggagg aaagcaatgt 240
 teageetgta aagagteetg ttactatatg eggtgatatt eatggaeaat tteatgatet 300
 tgetgaacte tteegaateg gtggaaagtg teeagataeg aactaettgt ttatgggaga 360
- (2) INFORMATION FOR SEQ ID NO:2524:

ttatgttgac cgtggttact actctgtcg

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..59
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601318
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

Arg Thr Phe Val Pro Leu Pro Pro Pro His Leu Ser Phe Ser Pro Pro 1 5 10 15

Pro Pro Ala Pro Ser Gln Glu Arg Ala Arg Ala Arg Pro Asp Leu Gly
20 25 30

Phe Arg Pro Arg Gln Asp Glu Gln Pro Ala Trp Arg Ser Arg Pro 35 40 45

Asp Arg Ala Ala His Ala Val Gln Ala Arg 50 55

- (2) INFORMATION FOR SEQ ID NO:2525:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601319
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Met Ser Ser Pro His Gly Gly Leu Asp Asp Gln Ile Glu Arg Leu Met 1 5 10 15

Gln Cys Lys Pro Leu Ala Glu Pro Glu Val Arg Ala Leu Cys Glu Lys 20 25 30

Ala Lys Glu Ile Leu Met Glu Glu Ser Asn Val Gln Pro Val Lys Ser 35 40 45

Pro Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe His Asp Leu Ala 50 55 60 Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro Asp Thr Asn Tyr Leu Phe

65 70 75

Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val
85 90

- (2) INFORMATION FOR SEQ ID NO:2526:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

Met Gln Cys Lys Pro Leu Ala Glu Pro Glu Val Arg Ala Leu Cys Glu
1 5 10 15

Lys Ala Lys Glu Ile Leu Met Glu Glu Ser Asn Val Gln Pro Val Lys 20 25 30

Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe His Asp Leu 35 40 45

Ala Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro Asp Thr Asn Tyr Leu 50 55 60

Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2527:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..517
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601325
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527: aaaatcacca tcaccaccta tcgtcggaga accacagaat ccaccgcatc gcagagacga 60 gtagaggtta gatttaggct gaggtaagat ggtgtgcatc cggcaggcga ccatcgaaga 120 cctgctggcg atgcaggcgt gcaacctgat gtgcctgccg gagaactacc agatgaagta 180 ctacttctac cacatgctct cgtggccgca gctcctcttc gtcgccgagg actacggagg 240 cagcatcgtc ggatacgtgc tcgccaagat ggaggaggac ccctccgagc cctgccacgg 300 ccacatcacc teectegegg teeteegete ccacegeaag etegggeteg ecactaaget catgtccgcc gcgcaggccg ccatggacca ggtcttcggc gctgagtacg tctcactcca 420 cgtccgcgat ccaaccgcgc tgccttcaac ctctacacct ctaccctcgg gtaccagatt caggatatcg aggccaagta ctatgccgat ggggagg
- (2) INFORMATION FOR SEQ ID NO:2528:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601326
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528: Met Val Cys Ile Arg Gln Ala Thr Ile Glu Asp Leu Leu Ala Met Gln

1 5 10 15 Ala Cys Asn Leu Met Cys Leu Pro Glu Asn Tyr Gln Met Lys Tyr Tyr

20 25 30
Phe Tyr His Met Leu Ser Trp Pro Gln Leu Leu Phe Val Ala Glu Asp

35 40 45

Tyr Gly Gly Ser Ile Val Gly Tyr Val Leu Ala Lys Met Glu Glu Asp
50 55 60

Pro Ser Glu Pro Cys His Gly His Ile Thr Ser Leu Ala Val Leu Arg

65 70 75 80

Ser His Arg Lys Leu Gly Leu Ala Thr Lys Leu Met Ser Ala Ala Gln

85 90 95

Ala Ala Met Asp Gln Val Phe Gly Ala Glu Tyr Val Ser Leu His Val

Arg Asp Pro Thr Ala Leu Pro Ser Thr Ser Thr Pro Leu Pro Ser Gly 120 115

Thr Arg Phe Arg Ile Ser Arg Pro Ser Thr Met Pro Met Gly Arg 135 140 130

- (2) INFORMATION FOR SEQ ID NO:2529:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

Met Gln Ala Cys Asn Leu Met Cys Leu Pro Glu Asn Tyr Gln Met Lys 5 10

Tyr Tyr Phe Tyr His Met Leu Ser Trp Pro Gln Leu Leu Phe Val Ala 25 20

Glu Asp Tyr Gly Gly Ser Ile Val Gly Tyr Val Leu Ala Lys Met Glu 45 4.0

Glu Asp Pro Ser Glu Pro Cys His Gly His Ile Thr Ser Leu Ala Val 55 60

Leu Arg Ser His Arg Lys Leu Gly Leu Ala Thr Lys Leu Met Ser Ala 75 70

Ala Gln Ala Ala Met Asp Gln Val Phe Gly Ala Glu Tyr Val Ser Leu 90 8.5

His Val Arg Asp Pro Thr Ala Leu Pro Ser Thr Ser Thr Pro Leu Pro 100 105 110

Ser Gly Thr Arg Phe Arg Ile Ser Arg Pro Ser Thr Met Pro Met Gly 120

Ara

- (2) INFORMATION FOR SEQ ID NO:2530:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

Met Cys Leu Pro Glu Asn Tyr Gln Met Lys Tyr Tyr Phe Tyr His Met 5 10 1 Leu Ser Trp Pro Gln Leu Leu Phe Val Ala Glu Asp Tyr Gly Gly Ser

25 30

Ile Val Gly Tyr Val Leu Ala Lys Met Glu Glu Asp Pro Ser Glu Pro 40

Cys His Gly His Ile Thr Ser Leu Ala Val Leu Arg Ser His Arg Lys 55

Leu Gly Leu Ala Thr Lys Leu Met Ser Ala Ala Gln Ala Ala Met Asp 75

Gln Val Phe Gly Ala Glu Tyr Val Ser Leu His Val Arg Asp Pro Thr 90 85

Ala Leu Pro Ser Thr Ser Thr Pro Leu Pro Ser Gly Thr Arg Phe Arg 105 100

Ile Ser Arg Pro Ser Thr Met Pro Met Gly Arg

- (2) INFORMATION FOR SEQ ID NO:2531:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..508
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601333
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

(~ ~					
aacacaggca	ccacagetga	gagacgatag	aagcacgcag	cagctgaaag	ggagggaac	60
taggaatgaa	aggaaggaag	gtccacgagc	acqaqqcaqa	cgtccccgcc	tccgacctct	120
eaggaatgaa	gggggggatg	cgcgccgcgg	aactcctqcc	ggaggtggtg	ccacacatac	180
gggcgattta	eggereere	cgcgccgcgg	adeceeegee	ggagoogooo		240
ttaccaaaat	ggagctcgtc	agcggcgacg	gcggtgttgg	taccatcttg	cagctaatat	240
tteeteecaa	gattcctggg	ctacagagtt	acaaqqaqaa	gttcatcaaa	gttgacaacg	300
		~~~~~~	atagggagat	tttgaagetg	aaattaaaa	360
agaactatat	caaggaggca	gaagccattg	acggcgacac	cccyaagecg	gggcccgagg	
catacatgat	acggtttgag	atcattccaa	aaqqqqccaa	ttcgtctgtc	atcaggtcga	420
cacacacgac	2299000909			aggtatagta	24424443	480
ctatcgagta	tgtgattgct	gatgcgcacc	eggagetega	agctatygty	aycacaycaa	400
ctttggctga	aactgctcag	aaattttc				

- (2) INFORMATION FOR SEQ ID NO:2532:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601334
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

Arg Arg Pro Arg Leu Arg Pro Leu Gly Asp Leu Arg Leu Pro Pro Arg

Arg Gly Thr Pro Ala Gly Ala Ala Pro Ala Arg Ala Cys Gln Gly Gly 50 55 60

Ala Arg Gln Arg Arg Arg Cys Trp Tyr His Leu Ala Ala Asn Ile 65 70 75 80
Ser Ser Arg Asp Ser Trp Ala Thr Glu Leu Gln Gly Glu Val His Gln

90

Ser

(2) INFORMATION FOR SEQ ID NO:2533:

85

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 147 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..147
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601335
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

Met Lys Gly Ser Lys Val His Glu His Glu Ala Asp Val Pro Ala Ser

10 Asp Leu Trp Ala Ile Tyr Gly Ser Leu Arg Ala Ala Glu Leu Leu Pro 25 Glu Leu Leu Pro His Val Leu Ala Lys Val Glu Leu Val Ser Gly Asp Gly Gly Val Gly Thr Ile Leu Gln Leu Ile Phe Pro Pro Gly Ile Pro Gly Leu Gln Ser Tyr Lys Glu Lys Phe Ile Lys Val Asp Asn Glu Asn 75 Tyr Ile Lys Glu Ala Glu Ala Ile Asp Gly Asp Ile Leu Lys Leu Gly 85 90 Phe Glu Ala Tyr Met Ile Arg Phe Glu Ile Ile Pro Lys Gly Ala Asn 105 110 100 Ser Ser Val Ile Arg Ser Thr Ile Glu Tyr Val Ile Ala Asp Ala His 120 115 Pro Glu Leu Glu Ala Met Val Ser Thr Ala Thr Leu Ala Glu Thr Ala 135 130 Gln Lys Phe 145 (2) INFORMATION FOR SEQ ID NO:2534: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..475 (D) OTHER INFORMATION: / Ceres Seq. ID 1601340 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534: 60 aatccacaca cacacaacac agcagagaga ttactacgat ccaacagttc tagagcaaga gagaggaaga cacaccgcag agttagcagg ctaataactt gcaggagcag caggaatggc 120 ggcgacgcgt cgcctctctt gccttctcct cgccgtgctt ctggcaggag tggccgctgc 180 caccgccttc gacgaagcgg ctgctgccgg cttcgggctt ggccacggcg cgcgtttcgc 240 gegcaageat ggacgagetg cegetgagat geeccageeg gagecacaae etaaaactaa 300 geoggagece catatgeage cactgeneca geoagaacet aaacegaaac etatgecaca 360 tocagagoca aagootgaac otcaaccaaa goocaaccot gaacctcaac caatgoocaa 420 gcctctacca aaatccaaac cagagccatt gcctacacng aagccagaac ctaag (2) INFORMATION FOR SEQ ID NO:2535: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 88 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..88 (D) OTHER INFORMATION: / Ceres Seq. ID 1601341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535: Asn Pro His Thr His Asn Thr Ala Glu Arg Leu Leu Arg Ser Asn Ser 10 Ser Arg Ala Arg Glu Arg Lys Thr His Arg Arg Val Ser Arg Leu Ile 30 Thr Cys Arg Ser Ser Arg Asn Gly Gly Asp Ala Ser Pro Leu Leu Pro 45 40 Ser Pro Arg Arg Ala Ser Gly Arg Ser Gly Arg Cys His Arg Leu Arg

55

Arg Ser Gly Cys Cys Arg Leu Arg Ala Trp Pro Arg Arg Ala Phe Arg

Ala Gln Ala Trp Thr Ser Cys Arg 85

- (2) INFORMATION FOR SEQ ID NO:2536:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..120
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601342
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

Met Ala Ala Thr Arg Arg Leu Ser Cys Leu Leu Leu Ala Val Leu Leu 1 5 10 15

Ala Gly Val Ala Ala Ala Thr Ala Phe Asp Glu Ala Ala Ala Gly  $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30 \hspace{1.5cm}$ 

Phe Gly Leu Gly His Gly Ala Arg Phe Ala Arg Lys His Gly Arg Ala 35 40 45

Ala Ala Glu Met Pro Gln Pro Glu Pro Gln Pro Lys Thr Lys Pro Glu
50 55 60

Pro His Met Gln Pro Leu Xaa Gln Pro Glu Pro Lys Pro Lys Pro Met 70 75 80

Pro His Pro Glu Pro Lys Pro Glu Pro Gln Pro Lys Pro Asn Pro Glu 85 90 95

Pro Gln Pro Met Pro Lys Pro Leu Pro Lys Ser Lys Pro Glu Pro Leu 100 105 110

Pro Thr Xaa Lys Pro Glu Pro Lys 115 120

- (2) INFORMATION FOR SEQ ID NO:2537:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1...75
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601343
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

Met Asp Glu Leu Pro Leu Arg Cys Pro Ser Arg Ser His Asn Leu Lys
1 5 10 15

Leu Ser Arg Ser Pro Ile Cys Ser His Cys Xaa Ser Gln Asn Leu Asn 20 25 30

Arg Asn Leu Cys His Ile Gln Ser Gln Ser Leu Asn Leu Asn Gln Ser 35 40 45

Pro Thr Leu Asn Leu Asn Gln Cys Pro Ser Leu Tyr Gln Asn Pro Asn 50 55 60

Gln Ser His Cys Leu His Xaa Ser Gln Asn Leu 70 75

- (2) INFORMATION FOR SEQ ID NO:2538:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 499 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -

- (B) LOCATION: 1..499
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601351
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538: ggaccgcacc cgctgtagcc gccatgtcgt ccgccgccgc cacagccttt gccggagtct 120 ccqtcqccac cccqaacctc accactccat ttcqcqgtcq cqtqcqcctt ccqctacqcq gggtctccgc tgccccacgc cgcgccgtcg cttcgatggc cgtgtccgcc cccaggtccg 180 240 gcgccgccgc ctcgttcctg gagcgccgcg agtccgagcg cgctctccac ttcgtcaagt accagggeet eggeaatgae tteattatgg tggacaacag ggattegteg gtgeegaagg 300 tgacgccgga ggaggccgcg aagctgtgcg accgaaactt cggcattggt gccgacggcg 360 tcatcttcgt catgccaggg gtcaatgatg ccgactacac catgaggatc ttcaactctg 420 acggcagcga gccagagatg tgtggtaatg gagtccgttg ctttgctcgg tttataggcg 480 aacttgaaaa atctgcagg
- (2) INFORMATION FOR SEQ ID NO:2539:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 165 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..165
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601352
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:
- Thr Ala Pro Ala Val Ala Ala Met Ser Ser Ala Ala Ala Thr Ala Phe 1  $\phantom{0}$  5  $\phantom{0}$  10  $\phantom{0}$  15 Ala Gly Val Ser Val Ala Thr Pro Asn Leu Thr Thr Pro Phe Arg Gly
- 20 25 30 25 Arg Arg Arg Ala
- Arg Val Arg Leu Pro Leu Arg Gly Val Ser Ala Ala Pro Arg Ala 35 40 45
- Val Ala Ser Met Ala Val Ser Ala Pro Arg Ser Gly Ala Ala Ala Ser 50 55 60
- Phe Leu Glu Arg Arg Glu Ser Glu Arg Ala Leu His Phe Val Lys Tyr 65 70 75 80
- Gln Gly Leu Gly Asn Asp Phe Ile Met Val Asp Asn Arg Asp Ser Ser 85 90 95 Val Pro Lys Val Thr Pro Glu Glu Ala Ala Lys Leu Cys Asp Arg Asn
- 100 105 110 Phe Gly Ile Gly Ala Asp Gly Val Ile Phe Val Met Pro Gly Val Asn
- Asp Ala Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro 130 135 140
- Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile Gly Glu 145 150 155 160

Leu Glu Lys Ser Ala

165

- (2) INFORMATION FOR SEQ ID NO:2540:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..158
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601353
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:
- Met Ser Ser Ala Ala Ala Thr Ala Phe Ala Gly Val Ser Val Ala Thr 1 5 10 15

Pro Asn Leu Thr Thr Pro Phe Arg Gly Arg Val Arg Leu Pro Leu Arg

180

240

```
25
           2.0
Gly Val Ser Ala Ala Pro Arg Arg Ala Val Ala Ser Met Ala Val Ser
                           40
Ala Pro Arg Ser Gly Ala Ala Ala Ser Phe Leu Glu Arg Arg Glu Ser
Glu Arg Ala Leu His Phe Val Lys Tyr Gln Gly Leu Gly Asn Asp Phe
                                       75
                   70
Ile Met Val Asp Asn Arg Asp Ser Ser Val Pro Lys Val Thr Pro Glu
                                   90
               85
Glu Ala Ala Lys Leu Cys Asp Arg Asn Phe Gly Ile Gly Ala Asp Gly
                               105
Val Ile Phe Val Met Pro Gly Val Asn Asp Ala Asp Tyr Thr Met Arg
                          120
                                               125
       115
Ile Phe Asn Ser Asp Gly Ser Glu Pro Glu Met Cys Gly Asn Gly Val
                    135
                                           140
Arg Cys Phe Ala Arg Phe Ile Gly Glu Leu Glu Lys Ser Ala
                  150
(2) INFORMATION FOR SEQ ID NO:2541:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 114 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
```

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..114
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

Met Ala Val Ser Ala Pro Arg Ser Gly Ala Ala Ala Ser Phe Leu Glu 1 5 10 15

Arg Arg Glu Ser Glu Arg Ala Leu His Phe Val Lys Tyr Gln Gly Leu 20 25 30

Gly Asn Asp Phe Ile Met Val Asp Asn Arg Asp Ser Ser Val Pro Lys 35 40 45

Val Thr Pro Glu Glu Ala Ala Lys Leu Cys Asp Arg Asn Phe Gly Ile 50 55 60

Gly Ala Asp Gly Val Ile Phe Val Met Pro Gly Val Asn Asp Ala Asp 65 70 75 80

Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro Glu Met Cys 85 90 95

Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile Gly Glu Leu Glu Lys
100 105 110

Ser Ala

- (2) INFORMATION FOR SEQ ID NO:2542:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..501
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601362
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

aaggccagtetgagtgtgegttcgattegettgtgetgeagetagggtttagaggtttetgggcgeggagegggaggeggeggeggetatggetgeggeggaggaggagategeggtgaaggagecgetggatetgataegeeteageeaagaageegegeegeegeeggeageaataatggaggagaattteeteeactteecaaaeectaceggeggegeageageateacaaee

accgcccgaagatggtgaagtttctcaagcccggcaaggccgtaatcctcctccagggcaggttcgccggccggaaggcggtgatcgtgcgcgtgttcgaggagggcacccgcgaccgtccctatgggcactgcctcgtcgccggcctggccaagtaccccaagaaggtgatccgcaaggactccgccaagaagacggccaagaagtcccgcgtcaagtgtttcatcaagctcgtcaatttcactcacctcatggcccacc

- (2) INFORMATION FOR SEQ ID NO:2543:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 59 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..59
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:
- Gly Gln Ser Glu Cys Ala Phe Asp Ser Leu Val Leu Gln Leu Gly Phe  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Arg Gly Phe Leu Gly Ala Glu Arg Glu Ala Ala Ala Ala Met Ala Ala 20 25 30

Ala Glu Glu Glu Ile Ala Val Lys Glu Pro Leu Asp Leu Ile Arg Leu 35 40 45

Ser Gln Glu Ala Arg Arg Arg Arg Arg Gln Gln 50 55

- (2) INFORMATION FOR SEQ ID NO:2544:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
      - (B) LOCATION: 1..106
      - (D) OTHER INFORMATION: / Ceres Seq. ID 1601364
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

Met Glu Glu Asn Phe Leu His Phe Pro Asn Pro Thr Gly Gly Ala Ala 1 5 10 15

Ala Ser Gln Pro Pro Pro Glu Asp Gly Glu Val Ser Gln Ala Arg Gln 20 25 30

Gly Arg Asn Pro Pro Pro Gly Gln Val Arg Arg Pro Glu Gly Gly Asp 35 40 45

Arg Ala Arg Val Arg Gly Gly His Pro Arg Pro Ser Leu Trp Ala Leu 50 60

Pro Arg Arg Pro Gly Gln Val Pro Gln Glu Gly Asp Pro Gln Gly 65 70 75 80

Leu Arg Gln Glu Asp Gly Gln Glu Val Pro Arg Gln Val Phe His Gln 85 90 95

Ala Arg Gln Phe His Ser Pro His Gly Pro 100 105

- (2) INFORMATION FOR SEQ ID NO:2545:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 83 amino acids(B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1601365 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545: Met Val Lys Phe Leu Lys Pro Gly Lys Ala Val Ile Leu Leu Gln Gly 10 Arg Phe Ala Gly Arg Lys Ala Val Ile Val Arg Val Phe Glu Gly 20 25 Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys 40 Tyr Pro Lys Lys Val Ile Arg Lys Asp Ser Ala Lys Lys Thr Ala Lys 60 55 Lys Ser Arg Val Lys Cys Phe Ile Lys Leu Val Asn Phe Thr His Leu 70 75 65 Met Ala His

## (2) INFORMATION FOR SEQ ID NO:2546:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 420 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..420
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601378
- (2) INFORMATION FOR SEQ ID NO:2547:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..107
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:

Thr Phe Asn Asn Glu Arg Pro Thr Gln Pro Asn Pro Thr His His Cys
1 10 15

Arg Pro Ser Pro Phe Pro Ser Pro His Arg Arg Pro Ala Ala Pro Pro 20 25 30

Pro Phe Pro Ala Pro Ser Ser Arg His His Arg Arg Arg Asn Phe Val 35 40 45

Glu Glu Glu Ala Arg Thr Arg Pro Arg Ser Asp Gly Gln Gln Pro 50 55 60

Pro Ala Ala Asp His Gln Gly Asp Ala Ala Thr Ala Gln Arg Ala Ser
65 70 75 80

Ala Gly Asp Gln Xaa Val Ala Leu Gly Gly Glu Xaa Ala Leu Leu Gln
85 90 95

Arg Tyr Asp Pro Trp Ala Gly Ala Val Xaa Leu 100 105

(2) INFORMATION FOR SEQ ID NO:2548:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..119
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601380
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

Leu Ser Ile Thr Ser Gly Gln Pro Asn Pro Thr Gln Pro Thr Ala 1 5 10 15

Val Pro Pro Arg Ser Pro Val Pro Thr Ala Asp Arg Leu Leu Leu 20 25 30

Leu Ser Pro Arg His Pro Arg Gly Ile Thr Gly Ala Ala Thr Ser Leu 35 40 45

Arg Arg Lys Pro Ala Pro Ala Pro Asp Pro Met Ala Asn Ser Asn Leu 50 55 60

Pro Arg Arg Ile Ile Lys Glu Thr Gln Arg Leu Leu Ser Glu Pro Ala 70 75 80

Pro Gly Ile Xaa Ala Ser Pro Ser Glu Glu Asn Xaa Arg Tyr Phe Asn 85 90 95

Val Met Ile Leu Gly Pro Ala Gln Ser Xaa Tyr Glu Gly Gly Val Phe 100 105 110

Lys Leu Glu Leu Xaa Phe Thr

- (2) INFORMATION FOR SEQ ID NO:2549:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 61 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..61
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

Met Ala Asn Ser Asn Leu Pro Arg Arg Ile Ile Lys Glu Thr Gln Arg

1 5 10 15

Leu Leu Ser Glu Pro Ala Pro Gly Ile Xaa Ala Ser Pro Ser Glu Glu 20 25 30

Asn Xaa Arg Tyr Phe Asn Val Met Ile Leu Gly Pro Ala Gln Ser Xaa 35 40 45

Tyr Glu Gly Gly Val Phe Lys Leu Glu Leu Xaa Phe Thr 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2550:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..484
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601386
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550: gtcatccgcg cgccgaggat cttctaccca gccatcaacg ccctcctcca tcaacggaag gtggccgagg atccgccca ccctcctccc cacgccgtcg tcgatggaag gtgcgatctc

180 ctacccctct gctccaccat caacgccctc ctccatcccc ttccattgtt gccgctccgc caccacacca cgtttcccaa acgcgcagat ccgaggatcc gccatcaacg ccgcgcccac 240 300 cetectecee etetgeteeg egacgacagg ggtetgagge egecateaac geceteetee ccacgccgtc gatggcgcgc gcagatccag tctccttcag gcaacaccgc gccatcagcg gaatctcctt ccgccatcag cagaaggtgc tgaggatctt gggcaagcag gagagggga 420 gaggaggcca aggacacaac cgcgaagcaa actcatccaa tccagtccct tctgtcggcc gcac

- (2) INFORMATION FOR SEQ ID NO:2551:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..130
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601387
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

Val Ile Arg Ala Pro Arg Ile Phe Tyr Pro Ala Ile Asn Ala Leu Leu 10 5

His Gln Arg Lys Val Ala Glu Asp Pro Pro His Pro Pro Pro His Ala 25 30 2.0

Val Val Asp Gly Arg Cys Asp Leu Leu Pro Leu Cys Ser Thr Ile Asn 40

Ala Leu Leu His Pro Leu Pro Leu Leu Pro Leu Arg His His Thr Thr 60 5.5

Phe Pro Lys Arg Ala Asp Pro Arg Ile Arg His Gln Arg Arg Ala His 75 7.0

Pro Pro Pro Pro Leu Leu Arg Asp Asp Arg Gly Leu Arg Pro Pro Ser 90 85

Thr Pro Ser Ser Pro Arg Arg Arg Trp Arg Ala Gln Ile Gln Ser Pro 110 105

Ser Gly Asn Thr Ala Pro Ser Ala Glu Ser Pro Ser Ala Ile Ser Arg 125 120

Arg Cys

130

- (2) INFORMATION FOR SEQ ID NO:2552:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 91 amino acids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS:
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..91
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601388
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

Ser Ser Ala Arg Arg Gly Ser Ser Thr Gln Pro Ser Thr Pro Ser Ser 10

Ile Asn Gly Arg Trp Pro Arg Ile Arg Pro Thr Leu Leu Pro Thr Pro 30 25 20

Ser Ser Met Glu Gly Ala Ile Ser Tyr Pro Ser Ala Pro Pro Ser Thr 45 40

Pro Ser Ser Ile Pro Phe His Cys Cys Arg Ser Ala Thr Thr Pro Arg 60 55

Phe Pro Asn Ala Gln Ile Arg Gly Ser Ala Ile Asn Ala Ala Pro Thr 75 70

Leu Leu Pro Leu Cys Ser Ala Thr Thr Gly Val 85

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide
(B) LOCATION: 1..82

(ix) FEATURE:

(2) INFORMATION FOR SEQ ID NO:2553: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1601389 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553: His Pro Arg Ala Glu Asp Leu Leu Pro Ser His Gln Arg Pro Pro Pro 5 10 Ser Thr Glu Gly Gly Arg Gly Ser Ala Pro Pro Ser Ser Pro Arg Arg 20 2.5 Arg Arg Trp Lys Val Arg Ser Pro Thr Pro Leu Leu His His Gln Arg 40 Pro Pro Pro Ser Pro Ser Ile Val Ala Pro Pro Pro His His Val 55 Ser Gln Thr Arg Arg Ser Glu Asp Pro Pro Ser Thr Pro Arg Pro Pro 70 75 Ser Ser Pro Ser Ala Pro Arg Gln Gly Ser Glu Ala Ala Ile Asn 85 90 Ala Leu Leu Pro Thr Pro Ser Met Ala Arg Ala Asp Pro Val Ser Phe 100 105 Arg Gln His Arg Ala Ile Ser Gly Ile Ser Phe Arg His Gln Gln Lys 120 Val Leu Arg Ile Leu Gly Lys Gln Glu Arg Gly Arg Gly Gly Gln Gly 135 His Asn Arg Glu Ala Asn Ser Ser Asn Pro Val Pro Ser Val Gly Arg 150 (2) INFORMATION FOR SEQ ID NO:2554: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 246 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..246 (D) OTHER INFORMATION: / Ceres Seq. ID 1601394 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554: aagaaaaaac attetttgte etetteteet eegeteeeca tttetettge tagggtttet accectecat atectegete caeggteatg gegaagaega ageagggaaa taaggaegtg 120 gattcgtaca ccatcggcgg caccaacaag gtcgtctatg tgggagactg cgtgctgatg 180 cgggcgtcgg actcggacaa ccagccgtat gtggcgcggg tggagaagat ggagggcgac 240 (2) INFORMATION FOR SEQ ID NO:2555: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1601395
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Lys Lys Lys His Ser Leu Ser Ser Pro Pro Leu Pro Ile Ser Leu
1 5 10 15

Ala Arg Val Ser Thr Pro Pro Tyr Pro Arg Ser Thr Val Met Ala Lys
20 25 30

Thr Lys Gln Gly Asn Lys Asp Val Asp Ser Tyr Thr Ile Gly Gly Thr
35 40 45

Asn Lys Val Val Tyr Val Gly Asp Cys Val Leu Met Arg Ala Ser Asp
50 55 60

Ser Asp Asn Gln Pro Tyr Val Ala Arg Val Glu Lys Met Glu Gly Asp
65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:2556:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 58 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

Gly Arg

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601396
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

Arg Lys Asn Ile Leu Cys Pro Leu Leu Leu Arg Ser Pro Phe Leu Leu  $1 ag{5} ag{15}$ 

Leu Gly Phe Leu Pro Leu His Ile Leu Ala Pro Arg Ser Trp Arg Arg 20 25 30

Arg Ser Arg Glu Ile Arg Thr Trp Ile Arg Thr Pro Ser Ala Ala Pro 35 40 45

Thr Arg Ser Ser Met Trp Glu Thr Ala Cys 50 55

- (2) INFORMATION FOR SEQ ID NO:2557:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 53 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..53
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601397
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

Gly Gly Thr Asn Lys Val Val Tyr Val Gly Asp Cys Val Leu Met Arg 20 25 30

Ala Ser Asp Ser Asp Asn Gln Pro Tyr Val Ala Arg Val Glu Lys Met 35 40 45

Glu Gly Asp Gly Arg 50

(2) INFORMATION FOR SEQ ID NO:2558:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601400
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

ccgaccaaga accagcatga agccactggt ggcggcctg ctectetget actecetget 60 ctggctggcg cccggcagg ccccgctacg cetgcagcac gatcatgtcc ggggccacgg 120 ccacggcat gccacccgc ctccgtacgc gcgtaacgcg acggcgtacg gcgtctcggc ggacgcgttgtg ccggggtggc ccgggtggc ggacgcgctc gagttcctct actaccacaa 240 cctggtgcgg tgggcgcgc agcgcgcgg ggactgcgg ctggcgcgc tggggcgcg agcgcgcgg ggactgcgg ctgcgcact ccttccccga 360 cggccagttc gcgctcggg agaacgtctt ctggggcggg c

- (2) INFORMATION FOR SEQ ID NO:2559:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 133 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..133
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601401
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

Arg Pro Arg Thr Ser Met Lys Pro Leu Val Ala Arg Leu Leu Cys
1 10 15

Tyr Ser Leu Leu Trp Leu Ala Pro Ala Ala Pro Leu Arg Leu Gln 20 25 30

His Asp His Val Arg Gly His Gly His Gly His Ala His Pro Pro Pro 35  $\phantom{\bigg|}40\phantom{\bigg|}45\phantom{\bigg|}$ 

Tyr Ala Arg Asn Ala Thr Ala Tyr Gly Val Ser Ala Ala Leu Cys Pro 50 55 60

Gly Cys Gly Ala Trp Ala Asp Ala Leu Glu Phe Leu Tyr Tyr His Asn 65 70 75 80
Leu Val Arg Leu Ala Ser Leu Glu Pro Pro Leu Ala Trp Ser Pro Arg

85 90 95 Leu Ala Ser Tyr Ala Gly Trp Trp Ala Ala Gln Arg Arg Gly Asp Cys

Leu Ala Ser Tyr Ala Gly Trp Trp Ala Ala Gln Arg Arg Gly Asp Cys
100 105 110

Ala Leu Arg His Ser Phe Pro Asp Gly Gln Phe Ala Leu Gly Glu Asn 115 120 125

Val Phe Trp Gly Gly 130

- (2) INFORMATION FOR SEQ ID NO:2560:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..128
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601402
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

Met Lys Pro Leu Val Ala Arg Leu Leu Cys Tyr Ser Leu Leu Trp

1 10 15

Leu Ala Pro Ala Ala Ala Pro Leu Arg Leu Gln His Asp His Val Arg 20 25 30

Gly His Gly His Gly His Ala His Pro Pro Pro Tyr Ala Arg Asn Ala 35 40 45

Thr Ala Tyr Gly Val Ser Ala Ala Leu Cys Pro Gly Cys Gly Ala Trp

- (2) INFORMATION FOR SEQ ID NO:2561:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..99
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601403
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

Val Thr Arg Arg Arg Thr Ala Ser Arg Arg Arg Cys Ala Arg Ala Ala
20 25 30

Ala Arg Gly Arg Thr Arg Ser Ser Ser Ser Thr Thr Thr Trp Cys 35 40 45

Gly Trp Arg Arg Trp Ser Arg Arg Trp Arg Gly Pro Arg Ala Trp Arg 50 55 60

Arg Thr Arg Ala Gly Gly Arg Arg Ser Ala Ala Gly Thr Ala Arg Cys 75 80

Ala Thr Pro Ser Pro Thr Ala Ser Ser Arg Ser Gly Arg Thr Ser Ser 85 90 95

Gly Ala Gly

- (2) INFORMATION FOR SEQ ID NO:2562:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..481
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601408
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

tcatatacgt gacagatgtt ggtcagcagc agcactttga catgttttc agtgctgcaa 60 agatggctgg ttggctgca ggtccaaacg aaaagaagtt tccgaaaaca agccatgttg 120 gatttggtct agttcttggt tcagatggca agcggttccg aacgcgcagt actgaggttg ttcgattggt agagctactt gatgaggcta aatctcggag caaatcagaa ctactacaac 240 ggctcactga aaatggcaaa attgttgact ggacggatga ggaattagag caaacttcag aggcagttgg atatggtgct gtgaagtatg ctgatctcaa gaataatcgt ctgacctaatt acacatttag ttttgaacaa attgctgagc gataagggaa atactgctgt gtaccttcag 420 tatgcacatg ctcgtatttt ggtccattat tcggaaatcc aacaaggatg tggaagatct 480

- (2) INFORMATION FOR SEQ ID NO:2563:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..130
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:
- Ile Tyr Val Thr Asp Val Gly Gln Gln His Phe Asp Met Phe Phe 1 5 10 15
- Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Gly Pro Asn Glu Lys Lys 20 25 30
- Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu Gly Ser Asp 35 40 45
- Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg Leu Val Glu
  50 55 60
- Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu Leu Gln Arg 65 70 75 80
- Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu Glu Leu Glu 85 90 95
- Gln Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu 100 105 110
- Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Ile Ala 115 120 125

Glu Arg 130

- (2) INFORMATION FOR SEQ ID NO:2564:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..117
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601410
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:
- Met Phe Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Gly Pro Asn 1 5 10 15
- Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu 20 25 30
- Gly Ser Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
  35 40 45
- Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu 50 55 60
- Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu 65 70 75 80
- Glu Leu Glu Gln Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr 85 90 95
- Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu 100 105 110
- Gln Ile Ala Glu Arg

- (2) INFORMATION FOR SEQ ID NO:2565:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 110 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..110 (D) OTHER INFORMATION: / Ceres Seq. ID 1601411 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565: Met Ala Gly Trp Leu Pro Gly Pro Asn Glu Lys Lys Phe Pro Lys Thr 10 Ser His Val Gly Phe Gly Leu Val Leu Gly Ser Asp Gly Lys Arg Phe 20 25 Arg Thr Arg Ser Thr Glu Val Val Arg Leu Val Glu Leu Leu Asp Glu 40 Ala Lys Ser Arg Ser Lys Ser Glu Leu Leu Gln Arg Leu Thr Glu Asn 60 55 Gly Lys Ile Val Asp Trp Thr Asp Glu Glu Leu Glu Gln Thr Ser Glu 75 70 Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys Asn Asn Arg 85 90 Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Ile Ala Glu Arg 105 100 (2) INFORMATION FOR SEQ ID NO:2566: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 363 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..363 (D) OTHER INFORMATION: / Ceres Seq. ID 1601416 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566: 60 accaggeace ageatagate tegtgetege cactattatt etgeacagea aegeateage 120 cttctqqaac catctcqccq ccqccacacc acaatccaca acccgtcgaa gcgaagcaag 180 caatggccgg agtcggatcg aaggccctcg ccgttgccgc cgttctggcg gccgtctcct 240 totogqtqqc eqeegeggcc gaggegeceg egeceagece egteteegec geegtegegg 300 cqtcqtcqcc cttcqccqcq gctctcqtcq cctccqccqc cqccttcctc ttcqccqccq 360 tecquactqa qecqatqqqq ceteqtqeet geaggetace tageagtact tecceegeeg (2) INFORMATION FOR SEQ ID NO: 2567: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..121 (D) OTHER INFORMATION: / Ceres Seq. ID 1601417 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567: Thr Arg His Gln His Arg Ser Arg Ala Arg His Tyr Tyr Ser Ala Gln Gln Arg Ile Ser Leu Leu Glu Pro Ser Arg Arg Arg His Thr Thr Ile 25 His Asn Pro Ser Lys Arg Ser Lys Gln Trp Pro Glu Ser Asp Arg Arg

35 40 45
Pro Ser Pro Leu Pro Pro Phe Trp Arg Pro Ser Pro Ser Arg Trp Pro

Pro Arg Pro Arg Pro Arg Pro Ala Pro Ser Pro Pro Pro Ser Arg

60

Arg Arg Pro Ser Pro Arg Leu Ser Ser Pro Pro Pro Pro Pro Ser 85 90 95

Ser Ser Pro Pro Ser Ala Leu Ser Arg Trp Gly Leu Val Pro Ala Gly 100 105 110

Tyr Leu Ala Val Leu Pro Pro Pro Pro 115 120

- (2) INFORMATION FOR SEQ ID NO:2568:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..102
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601418
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

Asn Ala Ser Ala Phe Trp Asn His Leu Ala Ala Ala Thr Pro Gln Ser

Thr Thr Arg Arg Ser Glu Ala Ser Asn Gly Arg Ser Arg Ile Glu Gly

Pro Arg Arg Cys Arg Arg Ser Gly Gly Arg Leu Leu Gly Gly Arg

Arg Gly Arg Gly Ala Arg Ala Gln Pro Arg Leu Arg Arg Arg Arg Gly 65 70 75 80

Val Val Ala Leu Arg Arg Gly Ser Arg Arg Leu Arg Arg Arg Leu Pro 85 90 95

Leu Arg Arg Pro His

100

- (2) INFORMATION FOR SEQ ID NO:2569:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..80
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601419
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

Met Ala Gly Val Gly Ser Lys Ala Leu Ala Val Ala Ala Val Leu Ala 1 5 10 15

Ala Val Ser Phe Ser Val Ala Ala Ala Ala Glu Ala Pro Ala Pro Ser 20 25 30

Pro Val Ser Ala Ala Val Ala Ala Ser Ser Pro Phe Ala Ala Ala Leu 35 40 45

Val Ala Ser Ala Ala Ala Phe Leu Phe Ala Ala Val Arg Thr Glu Pro 50 55 60

Met Gly Pro Arg Ala Cys Arg Leu Pro Ser Ser Thr Ser Pro Ala Ala 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:2570:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 494 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..494
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

acaccacacc	acacttacaa	taccagcaat	ccaqagcggg	gcagatctac	cgagacccgc	60
		cgccatggtg				120
		cttcttcccg				180
accgacccgc	tcctcgactg	ggcgcgcgag	gcgcactggt	ccatgggcgg	cttcggcgtg	240
aagggctcc	acctacaaaa	ccgcatcgag	ggctccatcg	acaagctccg	ccgccgcgcg	300
caccacaata	ccagggccaa	gaccaaggcc	cgctccgctg	gccacgtgcc	cgcctcgctg	360
tacacactca	gctccgagga	cgaggcggag	gaggtggcgg	cgccggagcg	ggggctcgtc	420
		cgggtccgac				480
tcgctgctat						
	-					

- (2) INFORMATION FOR SEQ ID NO:2571:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..164
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601421
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

Thr Glu Thr Arg Val Thr Glu Glu Arg Glu Ile Ala Met Val Val Ala
20 25 30

Leu Gly Pro Gly Arg Phe Tyr Gly Ser Gly Leu Pro Arg Pro Arg Phe 35 40 45

Phe Pro Gly Asp Arg Val Asp Pro Pro Ala Ser Val Thr Asp Pro Leu 50 55 60

Leu Asp Trp Ala Arg Glu Ala His Trp Ser Met Gly Gly Phe Gly Val

65 70 75 80
Lys Arg Leu Arg Leu Gln Gly Arg Ile Glu Gly Ser Ile Asp Lys Leu

85 90 95
Arg Arg Arg Ala Arg Arg Asp Ala Arg Ala Lys Thr Lys Ala Arg Ser
100 105 110

Ala Gly His Val Pro Ala Ser Leu Ser Pro Leu Gly Ser Glu Asp Glu
115 120 125

Ala Glu Glu Val Ala Ala Pro Glu Arg Gly Leu Val Val Asp Asp Val 130 135 140

Gly Ser Asn Gly Ser Asp Glu Ser Glu Gly Glu Glu Glu Asp Glu Pro 145 150 155 160

Ser Leu Leu Ser

- (2) INFORMATION FOR SEQ ID NO:2572:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..164
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572: Thr Ala Pro Arg Leu Gln Tyr Gln Gln Ser Arg Ala Gly Gln Ile Tyr 10 Arg Asp Pro Arg His Arg Gly Glu Arg Asp Arg His Gly Gly Ala Gly Thr Arg Pro Val Leu Arg Gln Arg Pro Ala Glu Ala Thr Leu Leu Pro Gly Arg Pro Arg Gly Pro Ala Gly Val Arg His Arg Pro Ala Pro Arg Leu Gly Ala Arg Gly Ala Leu Val His Gly Arg Leu Arg Arg Glu 70 Ala Pro Pro Pro Ala Gly Pro His Arg Gly Leu His Arg Gln Ala Pro 90 8.5 Pro Pro Arg Ala Pro Arg Cys Gln Gly Gln Asp Gln Gly Pro Leu Arg 105 Trp Pro Arg Ala Arg Leu Ala Val Pro Ala Arg Leu Arg Gly Arg Gly 115 120 Gly Gly Gly Gly Ala Gly Ala Gly Ala Arg Arg Arg Arg Gly 140 130 135 Leu Glu Arg Val Arg Arg Val Gly Gly Gly Gly Gly Arg Ala Leu 155 150 Ala Ala Ile Val

- (2) INFORMATION FOR SEQ ID NO:2573:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..136
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601423
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

Met Val Val Ala Leu Gly Pro Gly Arg Phe Tyr Gly Ser Gly Leu Pro 1 5 10 15

Arg Pro Arg Phe Phe Pro Gly Asp Arg Val Asp Pro Pro Ala Ser Val 20 25 30

Thr Asp Pro Leu Leu Asp Trp Ala Arg Glu Ala His Trp Ser Met Gly
35 40 45

Gly Phe Gly Val Lys Arg Leu Arg Leu Gln Gly Arg Ile Glu Gly Ser 50 55 60

Ile Asp Lys Leu Arg Arg Arg Ala Arg Asp Ala Arg Ala Lys Thr 65 70 75 80

Lys Ala Arg Ser Ala Gly His Val Pro Ala Ser Leu Ser Pro Leu Gly 85 90 95

Ser Glu Asp Glu Ala Glu Glu Val Ala Ala Pro Glu Arg Gly Leu Val

Val Asp Asp Val Gly Ser Asn Gly Ser Asp Glu Ser Glu Glu Glu 115 120 125

Glu Asp Glu Pro Ser Leu Leu Ser

- (2) INFORMATION FOR SEQ ID NO:2574:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 454 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601424
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574: cttaaccgca tcatcctttc cctcgcgccg ccgccaacgc aacccttgca gccccaatcc 60 ctcacagcaa ccatggctgg cgcgcaggag tccctctctc tggtgggcac gatgcgcggc 120 cacaacggcg aggtgacggc gatcgcgacc ccgatcgaca actcgccgtt catcgtttcc 180 tectecegeg acaagteect setggtgtgg gaeetgaeea acceggteea etecaeeeeg 240 gaateeggeg ecaeegeega etaeggegte ecetteegee geeteaeegg ecaeteeeae 300 360 ttegtecagg aegtegteet cagtteegae ggeeagtteg eeettteegg eteetgggat ggagagetee geetetggga eeteteeace ggeeteacea eeegeegett egteggeeac 420 gagaaggatg teeteteegt tgeettetee gttg
- (2) INFORMATION FOR SEQ ID NO:2575:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 151 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..151
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:
- Leu Asn Arg Ile Ile Leu Ser Leu Ala Pro Pro Pro Thr Gln Pro Leu 10 5
- Gln Pro Gln Ser Leu Thr Ala Thr Met Ala Gly Ala Gln Glu Ser Leu 25 30 2.0
- Ser Leu Val Gly Thr Met Arg Gly His Asn Gly Glu Val Thr Ala Ile 40
- Ala Thr Pro Ile Asp Asn Ser Pro Phe Ile Val Ser Ser Ser Arg Asp 55
- Lys Ser Xaa Leu Val Trp Asp Leu Thr Asn Pro Val His Ser Thr Pro 75 70
- Glu Ser Gly Ala Thr Ala Asp Tyr Gly Val Pro Phe Arg Arg Leu Thr 90 85 Gly His Ser His Phe Val Gln Asp Val Val Leu Ser Ser Asp Gly Gln
- 110 105 Phe Ala Leu Ser Gly Ser Trp Asp Gly Glu Leu Arg Leu Trp Asp Leu
- 125 120
- Ser Thr Gly Leu Thr Thr Arg Arg Phe Val Gly His Glu Lys Asp Val 140 135
- Leu Ser Val Ala Phe Ser Val
- 150 145
- (2) INFORMATION FOR SEQ ID NO:2576:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..127
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601426
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:
- Met Ala Gly Ala Gln Glu Ser Leu Ser Leu Val Gly Thr Met Arg Gly 5 10
- His Asn Gly Glu Val Thr Ala Ile Ala Thr Pro Ile Asp Asn Ser Pro 30 25
- Phe Ile Val Ser Ser Ser Arg Asp Lys Ser Xaa Leu Val Trp Asp Leu

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 40 35 Thr Asn Pro Val His Ser Thr Pro Glu Ser Gly Ala Thr Ala Asp Tyr 60 55 Gly Val Pro Phe Arg Arg Leu Thr Gly His Ser His Phe Val Gln Asp 75 70 Val Val Leu Ser Ser Asp Gly Gln Phe Ala Leu Ser Gly Ser Trp Asp 85 Gly Glu Leu Arg Leu Trp Asp Leu Ser Thr Gly Leu Thr Thr Arg Arg 105 Phe Val Gly His Glu Lys Asp Val Leu Ser Val Ala Phe Ser Val 120 125 115 (2) INFORMATION FOR SEQ ID NO:2577: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..114 (D) OTHER INFORMATION: / Ceres Seq. ID 1601427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577: Met Arg Gly His Asn Gly Glu Val Thr Ala Ile Ala Thr Pro Ile Asp 10 5 Asn Ser Pro Phe Ile Val Ser Ser Ser Arg Asp Lys Ser Xaa Leu Val 2.5 Trp Asp Leu Thr Asn Pro Val His Ser Thr Pro Glu Ser Gly Ala Thr 4.0 Ala Asp Tyr Gly Val Pro Phe Arg Arg Leu Thr Gly His Ser His Phe 55 Val Gln Asp Val Val Leu Ser Ser Asp Gly Gln Phe Ala Leu Ser Gly 75 70 Ser Trp Asp Gly Glu Leu Arg Leu Trp Asp Leu Ser Thr Gly Leu Thr 90 Thr Arg Arg Phe Val Gly His Glu Lys Asp Val Leu Ser Val Ala Phe 105 Ser Val (2) INFORMATION FOR SEQ ID NO:2578: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..292
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601428
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578: atccgaagtt ccgaacccaa gccaagcccc agggtccgac cgcagaaccg acccaaaatg tegecegect getecatget caccacegeg tegetetect eccegetece ageceegege ctccgcgccg ccgccgcctt cgctccgccg cgccgcgcgg cagtcacact cgtcgtgcgc 180 geggegteeg catettecaa gteecetgee aeggeggagg eggeeeegaa gaagaagagg 240 gcgaccggca tcacccagcc gaagtccgtg tcgccggcgc tgcaggcaat cg
- (2) INFORMATION FOR SEQ ID NO:2579:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..97
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601429
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:
- Ile Arg Ser Ser Glu Pro Lys Pro Ser Pro Arg Val Arg Pro Gln Asn 1 5 10 15
- Arg Pro Lys Met Ser Pro Ala Cys Ser Met Leu Thr Thr Ala Ser Leu 20 25 30
- Ser Ser Pro Leu Pro Ala Pro Arg Leu Arg Ala Ala Ala Ala Phe Ala 35 40 45
- Pro Pro Arg Arg Ala Ala Val Thr Leu Val Val Arg Ala Ala Ser Ala 50 55 60
- Ser Ser Lys Ser Pro Ala Thr Ala Glu Ala Ala Pro Lys Lys Lys Arg
  65 70 75 80
- Ala Thr Gly Ile Thr Gln Pro Lys Ser Val Ser Pro Ala Leu Gln Ala 85 90 95

Ile

- (2) INFORMATION FOR SEQ ID NO:2580:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601430
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:
- Ser Glu Val Pro Asn Pro Ser Gln Ala Pro Gly Ser Asp Arg Arg Thr 1 5 10 15
- Asp Pro Lys Cys Arg Pro Pro Ala Pro Cys Ser Pro Pro Arg Arg Ser 20 25 30
- Pro Pro Arg Ser Gln Pro Arg Ala Ser Ala Pro Pro Pro Pro Ser Leu 35 40 45
- Arg Arg Ala Ala Arg Gln Ser His Ser Ser Cys Ala Arg Arg Pro His 50 55 60
- Leu Pro Ser Pro Leu Pro Arg Arg Arg Arg Pro Arg Arg Arg Gly
  65 70 75 80
- Arg Pro Ala Ser Pro Ser Arg Ser Pro Cys Arg Arg Arg Cys Arg Gln 85 90 95

Ser

- (2) INFORMATION FOR SEQ ID NO:2581:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601431
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

  Pro Lys Phe Arg Thr Gln Ala Lys Pro Gln Gly Pro Thr Ala Glu Pro

  1 10 15

- (2) INFORMATION FOR SEQ ID NO:2582:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..496
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601445
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

aacagccatc acacgcacgc atacacagca cagagtgagg taagcatccg aaaaaagctg 60 tgatctgatc gacatggccg ccgccaccat ggctctcacc tcccgcgcgc tcgtcggcaa 120 gccggcgacc agcaccaggg acgtcttcgg cgaggggcgc atcaccatgc gcaagactgc 180 tggcaagccc aagccagegg egteeggeag eceetggtae ggggeegaec gegteetgta 240 cottgggcccc tgtccggcca gcccccaage tacctgaccg gcgagttccc cggcgactac 300 ggctgggaca ccgcggggct gtccgccgac ccggagactt tcgccaagaa ccgcgagctg 360 gaggtgatec actgeogetg ggccaatget gggcgcgcte gggtgcgtgt teceggaget 420 gctcgcccgc aacggcgtca agttcggcga ggccgtgtgg ttcaaggccg ggtccagatc ttcagcgagg gcgggc

- (2) INFORMATION FOR SEQ ID NO:2583:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..67
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601446
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

Pro Ala Thr Ser Thr Arg Asp Val Phe Gly Glu Gly Arg Ile Thr Met 20 25 30

Arg Lys Thr Ala Gly Lys Pro Lys Pro Ala Ala Ser Gly Ser Pro Trp  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Tyr Gly Ala Asp Arg Val Leu Tyr Leu Gly Pro Cys Pro Ala Ser Pro 50 60

Gln Ala Thr

- (2) INFORMATION FOR SEQ ID NO:2584:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 62 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..62 (D) OTHER INFORMATION: / Ceres Seq. ID 1601447 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584: Met Ala Leu Thr Ser Arg Ala Leu Val Gly Lys Pro Ala Thr Ser Thr 10 -5 Arg Asp Val Phe Gly Glu Gly Arg Ile Thr Met Arg Lys Thr Ala Gly 25 30 20 Lys Pro Lys Pro Ala Ala Ser Gly Ser Pro Trp Tyr Gly Ala Asp Arg 40 Val Leu Tyr Leu Gly Pro Cys Pro Ala Ser Pro Gln Ala Thr 50 55 (2) INFORMATION FOR SEQ ID NO:2585: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..37 (D) OTHER INFORMATION: / Ceres Seq. ID 1601448 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585: Met Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn 10 5 Gly Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Arg Ser 25 20 Ser Ala Arg Ala Gly 35 (2) INFORMATION FOR SEQ ID NO:2586: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 499 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..499 (D) OTHER INFORMATION: / Ceres Seq. ID 1601453 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586: aaaaaaccct atcqtccctc ccgcgcagcc accagcgaag cagcggggca cgcggacgag 60 ccgagcgagg cggaggcgga gagatggcgc gcggcgtggt ggctggggcg aagggtggtg 120 cggccggcgg cggcggcaag aagaagggct ccgtcacgtt cacgatcgac tgcaccaagc 180 240 ccgtcgagga caagatcatg gagatcgcca cgctcgagaa gttcctgcag gagcgcatca aggtcqctgg aggcaaggcc ggccagctcg gcgagggcgt caccgtcacc cgcgataagt 300 ccaaggtcac cgtcacctcc gacgggcctt tctctaagag gtacctgaaa tacttgacca 360 agaagtacct qaaqaagcac aatgtgcgtg actggctccg agttgtagcg gcaagcaagg 420 accgcagtgt astatgaget acggtacttc aacattgctg agaacgagga ggaataggcg 480 gcttagacct tatagacgc (2) INFORMATION FOR SEQ ID NO:2587: (i) SEQUENCE CHARACTERISTICS:
  - - (A) LENGTH: 115 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: peptide
    - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

Lys Lys Pro Tyr Arg Pro Ser Arg Ala Ala Thr Ser Glu Ala Ala Gly 1 5 10 15

His Ala Asp Glu Pro Ser Glu Ala Glu Ala Glu Arg Trp Arg Ala Ala 20 25 30

Trp Trp Leu Gly Arg Arg Val Val Arg Pro Ala Ala Ala Ala Arg Arg 35 40 45

Arg Ala Pro Ser Arg Ser Arg Ser Thr Ala Pro Ser Pro Ser Arg Thr 50 55 60

Arg Ser Trp Arg Ser Pro Arg Ser Arg Ser Ser Cys Arg Ser Ala Ser 65 70 75 80

Arg Ser Leu Glu Ala Arg Pro Ala Ser Ser Ala Arg Ala Ser Pro Ser 85 90 95

Pro Ala Ile Ser Pro Arg Ser Pro Ser Pro Pro Thr Gly Leu Ser Leu 100 105 110

Arg Gly Thr

115

- (2) INFORMATION FOR SEQ ID NO:2588:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 144 amino acids
      - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..144
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601455
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

Lys Thr Leu Ser Ser Leu Pro Arg Ser His Gln Arg Ser Ser Gly Ala 1 5 10 15

Arg Gly Arg Ala Glu Arg Gly Gly Gly Glu Met Ala Arg Gly Val 20 25 30

Val Ala Gly Ala Lys Gly Gly Ala Ala Gly Gly Gly Lys Lys
35
40
45

Gly Ser Val Thr Phe Thr Ile Asp Cys Thr Lys Pro Val Glu Asp Lys 50 60

Ile Met Glu Ile Ala Thr Leu Glu Lys Phe Leu Gln Glu Arg Ile Lys 65 70 75 80

Val Ala Gly Gly Lys Ala Gly Gln Leu Gly Glu Gly Val Thr Val Thr

85

90

95

Arg Asp Lys Ser Lys Val Thr Val Thr Ser Asp Gly Pro Phe Ser Lys 100 105 110

Arg Tyr Leu Lys Tyr Leu Thr Lys Lys Tyr Leu Lys Lys His Asn Val 115 120 125

Arg Asp Trp Leu Arg Val Val Ala Ala Ser Lys Asp Arg Ser Val Xaa 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2589:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide

- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

Met Ala Arg Gly Val Val Ala Gly Ala Lys Gly Gly Ala Ala Gly Gly 1 5 10 15

Pro Val Glu Asp Lys Ile Met Glu Ile Ala Thr Leu Glu Lys Phe Leu  $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$ 

Gln Glu Arg Ile Lys Val Ala Gly Gly Lys Ala Gly Gln Leu Gly Glu 50 55 60

Gly Val Thr Val Thr Arg Asp Lys Ser Lys Val Thr Val Thr Ser Asp 65 70 75 80

Gly Pro Phe Ser Lys Arg Tyr Leu Lys Tyr Leu Thr Lys Lys Tyr Leu 85 90 95

Lys Lys His Asn Val Arg Asp Trp Leu Arg Val Val Ala Ala Ser Lys  $100 \hspace{1cm} 105 \hspace{1cm} 110$ 

Asp Arg Ser Val Xaa

115

- (2) INFORMATION FOR SEQ ID NO:2590:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..492
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601457
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

60 ccaaataaat cttaacqaag gcattgaaga agatatccca ccgagccaat atgccaggtg tgaagagaaa ataactatga ctccagctgc catctcaagg gaagctggtc ttccaggata 120 tggtcctggt cctggagaaa actttcttca ggtcagttca aggaatacta gctgtgagca 180 gagtgtgata ctggctccta ccgctatcgc aagagaagtt ggtccaccag gatatgcgac 240 tggagaaaac cagcgcaatg gggctccatg gaatacaagt tatgagcgaa gactatttat 300 gaateetgtg accageteaa gageagteag teeteeagga tatgggeetg aagaaageeg 360 aggcagtggc atttcctgga atacaagcag tgaacaaata ttgtttatga gtcctacaac 420 catctcaaga gaacttggtc caccaggata tgggcctaga gaagaccagy gcagtggcac ttcatggaat gc

- (2) INFORMATION FOR SEQ ID NO:2591:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 163 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..163
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601458
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

Tyr Ala Arg Cys Glu Glu Lys Ile Thr Met Thr Pro Ala Ala Ile Ser 20 25 30

Arg Glu Ala Gly Leu Pro Gly Tyr Gly Pro Gly Pro Gly Glu Asn Phe
35 40 45

Leu Gln Val Ser Ser Arg Asn Thr Ser Cys Glu Gln Ser Val Ile Leu 50 60

Ala Pro Thr Ala Ile Ala Arg Glu Val Gly Pro Pro Gly Tyr Ala Thr

```
75
                  70
65
Gly Glu Asn Gln Arg Asn Gly Ala Pro Trp Asn Thr Ser Tyr Glu Arg
                                90
              85
Arg Leu Phe Met Asn Pro Val Thr Ser Ser Arg Ala Val Ser Pro Pro
                             105
          100
Gly Tyr Gly Pro Glu Glu Ser Arg Gly Ser Gly Ile Ser Trp Asn Thr
                                           125
                         120
       115
Ser Ser Glu Gln Ile Leu Phe Met Ser Pro Thr Thr Ile Ser Arg Glu
                                    140
                     135
Leu Gly Pro Pro Gly Tyr Gly Pro Arg Glu Asp Gln Xaa Ser Gly Thr
                          155
                  150
Ser Trp Asn
```

- (2) INFORMATION FOR SEQ ID NO:2592:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..138
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601459
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592: Met Thr Pro Ala Ala Ile Ser Arg Glu Ala Gly Leu Pro Gly Tyr Gly

1 5 10 15
Pro Gly Pro Gly Glu Asn Phe Leu Gln Val Ser Ser Arg Asn Thr Ser

Cys Glu Gln Ser Val Ile Leu Ala Pro Thr Ala Ile Ala Arg Glu Val

Gly Pro Pro Gly Tyr Ala Thr Gly Glu Asn Gln Arg Asn Gly Ala Pro
50 55 60

Trp Asn Thr Ser Tyr Glu Arg Arg Leu Phe Met Asn Pro Val Thr Ser 65 70 75 80 Ser Arg Ala Val Ser Pro Pro Gly Tyr Gly Pro Glu Glu Ser Arg Gly

85 90 95
Ser Gly Ile Ser Trp Asn Thr Ser Ser Glu Gln Ile Leu Phe Met Ser

100 105 110

Pro Thr Thr Ile Ser Arg Glu Leu Gly Pro Pro Gly Tyr Gly Pro Arg
115 120 125

- Glu Asp Gln Xaa Ser Gly Thr Ser Trp Asn 130 135
- (2) INFORMATION FOR SEQ ID NO:2593:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..484
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601476
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

  gtttctgga ggcttcctgc gcgtggagag acgggagaac gaagcagcag cagcagcag 60
  cgccatccgc tcgcttcctt ccccccaccg ccagcgtcgc ctctccgtgt gcgcgccccg 120
  ccgggggtgg cgtcactgca cccttggca gcgggcgcat acctacctac gtgcgggggg 180
  agccacacgc ctccctctcg cctcttggca tggacgcgg cggagagaag tgcggggag 240
  cggcggcgga gggcgggag ggtggcggag acctctacgc ggttctcggg ctcaagaagg 300
  agtgctccga cgccgagctt acggaagct accggaagct cgccaagaaa tggcacccgg 360

acaaatgctc gtcctccagc agcgtgaagc acatggagga agccaaggag aagttccaag 420 agatccaggg cgcctattcc gtactctccg acgccaataa acggctcctc tacgatgtgg 480 gagt

- (2) INFORMATION FOR SEQ ID NO:2594:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..128
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:
- Val Phe Trp Arg Leu Pro Ala Arg Gly Glu Thr Gly Glu Arg Ser Ser
- Ser Ser Ser Arg Arg His Pro Leu Ala Ser Phe Pro Pro Pro Pro Ala 20 25 30
- Ser Pro Leu Arg Val Arg Ala Pro Pro Gly Val Ala Ser Leu His Pro
- Trp Ala Ala Gly Ala Tyr Leu Pro Thr Cys Gly Gly Ser His Thr Pro 50 55 60
- Pro Ser Arg Leu Leu Ala Trp Thr Pro Ala Glu Arg Ser Ala Ala Thr 65 70 75 80
- Arg Arg Arg Ala Gly Arg Val Ala Glu Thr Ser Thr Arg Phe Ser 85 90 95
- Gly Ser Arg Arg Ser Ala Pro Thr Pro Ser Leu Arg Ser Leu Thr Gly
  100 105 110
- Ser Ser Pro Arg Asn Gly Thr Arg Thr Asn Ala Arg Pro Pro Ala Ala 115 120 125
- (2) INFORMATION FOR SEQ ID NO:2595:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..106
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601478
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:
- Phe Ser Gly Gly Phe Leu Arg Val Glu Arg Arg Glu Asn Glu Ala Ala

  1 10 15
- Ala Ala Gly Ala Ile Arg Ser Leu Pro Ser Pro His Arg Gln Arg 20 25 30
- Arg Leu Ser Val Cys Ala Pro Arg Arg Gly Trp Arg His Cys Thr Leu 35 40 45
- Gly Gln Arg Ala His Thr Tyr Leu Arg Ala Gly Gly Ala Thr Arg Leu 50 55 60
- Pro Leu Ala Ser Trp His Gly Arg Arg Arg Glu Val Arg Arg Arg 65 70 75 80
- Gly Gly Gly Arg Gly Gly Trp Arg Arg Pro Leu Arg Gly Ser Arg 85 90 95
- Ala Gln Glu Gly Val Leu Arg Arg Ala 100 105
- (2) INFORMATION FOR SEQ ID NO:2596:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..160
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601479
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:

Phe Leu Glu Ala Ser Cys Ala Trp Arg Asp Gly Arg Thr Lys Gln Gln 1 5 10 15

Gln Gln Gln Ala Pro Ser Ala Arg Phe Leu Pro Pro Thr Ala Ser Val $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$ 

Ala Ser Pro Cys Ala Arg Pro Ala Gly Gly Gly Val Thr Ala Pro Leu 35 40 45

Gly Ser Gly Arg Ile Pro Thr Tyr Val Arg Gly Glu Pro His Ala Ser 50 55 60

Leu Ser Pro Leu Gly Met Asp Ala Gly Gly Glu Lys Cys Gly Asp Ala 65 70 75 80

Ala Ala Glu Gly Gly Gly Gly Gly Asp Leu Tyr Ala Val Leu Gly 85 90 95

Leu Ala Lys Lys Trp His Pro Asp Lys Cys Ser Ser Ser Ser Ser Val115 120 125

Lys His Met Glu Glu Ala Lys Glu Lys Phe Gln Glu Ile Gln Gly Ala 130  $\phantom{000}$  135  $\phantom{000}$  140

Tyr Ser Val Leu Ser Asp Ala Asn Lys Arg Leu Leu Tyr Asp Val Gly 145 150 155 160

- (2) INFORMATION FOR SEQ ID NO:2597:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..491
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601480
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:

acgtagtaag ctgggattct tcgtatagac cggattaaaa ccctaggccc tagccaccgc 60 ccaccytege etcageaaat ceteeteeg ttteaceatg eegeeetget geteeceeae 120 caecteegee gteacegetg eggeggeate teeeggegee tegegeageg ggggeeteet 180 gegeegeteg egeceagece eegeegeegt gaattgtaaa aagattgatt etetgaggte 240 aatcaatgga gcaccacctt gcattccggt gtccaacagg tcgttattga ctcctgtaac 300 360 cttqccaqtt ttccqqqatc caaacatqaq qaacqacacq agqctqcqca tcttctcaqq cacaqccaat ccttcccttt cccaqqaqat aqcaaqttac ttqqqqctaq aacttqqgaa 420 gataaccata aagaggtttg ctgatggtga aatatatgtt cagttgcaag aaagtgtacg 480 gggctgtgat g

- (2) INFORMATION FOR SEQ ID NO:2598:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601481
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:

Met Pro Pro Cys Cys Ser Pro Thr Thr Ser Ala Val Thr Ala Ala Ala 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15

Ala Ser Pro Gly Ala Ser Arg Ser Gly Gly Leu Leu Arg Arg Ser Arg  $20 \\ 25 \\ 30$ 

Pro Ala Pro Ala Ala Val As<br/>n Cys Lys Lys Ile Asp Ser Leu Arg Ser 35 40 45

Ile Asn Gly Ala Pro Pro Cys Ile Pro Val Ser Asn Arg Ser Leu Leu 50 55 60

Thr Pro Val Thr Leu Pro Val Phe Arg Asp Pro Asn Met Arg Asn Asp 65 70 75 80

Thr Arg Leu Arg Ile Phe Ser Gly Thr Ala Asn Pro Ser Leu Ser Gln 85 90 95

Glu Ile Ala Ser Tyr Leu Gly Leu Glu Leu Gly Lys Ile Thr Ile Lys 100 105 110

Arg Phe Ala Asp Gly Glu Ile Tyr Val Gl<br/>n Leu Gl<br/>n Glu Ser Val Arg 115 120 125

Gly Cys Asp 130

- (2) INFORMATION FOR SEQ ID NO:2599:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..408
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601483
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

aatctactcc tocattctcc accgcgcccc aacctcgaag agttccgaag tttccacacc 60 ctcaaagcga agcagcatga gttccaccgg aggcagcggc cgtgggaagg cgaagccagc 120 gaccaagtct gtgtcgcggt cttccaaggc tgggctccag ttccccgtcg gccgcatcgc 180 gcggtacctc aaggccggca agtacgcgga gcgcgtaggc gccggggctc ccgtgtacct 240 ctccgccgtc ctcgagtacc tcgccgccga ggtgctggag ctggccggga acgctgctcg ggaccacacaag aagaaccgga tcgtgccgcg ccacattcag ctggcggtc ggaacgacga 360 ggagctgagc aagcttctgg gcactgtgac gatcgcggcc ggcggcgt

- (2) INFORMATION FOR SEQ ID NO:2600:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..136
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601484
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Asn Leu Leu His Ser Pro Pro Arg Pro Asn Leu Glu Glu Phe Arg 1 5 10 15

Ser Phe His Thr Leu Lys Ala Lys Gln His Glu Phe His Arg Arg Gln 20 25 30

Arg Pro Trp Glu Gly Glu Ala Ser Asp Gln Val Cys Val Ala Val Phe 35 40 45

Gln Gly Trp Ala Pro Val Pro Arg Arg Pro His Arg Ala Val Pro Gln 50 55

Gly Arg Gln Val Arg Gly Ala Arg Arg Arg Arg Gly Ser Arg Val Pro 65 70 75 80
Leu Arg Arg Pro Arg Val Pro Arg Arg Arg Gly Ala Gly Ala Gly Arg

85 90 95

Glu Arg Cys Ser Gly Gln Gln Glu Glu Pro Asp Arg Ala Ala Pro His
100 105 110

Ser Ala Gly Gly Ala Glu Arg Arg Gly Ala Glu Gln Ala Ser Gly His 115 120 125

Cys Asp Asp Arg Gly Arg Arg Arg 130 135

- (2) INFORMATION FOR SEQ ID NO:2601:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 135 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..135
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

Ile Tyr Ser Ser Ile Leu His Arg Ala Pro Thr Ser Lys Ser Ser Glu  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Val Ser Thr Pro Ser Lys Arg Ser Ser Met Ser Ser Thr Gly Gly Ser 20 25 30

Gly Arg Gly Lys Ala Lys Pro Ala Thr Lys Ser Val Ser Arg Ser Ser 35 40 45

Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Ala Arg Tyr Leu Lys 50 60

Ala Gly Lys Tyr Ala Glu Arg Val Gly Ala Gly Ala Pro Val Tyr Leu 65 70 75 80 Ser Ala Val Leu Glu Tyr Leu Ala Ala Glu Val Leu Glu Leu Ala Gly

85 90 95
Asn Ala Ala Arg Asp Asn Lys Lys Asn Arg Ile Val Pro Arg His Ile

100 105 110 Gln Leu Ala Val Arg Asn Asp Glu Glu Leu Ser Lys Leu Leu Gly Thr

120

115 Val Thr Ile Ala Ala Gly Gly 130

- (2) INFORMATION FOR SEQ ID NO:2602:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 110 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..110
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

Lys Ser Val Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro Val Gly 20 25 30

Arg Ile Ala Arg Tyr Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly 35 40 45

Ala Gly Ala Pro Val Tyr Leu Ser Ala Val Leu Glu Tyr Leu Ala Ala 50 55 60 60 Glu Val Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Asn

65 70 75 Arg Ile Val Pro Arg His Ile Gln Leu Ala Val Arg Asn Asp Glu Glu 85 90 Leu Ser Lys Leu Leu Gly Thr Val Thr Ile Ala Ala Gly Gly 105 (2) INFORMATION FOR SEQ ID NO: 2603: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..482 (D) OTHER INFORMATION: / Ceres Seq. ID 1601495 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603: acacgatcaa aaacaaaacc aagctccaag cacccatagc cacaccac accaagtcaa 60 120 gcaaggaget cgatcgacag caacaacgge catcatgaac tecagettea tegggeteaa gcccgctgcg gcagcagccc aggccaccgc ggctgcctcg tcgccgatga agcagcagca 180 ggtgcaggtc gcgccccaga gccgccgcgc cgcgctgctc ggcctggcgg ccgtcttcgc 240 300 cgtcaccgcc accacggccg gatcagccaa ggctggggtc ttcgacgagt acctcgagaa 360 gagcaaggct aacaaggagc tgaacgacaa gaagaggatg gccaccagcg ctgccaactt tgcgcgcgcc tacacagtcg agttcggcag ctgccagttc ccctacaact tcactgggtg 420 ccaggacctc gccaagcaga agaaagtccc tttcctcagc gacgacctcg agatcgagtg 480 cg (2) INFORMATION FOR SEQ ID NO:2604: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1601496 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604: His Asp Gln Lys Gln Asn Gln Ala Pro Ser Thr His Ser His Thr Pro 10 His Gln Val Lys Gln Gly Ala Arg Ser Thr Ala Thr Thr Ala Ile Met 2.0 25

Asn Ser Ser Phe Ile Gly Leu Lys Pro Ala Ala Ala Ala Gln Ala 40 Thr Ala Ala Ala Ser Ser Pro Met Lys Gln Gln Val Gln Val Ala 55 Pro Gln Ser Arg Arg Ala Ala Leu Leu Gly Leu Ala Ala Val Phe Ala 75 Val Thr Ala Thr Thr Ala Gly Ser Ala Lys Ala Gly Val Phe Asp Glu 90 Tyr Leu Glu Lys Ser Lys Ala Asn Lys Glu Leu Asn Asp Lys Lys Arg 105 Met Ala Thr Ser Ala Ala Asn Phe Ala Arg Ala Tyr Thr Val Glu Phe 120 Gly Ser Cys Gln Phe Pro Tyr Asn Phe Thr Gly Cys Gln Asp Leu Ala 135 140 Lys Gln Lys Lys Val Pro Phe Leu Ser Asp Asp Leu Glu Ile Glu Cys 145 150 155 160

Client Docket No. 80146.003 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..129 (D) OTHER INFORMATION: / Ceres Seq. ID 1601497 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605: Met Asn Ser Ser Phe Ile Gly Leu Lys Pro Ala Ala Ala Ala Gln 1 5 10 Ala Thr Ala Ala Ala Ser Ser Pro Met Lys Gln Gln Gln Val Gln Val 20 25 Ala Pro Gln Ser Arg Arg Ala Ala Leu Leu Gly Leu Ala Ala Val Phe 40 Ala Val Thr Ala Thr Thr Ala Gly Ser Ala Lys Ala Gly Val Phe Asp 55 Glu Tyr Leu Glu Lys Ser Lys Ala Asn Lys Glu Leu Asn Asp Lys Lys 70 Arg Met Ala Thr Ser Ala Ala Asn Phe Ala Arg Ala Tyr Thr Val Glu 90 85 Phe Gly Ser Cys Gln Phe Pro Tyr Asn Phe Thr Gly Cys Gln Asp Leu 100 105 110 Ala Lys Gln Lys Lys Val Pro Phe Leu Ser Asp Asp Leu Glu Ile Glu 125 120 Cys (2) INFORMATION FOR SEQ ID NO:2606: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..105 (D) OTHER INFORMATION: / Ceres Seq. ID 1601498 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606: Met Lys Gln Gln Gln Val Gln Val Ala Pro Gln Ser Arg Arg Ala Ala 5 10 Leu Leu Gly Leu Ala Ala Val Phe Ala Val Thr Ala Thr Thr Ala Gly 25 2.0 Ser Ala Lys Ala Gly Val Phe Asp Glu Tyr Leu Glu Lys Ser Lys Ala 45 40 35 Asn Lys Glu Leu Asn Asp Lys Lys Arg Met Ala Thr Ser Ala Ala Asn 60 55 Phe Ala Arg Ala Tyr Thr Val Glu Phe Gly Ser Cys Gln Phe Pro Tyr 75 70 Asn Phe Thr Gly Cys Gln Asp Leu Ala Lys Gln Lys Lys Val Pro Phe

90

100 (2) INFORMATION FOR SEQ ID NO:2607:

Leu Ser Asp Asp Leu Glu Ile Glu Cys

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE:

  - (A) NAME/KEY: -
  - (B) LOCATION: 1..474
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601499
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

ccaatcgctg ctgcgggcgt gtaactcgaa tgagagagag ctattaataa gtcatgtaga 60 aaacgtgcac cttcaagctg agctaaaacc tttcatttat tttcaccatt catcctgttg 120 cgaccatctt tggattataa atagcttgcc agagccagcg gatccagcag agcacgagac 180 acccaagaaa cacacagaag cgaggagcac tacttgttgg ttggattctc ttcagtctag 240 cagctagtcc agttaagttt cagacacaca tggggagcat tggcagaggc acggccaact 300 gcgccaccgt gccgcagccg ccgccgtcga cagggaagct catcacgatc ctgagcatcg 360 atggcggcgg catccgcggc cttatcccgg cgaccatcat tgcgtacctc gaggccaage 420 tccaggagct ggacggcccg gacgctcgga tcgccgacta cttcgatgtg attg

- (2) INFORMATION FOR SEQ ID NO:2608:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..81
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601500
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

Gln Ser Leu Leu Arg Ala Cys Asn Ser Asn Glu Arg Glu Leu Leu Ile 10

Ser His Val Glu Asn Val His Leu Gln Ala Glu Leu Lys Pro Phe Ile 20 25

Tyr Phe His His Ser Ser Cys Cys Asp His Leu Trp Ile Ile Asn Ser 40

Leu Pro Glu Pro Ala Asp Pro Ala Glu His Glu Thr Pro Lys Lys His 55 60

Thr Glu Ala Arg Ser Thr Thr Cys Trp Leu Asp Ser Leu Gln Ser Ser 65 70 7.5 Ser

- (2) INFORMATION FOR SEQ ID NO: 2609:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..68
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601501
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:

Met Gly Ser Ile Gly Arg Gly Thr Ala Asn Cys Ala Thr Val Pro Gln 10

Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly 25

Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu 40

Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr 50

Phe Asp Val Ile

(2) INFORMATION FOR SEQ ID NO:2610:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 539 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..539
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601502
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610: 60 aaaccctcat ttttctctct cctgcgccgc gacgtccctc gccttcgccg ccgaatccga gactecgate tegggtteac egeagegeae agageageet egactecegg ecegateege 120 180 gctctcctct ccgtcgcttc agtcatggca ggaatggcac ctgagggttc tcagttcgat gctaagcact atgattctaa gatgcaggag ctgctgagca ccggtgagac tgaggagttc 240 ttcacttcat atgatgaagt ttttgagagt tttgatgata tgggcctcca agagaatctt 300 ctgagaggca tttatgctta tggttttgag aagccatctg caattcagca gagaggaatt 360 gttcccttct gcaagggtct tgatgtcatt cagcaagcac aatctggtac aggaaagaca 420 gcaaccttct gttctgggat cttgcagcag ctggactatg gcctggttga atgccaggcc 480 ctggtccttg ctcccacccc gtgagcttgc acagcaaatc gagaaagtca tgcgcgcgc
- (2) INFORMATION FOR SEQ ID NO:2611: (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..167
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601503
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

20 25 30

Ala Ser Thr Pro Gly Pro Ile Arg Ala Leu Leu Ser Val Ala Ser Val

35 40 45
Met Ala Gly Met Ala Pro Glu Gly Ser Gln Phe Asp Ala Lys His Tyr

Met Ala Gly Met Ala Pro Glu Gly Ser Gln Phe Asp Ala Lys Mis Tyl
50 55 60
Asp Ser Lys Met Gln Glu Leu Leu Ser Thr Gly Glu Thr Glu Glu Phe

65 70 75 80
Phe Thr Ser Tyr Asp Glu Val Phe Glu Ser Phe Asp Asp Met Gly Leu
85 90 95

65 90 95

Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro
100 105 110

Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp

Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys

Ser Gly Ile Leu Gln Gln Leu Asp Tyr Gly Leu Val Glu Cys Gln Ala 145 150 155 160

Leu Val Leu Ala Pro Thr Pro

- (2) INFORMATION FOR SEQ ID NO: 2612:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 119 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

Met Ala Gly Met Ala Pro Glu Gly Ser Gln Phe Asp Ala Lys His Tyr 1 5 10 15

Asp Ser Lys Met Gln Glu Leu Leu Ser Thr Gly Glu Thr Glu Glu Phe 20 25 30

Phe Thr Ser Tyr Asp Glu Val Phe Glu Ser Phe Asp Asp Met Gly Leu 35 40 45

Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro 50 55 60

Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp
65 70 75 80

Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys
85 90 95

Ser Gly Ile Leu Gln Gln Leu Asp Tyr Gly Leu Val Glu Cys Gln Ala  $100 \,$   $105 \,$   $110 \,$ 

Leu Val Leu Ala Pro Thr Pro 115

- (2) INFORMATION FOR SEQ ID NO:2613:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 116 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..116
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

Met Ala Pro Glu Gly Ser Gln Phe Asp Ala Lys His Tyr Asp Ser Lys

1 10 15

Met Gln Glu Leu Leu Ser Thr Gly Glu Thr Glu Glu Phe Phe Thr Ser 20 25 30

Tyr Asp Glu Val Phe Glu Ser Phe Asp Asp Met Gly Leu Gln Glu Asn 35 40 45

Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
50 55 60

Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp Val Ile Gln
65 70 75 80

Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser Gly Ile 85 90 95 Leu Gln Gln Leu Asp Tyr Gly Leu Val Glu Cys Gln Ala Leu Val Leu

105

Ala Pro Thr Pro

115

- (2) INFORMATION FOR SEQ ID NO: 2614:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..472
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601510
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

ctagcetecg cccatacaca cacageecca tecegeege geaggegaga accagegeca 60 cettaggtta gggeggeege egeeggagaa gtgegeggtt gecaagatge agatetegt 120 gaagaceetg acggggaaga ccateaeget ggaggtggag teeteggaca ceategacaa 180 cgtgaaggee aagateeagg acaaggaggg cateeeggeeg gaeeageage geeteatett 240 cgeeggeaat cagetegag atggeegeae cetegeegae tacaacatee agaaggagte 300 caceaaggee aagaagatea ageecaagga aggegeeaag aageegeaga agaagaegta 360 caceaaggtt gaegaegee eeggeaaggt cacegeetee geaaggatg ce

- (2) INFORMATION FOR SEQ ID NO:2615:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 122 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..122
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601511
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu 1 5 10 15

Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Asn 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ala Lys Lys Arg 65 70 75 80
Lys Lys Lys Thr Tyr Thr Lys Pro Lys Lys Lys His Lys His Lys Lys

85 90 95
Lys Val Lys Leu Ala Val Leu Gln Phe Tyr Lys Val Asp Asp Ala Thr

110

100 105
Gly Lys Val Thr Ala Ser Ala Arg Ser Ala
115 120

- 115 120 (2) INFORMATION FOR SEQ ID NO:2616:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 410 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..410
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601516
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

aatcagggaa aaaatccatt tecettett etgaagtegt eetettette eegtegette 60 geegtgeege acetgegag agaggagaet tegeegegaa geteaceatg atetegeegg 120 agaggagete geegteegg eggeggeggg ggegeegtte etgtegatet 180 eegteacgga teeegtaaag atgggtaeeg gegtgeagte etacatetee tacegegtea gteaceagae eaaceteeet gaatttgagg gaccagagaa aattgttatt eggeggetata 300 gtgattttga atggttgeat gateggettg etgagaggta eaaaggeatt tetataeeee ctetteegga gaagaatget gttgagaaat teeggtttag caagggagtte

- (2) INFORMATION FOR SEQ ID NO:2617:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..136
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601517
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

Ser Gly Lys Lys Ser Ile Ser Leu Ser Ser Glu Val Val Leu Phe Phe 1 5 10 15

Lys Leu Thr Met Ile Ser Pro Glu Arg Ser Ser Ser Gln Ser Gln Arg 35 40 45

Ser Ala Ala Ala Gly Ala Pro Phe Leu Ser Ile Ser Val Thr Asp Pro 50 55 60

Val Lys Met Gly Thr Gly Val Gln Ser Tyr Ile Ser Tyr Arg Val Ile 65 70 75 80

Arg Arg Tyr Ser Asp Phe Glu Trp Leu His Asp Arg Leu Ala Glu Arg 100 105 110

Tyr Lys Gly Ile Phe Ile Pro Pro Leu Pro Glu Lys Asn Ala Val Glu 115 120 125

Lys Phe Arg Phe Ser Lys Glu Phe 130 135

- (2) INFORMATION FOR SEQ ID NO:2618:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..101
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601518
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

Met Ile Ser Pro Glu Arg Ser Ser Ser Gln Ser Gln Arg Ser Ala Ala 1 5 10 15

Ala Gly Ala Pro Phe Leu Ser Ile Ser Val Thr Asp Pro Val Lys Met 20 25 30

Gly Thr Gly Val Gln Ser Tyr Ile Ser Tyr Arg Val Ile Thr Lys Thr 35 40 45

Asn Leu Pro Glu Phe Glu Gly Pro Glu Lys Ile Val Ile Arg Arg Tyr 50 55 60

Ser Asp Phe Glu Trp Leu His Asp Arg Leu Ala Glu Arg Tyr Lys Gly 65 70 75 80

Ile Phe Ile Pro Pro Leu Pro Glu Lys Asn Ala Val Glu Lys Phe Arg 85 90 95

Phe Ser Lys Glu Phe

- (2) INFORMATION FOR SEQ ID NO:2619:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..70
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601519

120

180

240

300

360

420

480

30

95

110

45

60

75

90

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Client Docket No. 80146.003
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:
Met Gly Thr Gly Val Gln Ser Tyr Ile Ser Tyr Arg Val Ile Thr Lys
                                     10
Thr Asn Leu Pro Glu Phe Glu Gly Pro Glu Lys Ile Val Ile Arg Arg
                                 25
            20
Tyr Ser Asp Phe Glu Trp Leu His Asp Arg Leu Ala Glu Arg Tyr Lys
                            40
Gly Ile Phe Ile Pro Pro Leu Pro Glu Lys Asn Ala Val Glu Lys Phe
Arg Phe Ser Lys Glu Phe
(2) INFORMATION FOR SEQ ID NO:2620:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 495 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..495
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601523
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:
gggatcccgc ctcacaccgc cgcaaggact cgcgacggac ggagcaacgg aggaagcaac
tacgcggcag ccatggtgaa cgttccgaaa accaagaaga cctactgtaa gaacaaggaa
tgcaggaagc acaccctgca caaggttacc cagtacaaga aaggtaagga tagcctttca
gctcaaggga agcgacgtta tgaccgcaaa cagtctggat atggtggtca gacaaagcct
gttttccaca agaaggcaaa aacaacaaag aagattgtgc tgaagctgca gtgccagagc
tgcaagcact actctcaaca cccgatcaag aggtgcaagc actttgagat cggtggtgac
 aagaaaggca agggaacctc tctgttctaa gcgtatcata aacttgctca gggtctcaag
 tatctgtcag aatttaccat tacaaacacc ctgtgcttag cttctgcata tgttcttttg
 tcacatcttt ttggt
 (2) INFORMATION FOR SEQ ID NO:2621:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 129 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..129
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601524
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:
 Gly Ile Pro Pro His Thr Ala Ala Arg Thr Arg Asp Gly Arg Ser Asn
                                      10
                 5
 Gly Gly Ser Asn Tyr Ala Ala Ala Met Val Asn Val Pro Lys Thr Lys
```

25 Lys Thr Tyr Cys Lys Asn Lys Glu Cys Arg Lys His Thr Leu His Lys

Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu Ser Ala Gln Gly Lys

Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly Gln Thr Lys Pro

Val Phe His Lys Lys Ala Lys Thr Thr Lys Lys Ile Val Leu Lys Leu

Gln Cys Gln Ser Cys Lys His Tyr Ser Gln His Pro Ile Lys Arg Cys

Lys His Phe Glu Ile Gly Gly Asp Lys Lys Gly Lys Gly Thr Ser Leu 120

70

85

Phe

(2) INFORMATION FOR SEQ ID NO: 2622: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..105 (D) OTHER INFORMATION: / Ceres Seq. ID 1601525 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622: Met Val Asn Val Pro Lys Thr Lys Lys Thr Tyr Cys Lys Asn Lys Glu 5 10 Cys Arg Lys His Thr Leu His Lys Val Thr Gln Tyr Lys Lys Gly Lys 25 Asp Ser Leu Ser Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser 40 Gly Tyr Gly Gly Gln Thr Lys Pro Val Phe His Lys Lys Ala Lys Thr 55 Thr Lys Lys Ile Val Leu Lys Leu Gln Cys Gln Ser Cys Lys His Tyr 70 75 Ser Gln His Pro Ile Lys Arg Cys Lys His Phe Glu Ile Gly Gly Asp 85 90 Lys Lys Gly Lys Gly Thr Ser Leu Phe 100 (2) INFORMATION FOR SEQ ID NO: 2623: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..382 (D) OTHER INFORMATION: / Ceres Seq. ID 1601526 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623: agaacatcet aategaacac caatggcatt cttgcattga aggaacette cetecacete caccgcccga gagcgagcgg ccggacgggg ttttggttgg gcatggctgc cccggcgatg 120 ctccaagtgg tgatcctcgc cgcggtcctc cttctcccgt tcctcagcgt gccgggcgcc 180 240 gaggeacaga ccaagaagtt etgeeteacg eagttegeea tegetageea ggeetgegee 300 atectgecae ecaceaqtee tgageaceae caceateate acgatgaega ggacaatgae gaggacaacg acgaagatga ggacgaagac gaggacaacg atgaagatga agacgaggac aatgacgacg atagcggcgg tg (2) INFORMATION FOR SEQ ID NO:2624: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..74 (D) OTHER INFORMATION: / Ceres Seq. ID 1601527 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624: Asn Ile Leu Ile Glu His Gln Trp His Ser Cys Ile Glu Gly Thr Phe

10

Pro Pro Pro Pro Pro Glu Ser Glu Arg Pro Asp Gly Val Leu Val

Client Docket No. 80146.003 2.5 20 Gly His Gly Cys Pro Gly Asp Ala Pro Ser Gly Asp Pro Arg Arg Gly 4.5 40 Pro Pro Ser Pro Val Pro Gln Arg Ala Gly Arg Arg Gly Thr Asp Gln 55 Glu Val Leu Pro His Ala Val Arg His Arg 70 (2) INFORMATION FOR SEQ ID NO:2625: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1601528 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625: Met Ala Ala Pro Ala Met Leu Gln Val Val Ile Leu Ala Ala Val Leu 10 5 Leu Leu Pro Phe Leu Ser Val Pro Gly Ala Glu Ala Gln Thr Lys Lys 20 25 Phe Cys Leu Thr Gln Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile Leu 40 Pro Pro Thr Ser Pro Glu His His His His His Asp Asp Glu Asp 55 Asn Asp Glu Asp Asn Asp Glu Asp Glu Asp Glu Asp Asn Asp 70 Glu Asp Glu Asp Glu Asp Asn Asp Asp Ser Gly Gly 85 (2) INFORMATION FOR SEQ ID NO:2626: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 88 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..88 (D) OTHER INFORMATION: / Ceres Seq. ID 1601529 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626: Met Leu Gln Val Val Ile Leu Ala Ala Val Leu Leu Pro Phe Leu 10 5 Ser Val Pro Gly Ala Glu Ala Gln Thr Lys Lys Phe Cys Leu Thr Gln 25 20 Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile Leu Pro Pro Thr Ser Pro 4.5 40 Glu His His His His His Asp Asp Glu Asp Asn Asp Glu Asp Asn 60 55 Asp Glu 7.5 70 Asp Asn Asp Asp Ser Gly Gly 85 (2) INFORMATION FOR SEQ ID NO:2627: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..493
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601536
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627: 60 actacaatac tgctgcgcgc tagcggtagc gctcgcgctc ccactcgcac cacagcacgc caccgctgct gcggctcctc cccgcgctcg cattgcgatt tgcgacctag cgcgagggta 120 180 ccgggggtgg tgcgcgtgct ccgtgatccg ggaagcgccg cgagatggcc gggggcggag geggeggtge egegeegaag caegaegaet teaegeegea eeeegteaag gaeeagetee 240 ctggggtctc ctactgcatc accagccctc ccccgtggcc tgaagccgtt cttcttgggt 300 360 tocaacatta totggtcatg ottggtacca otgtgatcat accaactgca ottgttccac aaatgggagg aaacaatgag gacaaagcag tggttatcca gacattgctg ttcgttgcag 420 480 gtatcaacac cctcctgcag agtttctttg gtaccatgtt gcctgcagtg atcggcgggt catacacctt tgt
- (2) INFORMATION FOR SEQ ID NO:2628:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 111 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..111
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:
- Thr Thr Ile Leu Leu Arg Ala Ser Gly Ser Ala Arg Ala Pro Thr Arg
  1 5 10 15
- Thr Thr Ala Arg His Arg Cys Cys Gly Ser Ser Pro Arg Ser His Cys
  20 25 30
- Asp Leu Arg Pro Ser Ala Arg Val Pro Gly Val Val Arg Val Leu Arg 35 40 45
- Asp Pro Gly Ser Ala Ala Arg Trp Pro Gly Ala Glu Ala Ala Val Pro 50 60
- Arg Arg Ser Thr Thr Thr Ser Arg Arg Thr Pro Ser Arg Thr Ser Ser 65 70 75 80
- Leu Gly Ser Pro Thr Ala Ser Pro Ala Leu Pro Arg Gly Leu Lys Pro 85 90 95
- Phe Phe Leu Gly Ser Asn Ile Ile Trp Ser Cys Leu Val Pro Leu 100 105 110
- (2) INFORMATION FOR SEQ ID NO:2629:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 93 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..93
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601538
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:
- Leu Gln Tyr Cys Cys Ala Leu Ala Val Ala Leu Ala Leu Pro Leu Ala
- Pro Gln His Ala Thr Ala Ala Ala Ala Pro Pro Arg Ala Arg Ile Ala 20 25 30
- Ile Cys Asp Leu Ala Arg Gly Tyr Arg Gly Trp Cys Ala Cys Ser Val 35 40 45
- Ile Arg Glu Ala Pro Arg Asp Gly Arg Gly Arg Arg Arg Arg Cys Arg 50 55 60

Ala Glu Ala Arg Arg Leu His Ala Ala Pro Arg Gln Gly Pro Ala Pro 65 70 75 80

Trp Gly Leu Leu Heis His Gln Pro Ser Pro Val Ala

Trp Gly Leu Leu His His Gln Pro Ser Pro Val Ala 85 90

- (2) INFORMATION FOR SEQ ID NO:2630:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 109 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..109
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601539
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

Met Ala Gly Gly Gly Gly Gly Ala Ala Pro Lys His Asp Asp Phe 1 5 10 15

Thr Pro His Pro Val Lys Asp Gln Leu Pro Gly Val Ser Tyr Cys Ile 20 25 30

Thr Ser Pro Pro Pro Trp Pro Glu Ala Val Leu Leu Gly Phe Gln His

Tyr Leu Val Met Leu Gly Thr Thr Val Ile Ile Pro Thr Ala Leu Val 50 55 60

Pro Gln Met Gly Gly Asn Asn Glu Asp Lys Ala Val Val Ile Gln Thr 65 70 75 80

Leu Leu Phe Val Ala Gly Ile Asn Thr Leu Leu Gln Ser Phe Phe Gly 85 90 95

Thr Met Leu Pro Ala Val Ile Gly Gly Ser Tyr Thr Phe  $100 \hspace{1cm} 105$ 

- (2) INFORMATION FOR SEQ ID NO:2631:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 423 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..423
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601540
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

atcoatctat ccatcatcac cagctagcac ctectttece acgaeteceg agegetetge 60 gtgtggegeg eggeagetg gegactgega aegggageag caaggggteg ttegaggte 120 ccaaggtgga ggteaggtte accaagetet teategaegg eagttegte gaegeegtet 240 agggageaa ggeegaegte gaeetegeeg teaaggeege eegggagee ttegaeaeg 240 agggageaa ggeegaegte gaeetegeeg teaaggeege eegggagee ttegaeaeg 300 ggeectggee eaggatgaeg ggataegaeg gtggteggat eeteeaeagg ttegeggaee tgategaeg ggataegaeg egetggaeae ggtggaeege ggeaagetgt 420 teg

- (2) INFORMATION FOR SEQ ID NO:2632:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632: Ser Ile Tyr Pro Ser Ser Pro Ala Ser Thr Ser Phe Pro Thr Thr Pro 10 Glu Arg Ser Ala Cys Gly Ala Arg Gln His Gly Asp Cys Glu Arg Glu 25 Gln Gln Gly Val Val Arg Gly Ala Gln Gly Gly Gly Gln Val His Gln Ala Leu His Arg Arg Gln Val Arg Arg Arg Arg Leu Arg Gln Asp Val Arg Asp Pro Gly Pro Ser His Arg Arg Gly Asp Arg Gln His Arg Gly Gly Arg Gln Gly Arg Arg Pro Arg Arg Gln Gly Arg Pro Gly Gly 90 85 Leu Arg Gln Arg Ala Leu Ala Gln Asp Asp Gly Ile Arg Ala Trp Ser 100 105 Asp Pro Pro Gln Val Arg Gly Pro Asp Arg Arg Ala Arg Gly Gly Ala 115 120 125 Gly Gly Ala Gly His Gly Gly Arg Arg Gln Ala Val 135 (2) INFORMATION FOR SEQ ID NO:2633: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..140 (D) OTHER INFORMATION: / Ceres Seq. ID 1601542 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633: Pro Ser Ile His His Gln Leu Ala Pro Pro Phe Pro Arg Leu Pro 10 5 Ser Ala Leu Arg Val Ala Arg Gly Ser Met Ala Thr Ala Asn Gly Ser 25 Ser Lys Gly Ser Phe Glu Val Pro Lys Val Glu Val Arg Phe Thr Lys 4.0 Leu Phe Ile Asp Gly Lys Phe Val Asp Ala Val Ser Gly Lys Thr Phe 60 5.5 Glu Thr Arg Asp Pro Arg Thr Gly Glu Val Ile Ala Ser Ile Ala Glu 75 70 Gly Asp Lys Ala Asp Val Asp Leu Ala Val Lys Ala Ala Arg Glu Ala 85 90 Phe Asp Asn Gly Pro Trp Pro Arg Met Thr Gly Tyr Glu Arg Gly Arg 100 105 110 Ile Leu His Arg Phe Ala Asp Leu Ile Asp Glu His Val Glu Glu Leu 120 125 Ala Ala Leu Asp Thr Val Asp Ala Gly Lys Leu Phe 135 (2) INFORMATION FOR SEQ ID NO:2634: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide

(B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

(D) OTHER INFORMATION: / Ceres Seq. ID 1601543

```
Met Ala Thr Ala Asn Gly Ser Ser Lys Gly Ser Phe Glu Val Pro Lys
                                    10
Val Glu Val Arg Phe Thr Lys Leu Phe Ile Asp Gly Lys Phe Val Asp
                                                     30
                                25
Ala Val Ser Gly Lys Thr Phe Glu Thr Arg Asp Pro Arg Thr Gly Glu
                            40
Val Ile Ala Ser Ile Ala Glu Gly Asp Lys Ala Asp Val Asp Leu Ala
                        55
Val Lys Ala Ala Arg Glu Ala Phe Asp Asn Gly Pro Trp Pro Arg Met
                                        75
                    7.0
Thr Gly Tyr Glu Arg Gly Arg Ile Leu His Arg Phe Ala Asp Leu Ile
                                    90
                8.5
Asp Glu His Val Glu Glu Leu Ala Ala Leu Asp Thr Val Asp Ala Gly
                                                     110
            100
                                105
Lys Leu Phe
```

- (2) INFORMATION FOR SEQ ID NO:2635:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..472
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601547
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635: cetteetttt egteetette teeagtegte eeccagtete agteeaceae egtegeagee 60 ggaggggaga ggacggaagg caatgccgtg ctgccagact gtgctcagtg ccgcggcggc 120 cgccgccgcc agcagaacgc cgtcatggct ccatcggctg cacgccaaag ggggtctatc 180 cttcccctcc cacctcaaca ttgacgacct cctctacggg ggccgacagg cccaaactcc 240 cectececet ecetegeece tgecacette ttettecaat gateacaaeg acetegtegt 300 tgttgtcagg gagtcgccta caaaggccgc cgctaagccc aagccgccgc cggcggctca 360 gegteegeee egeaaceett egegaeeaaa eectagetet ageaatteet egeageegee 420 geogeaacca cagetteage tegttgeegt gateteegat gtettegegg te
- (2) INFORMATION FOR SEQ ID NO:2636:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..157
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601548
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:
- Leu Pro Phe Arg Pro Leu Leu Gln Ser Ser Pro Ser Leu Ser Pro Pro 1.0 5 1
- Pro Ser Gln Pro Glu Gly Arg Gly Arg Lys Ala Met Pro Cys Cys Gln 25 30
- Thr Val Leu Ser Ala Ala Ala Ala Ala Ala Ala Ser Arg Thr Pro Ser 45
- Trp Leu His Arg Leu His Ala Lys Gly Gly Leu Ser Phe Pro Ser His
- Leu Asn Ile Asp Asp Leu Leu Tyr Gly Gly Arg Gln Ala Gln Thr Pro 75 70
- Pro Pro Pro Pro Ser Pro Leu Pro Pro Ser Ser Ser Asn Asp His Asn
- Asp Leu Val Val Val Arg Glu Ser Pro Thr Lys Ala Ala Ala Lys

100 105 Pro Lys Pro Pro Pro Ala Ala Gln Arg Pro Pro Arg Asn Pro Ser Arg 115 120 125 Pro Asn Pro Ser Ser Ser Asn Ser Ser Gln Pro Pro Pro Gln Pro Gln 130 135 140 Leu Gln Leu Val Ala Val Ile Ser Asp Val Phe Ala Val 150 155 (2) INFORMATION FOR SEQ ID NO: 2637: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..149 (D) OTHER INFORMATION: / Ceres Seq. ID 1601549 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637: Phe Leu Phe Val Leu Phe Ser Ser Arg Pro Pro Val Ser Val His His 10 5 Arg Arg Ser Arg Arg Gly Glu Asp Gly Arg Gln Cys Arg Ala Ala Arg 25 Leu Cys Ser Val Pro Arg Arg Pro Pro Pro Pro Ala Glu Arg Arg His 45 40 Gly Ser Ile Gly Cys Thr Pro Lys Gly Val Tyr Pro Ser Pro Pro Thr 55 60 Ser Thr Leu Thr Thr Ser Ser Thr Gly Ala Asp Arg Pro Lys Leu Pro 75 70 Leu Pro Leu Pro Arg Pro Cys His Leu Leu Leu Pro Met Ile Thr Thr 90 Thr Ser Ser Leu Leu Ser Gly Ser Arg Leu Gln Arg Pro Pro Leu Ser 110 100 105 Pro Ser Arg Arg Arg Leu Ser Val Arg Pro Ala Thr Leu Arg Asp 120 125 115 Gln Thr Leu Ala Leu Ala Ile Pro Arg Ser Arg Arg Arg Asn His Ser 140 135 130 Phe Ser Ser Leu Pro (2) INFORMATION FOR SEQ ID NO:2638: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..130 (D) OTHER INFORMATION: / Ceres Seq. ID 1601550 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638: Met Pro Cys Cys Gln Thr Val Leu Ser Ala Ala Ala Ala Ala Ala Ala 10 Ser Arg Thr Pro Ser Trp Leu His Arg Leu His Ala Lys Gly Gly Leu 25 20 Ser Phe Pro Ser His Leu Asn Ile Asp Asp Leu Leu Tyr Gly Gly Arg 40 Gln Ala Gln Thr Pro Pro Pro Pro Ser Pro Leu Pro Pro Ser Ser 60 55 Ser Asn Asp His Asn Asp Leu Val Val Val Arg Glu Ser Pro Thr 75 70

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Lys Ala Ala Ala Lys Pro Lys Pro Pro Pro Ala Ala Gln Arg Pro Pro
                                    90
                85
Arg Asn Pro Ser Arg Pro Asn Pro Ser Ser Ser Asn Ser Ser Gln Pro
                                                 110
           100
                            105
Pro Pro Gln Pro Gln Leu Gln Leu Val Ala Val Ile Ser Asp Val Phe
                            120
                                                125
Ala Val
    130
(2) INFORMATION FOR SEQ ID NO:2639:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 485 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..485
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601559
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:
cgcccactcc cagaggetet tetecteete geeteetete ectageetee acgaegeaag
                                                                        60
ggagagtgac ggaaagcgac gcggcgcgag cgaggagggc caaggggaag aggggaagca
                                                                       120
ccgcaccagg accettgttc gccgccgccg cctctgatct ccgcgaggtt gtcaggattc
                                                                       180
aatatgtcga ccagcacatt cgctacttcc tgcacgctgt tgggcaatgt tagaacaacg
                                                                       240
caggeeteee agacageggt gaagageeet tegtetetaa gettetteag eeaagttaeg
                                                                       300
aaggttccaa gcctgaagac ctccaagaaa ctggatgtct ccgccatggc tgtatacaag
                                                                       360
gtgaagettg tegggeetga aggtgaagag cacgagtttg atgetecaga egaegeetae
                                                                       420
atccttgacg cagecgagac tgcggtgtgg agttgccata ctcgtgccgt gctggggctt
                                                                       480
gytcc
(2) INFORMATION FOR SEQ ID NO:2640:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 51 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..51
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601560
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:
Ala His Ser Gln Arg Leu Phe Ser Ser Ser Pro Pro Leu Pro Ser Leu
                5
                                     10
 His Asp Ala Arg Glu Ser Asp Gly Lys Arg Arg Gly Ala Ser Glu Glu
                                25
            20
 Gly Gln Gly Glu Glu Gly Lys His Arg Thr Arg Thr Leu Val Arg Arg
                             40
         35
 Arg Arg Leu
     50
 (2) INFORMATION FOR SEQ ID NO:2641:
      (i) SEQUENCE CHARACTERISTICS:
```

- - (A) LENGTH: 76 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..76
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

```
        Pro
        Thr
        Pro
        Arg
        Gly
        Ser
        Ser
        Pro
        Pro
        Arg
        Leu
        Leu
        Ser
        Leu
        Ala
        Ser
        Ala
        Arg
        Leu
        Ala
        Ala
        Ala
        Arg
        Ala
        Arg
        Ala
        Ala
        Pro
        Arg
        Arg</th
```

- (2) INFORMATION FOR SEQ ID NO:2642:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..99
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601562
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

Met Ser Thr Ser Thr Phe Ala Thr Ser Cys Thr Leu Leu Gly Asn Val 1 5 10 15

Arg Thr Thr Gln Ala Ser Gln Thr Ala Val Lys Ser Pro Ser Ser Leu 20 25 30

Ser Phe Phe Ser Gln Val Thr Lys Val Pro Ser Leu Lys Thr Ser Lys 35 40 45

Lys Leu Asp Val Ser Ala Met Ala Val Tyr Lys Val Lys Leu Val Gly 50 55 60

Pro Glu Gly Glu Glu His Glu Phe Asp Ala Pro Asp Asp Ala Tyr Ile 65 70 75 80

Leu Asp Ala Ala Glu Thr Ala Val Trp Ser Cys His Thr Arg Ala Val 85 90 95

Leu Gly Leu

- (2) INFORMATION FOR SEQ ID NO:2643:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..437
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

acacataacc agcacacage tetegeette teteteccat eggeacacce gagetegete 60 cetectteca egtegaggte egagteetge tttgatggeg acegaegtgg etgagactee 120 eggegeegttg gtggatgegg ececagagge geegeegta egeegagatg gteteggagg egateaegte geteaaggag aggaegggt ecageageta tgegattgee aagttegtgg aggaeaagea eaaggaeaag eteeegeea aetteegeaa gettetgaae gteagetea agaagetegt egeegegge aagetgacea aggtgaagaa etegtaeaag etgtegteeg aggaeaceaa geegaateee aageecaagg eegeecegaa gaageecaag aceggegeta 420 agaageeaag geegetg

- (2) INFORMATION FOR SEQ ID NO:2644:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..139
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601568
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:
- His Ile Thr Ser Thr Gln Leu Ser Pro Ser Leu Ser His Arg His Thr 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15
- Arg Ala Arg Ser Leu Leu Pro Arg Gly Pro Ser Pro Ala Leu Met 20 25 30
- Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala Pro 35 40 45
- Glu Ala Pro Ala Val Arg Arg Asp Gly Leu Gly Gly Asp His Val Ala 50 60
- Gln Gly Glu Asp Gly Val Gln Gln Leu Cys Asp Cys Gln Val Arg Gly 65 70 75 80
- Gly Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu 85 90 95
- Arg Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Glu 100 105 110
- Glu Leu Val Gln Ala Val Val Arg Arg His Gln Ala Glu Ser Gln Ala 115 120 125
- Gln Gly Arg Pro Glu Glu Ala Gln Asp Arg Arg 130 135
- (2) INFORMATION FOR SEQ ID NO:2645:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..108
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:
- Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala 1 5 10 15
- Pro Glu Ala Pro Ala Val Arg Arg Asp Gly Leu Gly Gly Asp His Val 20 25 30
- Ala Gln Gly Glu Asp Gly Val Gln Gln Leu Cys Asp Cys Gln Val Arg 35 40 45
- Gly Gly Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser 50 55 60
- Glu Arg Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly 65 70 75 80
- Glu Glu Leu Val Gln Ala Val Val Arg Arg His Gln Ala Glu Ser Gln 85 90 95
- Ala Gln Gly Arg Pro Glu Glu Ala Gln Asp Arg Arg
  100 105
- (2) INFORMATION FOR SEQ ID NO:2646:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..101

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(D) OTHER INFORMATION: / Ceres Seq. ID 1601570
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:
Met Arg Pro Gln Arg Arg Pro Pro Tyr Ala Glu Met Val Ser Glu Ala
                                    10
Ile Thr Ser Leu Lys Glu Arg Thr Gly Ser Ser Ser Tyr Ala Ile Ala
            20
                                25
Lys Phe Val Glu Asp Lys His Lys Asp Lys Leu Pro Pro Asn Phe Arg
                            40
Lys Leu Leu Asn Val Gln Leu Lys Lys Leu Val Ala Gly Gly Lys Leu
                        5.5
Thr Lys Val Lys Asn Ser Tyr Lys Leu Ser Ser Ala Ala Thr Lys Pro
                    70
                                        75
Asn Pro Lys Pro Lys Ala Ala Pro Lys Lys Pro Lys Thr Gly Ala Lys
                                    90
                8.5
Lys Pro Arg Pro Leu
            100
(2) INFORMATION FOR SEQ ID NO: 2647:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 481 base pairs
           (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
           (B) LOCATION: 1..481
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601571
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:
gtcaaagcag agtctgcccc tccccgcgcc gttctttttg gttccccact ccccagtccc
cgccgccgcc gaaacccgca gatggaggtc gtcgtcgccg cgaagcagaa ggcgaagaaa
cacatacacc tcttctactg ctcagaatgc gaggagctcg cccttaagat cgccgccagc
tecgaegeca tegageteca atecateaac tggeggaget tegaegaegg gttecegaac
                                                                       300
ctgttcatca acaaggcgca cgacatccgt gggcagcacg tggcgttcct ggcctccttc
agetegeegt eggteatatt egageagate teegteatet tegegetgee caagetatte
                                                                       420
 attgcctcat tcactctcgt gctgcctttc ttccccacgg gctcattcga gcgcgttgag
gaggaggeg atgtegecae egegtteace etegegegea ttetetegan gatececaag
                                                                       480
 (2) INFORMATION FOR SEQ ID NO:2648:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 160 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..160
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601572
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:
 Val Lys Ala Glu Ser Ala Pro Pro Arg Ala Val Leu Phe Gly Ser Pro
                                     10
 Leu Pro Ser Pro Arg Arg Arg Asn Pro Gln Met Glu Val Val Val
                                 25
             20
 Ala Ala Lys Gln Lys Ala Lys Lys His Ile His Leu Phe Tyr Cys Ser
                                                  45
                             40
 Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala Ser Ser Asp Ala Ile
                                              60
                          55
 Glu Leu Gln Ser Ile Asn Trp Arg Ser Phe Asp Asp Gly Phe Pro Asn
                      70
                                         75
 Leu Phe Ile Asn Lys Ala His Asp Ile Arg Gly Gln His Val Ala Phe
```

- (2) INFORMATION FOR SEQ ID NO: 2649:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 160 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..160
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601573
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

Ser Lys Gln Ser Leu Pro Leu Pro Ala Pro Phe Phe Leu Val Pro His 1 5 10 15

Ser Pro Val Pro Ala Ala Ala Glu Thr Arg Arg Trp Arg Ser Ser Ser 20 25 30

Pro Arg Ser Arg Arg Arg Arg Asn Thr Tyr Thr Ser Ser Thr Ala Gln 35 40 45

Asn Ala Arg Ser Ser Pro Leu Arg Ser Pro Pro Ala Pro Thr Pro Ser 50 55 60

Ser Ser Asn Pro Ser Thr Gly Gly Ala Ser Thr Thr Gly Ser Arg Thr 65 70 75 80

Cys Ser Ser Thr Arg Arg Thr Thr Ser Val Gly Ser Thr Trp Arg Ser 85 90 95 Trp Pro Pro Ser Ala Arg Arg Arg Ser Tyr Ser Ser Arg Ser Pro Ser

\$100\$ \$105\$ \$110\$ Ser Ser Arg Cys Pro Ser Tyr Ser Leu Pro His Ser Leu Ser Cys Cys

Leu Ser Ser Pro Arg Ala His Ser Ser Ala Leu Arg Arg Ala Met
130
135
140
Ser Pro Arg Ser Pro Ser Arg Ala Phe Ser Arg Yaa Ser Pro Ser

Ser Pro Pro Arg Ser Pro Ser Arg Ala Phe Ser Arg Xaa Ser Pro Ser 145 150 155 160

- (2) INFORMATION FOR SEQ ID NO:2650:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 133 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..133
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601574
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Met Glu Val Val Val Ala Ala Lys Gln Lys Ala Lys Lys His Ile His 1  $\phantom{-}$  5  $\phantom{-}$  10  $\phantom{-}$  15

Leu Phe Tyr Cys Ser Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala 20 25 30

Ser Ser Asp Ala Ile Glu Leu Gln Ser Ile Asn Trp Arg Ser Phe Asp

35 4Ω Asp Gly Phe Pro Asn Leu Phe Ile Asn Lys Ala His Asp Ile Arg Gly 55 60 Gln His Val Ala Phe Leu Ala Ser Phe Ser Ser Pro Ser Val Ile Phe 70 75 Glu Gln Ile Ser Val Ile Phe Ala Leu Pro Lys Leu Phe Ile Ala Ser 85 90 Phe Thr Leu Val Leu Pro Phe Phe Pro Thr Gly Ser Phe Glu Arg Val 100 105 Glu Glu Gly Asp Val Ala Thr Ala Phe Thr Leu Ala Arg Ile Leu 115 120 Ser Xaa Ile Pro Lys 130

- (2) INFORMATION FOR SEQ ID NO:2651:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..466
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601575
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

  agggcaaggt gcgaaaggca ccttccctgc ccgattggcg atttaagtgg tgggggaggg 60

  aaggccgatg gtcagtgaaa gagaggtagg tggccggacg gtggttgcat cgccaattca 120

  actccgcatc tgaatcggca ctcggcagcg cgccagctcc atagtgtagg aggaggagat 180

  ggcgctcaca agaatcggtc ttgctggcct tgcggtcatg gggcagaacc ttgccctcaa 240

  cattgcagag aaagggttcc ccatctctgt gtacaacagg acaacctcca aggtggacga 300

  gaccgtgcag cgtgccaagg cagaaggaaa ccttcccgtc tacggcttcc atgaccccgc 360

  gtcctttgtg aactccattc agaagccacg ggtggtgatc atgctcgtca aggccggcgc 420

  gccagttgac cagacatcgc gacgctcgca gctcacttgg agcagg
- (2) INFORMATION FOR SEQ ID NO:2652:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:
- Met Ala Leu Thr Arg Ile Gly Leu Ala Gly Leu Ala Val Met Gly Gln
  1 10 15
- Asn Leu Ala Leu Asn Ile Ala Glu Lys Gly Phe Pro Ile Ser Val Tyr 20 25 30
- Asn Arg Thr Thr Ser Lys Val Asp Glu Thr Val Gln Arg Ala Lys Ala 35 40 45
- Glu Gly Asn Leu Pro Val Tyr Gly Phe His Asp Pro Ala Ser Phe Val 50 60
- Asn Ser Ile Gln Lys Pro Arg Val Val Ile Met Leu Val Lys Ala Gly 65 70 75 80
- Ala Pro Val Asp Gln Thr Ser Arg Arg Ser Gln Leu Thr Trp Ser Arg 85 90 95
- (2) INFORMATION FOR SEQ ID NO:2653:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..83
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

Ser Val Tyr Asn Arg Thr Thr Ser Lys Val Asp Glu Thr Val Gln Arg 20 25 30

Ala Lys Ala Glu Gly Asn Leu Pro Val Tyr Gly Phe His Asp Pro Ala 35 40 45

Ser Phe Val Asn Ser Ile Gln Lys Pro Arg Val Val Ile Met Leu Val 50 55 60

Lys Ala Gly Ala Pro Val Asp Gln Thr Ser Arg Arg Ser Gln Leu Thr 65 70 75 80

Trp Ser Arg

- (2) INFORMATION FOR SEQ ID NO: 2654:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 490 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..490
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601582
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

gcaacgycgt tgetteaact egacteeage atecetegte eeegcateae egegeegee 60
asacteeget egettteget eeegagacee gggeetgeeg tageegeege eatggaegag 120
gagtaegaeg tgategttet gggeaegggg etcaaggagt geateeteag eggteteete 180
ytetgtegae ggeeteaagg ttetacacat ggatagaaat gattaetaeg gaggagatte 240
caceteecta aacetgaace ayetetggaa tgakgtttag ggggkaagae aageeaeegg 300
cacatetagg tgeaageaga gattaeaatk tagaeatggt tecaaagttt atgatggeaa 360
aegggaettt ggttegeaet etcatteaea etgatgtgae aaaatatttg teatteaaag 420
etgttgatgg aagetatgte tyeageaaae ggaagattea eaaggtteet genaeegata 480
tggaggetet

- (2) INFORMATION FOR SEQ ID NO:2655:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..71
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601583
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

Ala Thr Xaa Leu Leu Gln Leu Asp Ser Ser Ile Pro Arg Pro Arg Ile 1 5 10 15

Thr Ala Pro Pro Xaa Leu Arg Ser Leu Ser Leu Pro Arg Pro Gly Pro 20 25 30

Ala Val Ala Ala Met Asp Glu Glu Tyr Asp Val Ile Val Leu Gly 35 40 45

Thr Gly Leu Lys Glu Cys Ile Leu Ser Gly Leu Leu Xaa Cys Arg Arg 50 55 60

Pro Gln Gly Ser Thr His Gly 65 70

- (2) INFORMATION FOR SEQ ID NO:2656:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..82
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601584
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:

Asn Xaa Val Ala Ser Thr Arg Leu Gln His Pro Ser Ser Pro His His 1 10 15

Arg Ala Ala Xaa Thr Pro Leu Ala Phe Ala Pro Glu Thr Arg Ala Cys 20 25 30

Arg Ser Arg Arg His Gly Arg Gly Val Arg Arg Asp Arg Ser Gly His

Gly Ala Gln Gly Val His Pro Gln Arg Ser Pro Xaa Leu Ser Thr Ala
50 55 60

Ser Arg Phe Tyr Thr Trp Ile Glu Met Ile Thr Thr Glu Glu Ile Pro 65 70 75 80

Pro Pro

- (2) INFORMATION FOR SEQ ID NO:2657:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..73
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601585
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

Met Xaa Phe Arg Gly Xaa Asp Lys Pro Pro Ala His Leu Gly Ala Ser 1 5 10 15

Arg Asp Tyr Asn Xaa Asp Met Val Pro Lys Phe Met Met Ala Asn Gly 20 25 30

Thr Leu Val Arg Thr Leu Ile His Thr Asp Val Thr Lys Tyr Leu Ser

Phe Lys Ala Val Asp Gly Ser Tyr Val Xaa Ser Lys Arg Lys Ile His

Lys Val Pro Xaa Thr Asp Met Glu Ala 70

- (2) INFORMATION FOR SEQ ID NO:2658:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..492
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601586

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658: ctcaggatga atcggaagag agaatcctac caaacctagc taccaactcg atcgtcgtca 60 tcacgctcga ccgcacaact gcaccaaggg gggaggagac ctaaaaacta ctacatcttt 120 tagctacaca tctagctaaa gatcgagagg ggtaaataag gacgagcggg cgcgagctag 180 aagagcagct gcaggtacta ccatcatcgt cgtcgtcgtc gccaggatga ccgtcgtcga 240 egecgtegte tectecaceg atgeeggege eeetgetgee geegeeaceg eggtacegge 300 ggggaacggg cagaccgtgt gcgtgaccgg cgcggccggg tacatcgcct cgtggttggt 360 gaagctgctg ctcgagaagg gatacactgt gaagggcacc gtcaggaacc cagatgaccc 420 gaagaacgcg cacctcaagg cgctggacgg cgccgccgag cggctgatcc tctgcaaggc 480 ccgatctgct gg
- (2) INFORMATION FOR SEQ ID NO:2659:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..88
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601587
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659: Met Thr Val Val Asp Ala Val Val Ser Ser Thr Asp Ala Gly Ala Pro

1 5 10 15 Ala Ala Ala Ala Thr Ala Val Pro Ala Gly Asn Gly Gln Thr Val Cys 20 25 30

Val Thr Gly Ala Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu 35 40 45

Leu Glu Lys Gly Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp 50 55 60

Pro Lys Asn Ala His Leu Lys Ala Leu Asp Gly Ala Ala Glu Arg Leu 65 70 75 80

Ile Leu Cys Lys Ala Arg Ser Ala 85

- (2) INFORMATION FOR SEQ ID NO:2660:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 486 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..486
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601596
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:

acattccatc ggtcgtgaaa agaaaaaggg aaacaaacca agctagagaa aagaagga 60 tactacatac tagctagcta gcttagctat gggcaccatc gtcgacgctg acgtcgggtt 120 cgcggtgaag aggacgagca ggtcgctggt gccgcctgcg tcggcgacgc cgcgggagac 180 getgeggetg teggtgateg acegegtgge ggggetgege cacetggtge ggtegetgea 240 cgtgttcgcc gcgggcggcg acaagaagcg gcagcaggcg acggcgacgc cggccaaggc 300 gctgcgggag gcgctggga aggcgctggt ggactactac ccgttcgcgg ggcggttcgt 360 ggtggtggac gcggaggcg gcggggagac gcgggtggcg tgcaccggcg agggcgcctg 420 gttcgtggag gccaacgccg cgtgctcgct cgaggaggcc cgccacctcg accacccat 480 gctcat

- (2) INFORMATION FOR SEQ ID NO:2661:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..132
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601597
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:

Met Gly Thr Ile Val Asp Ala Asp Val Gly Phe Ala Val Lys Arg Thr 1 5 10 15

Ser Arg Ser Leu Val Pro Pro Ala Ser Ala Thr Pro Arg Glu Thr Leu 20 25 30

Arg Leu Ser Val Ile Asp Arg Val Ala Gly Leu Arg His Leu Val Arg 35 40 45

Ser Leu His Val Phe Ala Ala Gly Gly Asp Lys Lys Arg Gln Gln Ala 50 55 60

Thr Ala Thr Pro Ala Lys Ala Leu Arg Glu Ala Leu Gly Lys Ala Leu 65 70 75 80

Val Asp Tyr Tyr Pro Phe Ala Gly Arg Phe Val Val Val Asp Ala Glu 85 90 95

Gly Gly Glu Thr Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe  $100 \,$   $105 \,$   $110 \,$ 

Val Glu Ala As<br/>n Ala Ala Cys Ser Leu Glu Glu Ala Arg His Leu Asp\$115\$ <br/> \$120\$ <br/> \$125\$

His Pro Met Leu

130

- (2) INFORMATION FOR SEQ ID NO: 2662:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..381
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601598
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

atcacegteg ccatcactac cectetecte tetetcateg getecaatgg eggacgeega 60 egecaagtee cageegeeg aegeegge atceceggat geetegatet ceteeecete 120 etcectagge geggeggeg gegacgegge egacgeggac gegaytegag aageageteg 180 eegtaceagt ecceateceg geeggtggt teeeegagee ategggatgg gaegatggee 240 eegtaceagt ecceateceg geegatgtee ttgteggegg tgatgagggt geeggegaga 300 ageeggegge getggeegg gegeegactg gggeggtgga tgtgaaggtg eggtteeege 360 geeggeeggg ggageeggae t

- (2) INFORMATION FOR SEQ ID NO:2663:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..114
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:
- Ile Thr Val Ala Ile Thr Thr Pro Leu Leu Ser Leu Ile Gly Ser Asn 1 5 10 15
- Gly Gly Arg Arg Gln Val Pro Ala Ala Arg Arg Arg Gly Ile Pro 20 25 30
- Gly Cys Leu Asp Leu Leu Pro Leu Leu Pro Arg Arg Arg Arg Arg Arg 35 40 45

 Arg
 Gly
 Arg
 Gly
 Arg
 Xaa
 Ser
 Arg
 Ser
 Ser
 Ser
 Pro
 Ala
 Trp
 Ala

 Ser
 Pro
 Ser
 Pro
 Val
 Gly
 Ser
 Pro
 Ser
 His
 Arg
 Asp
 Gly
 Thr
 Met
 Ala

 80
 Pro
 Tyr
 Gln
 Ser
 Pro
 Ser
 Arg
 Pro
 Met
 Ser
 Leu
 Ser
 Ala
 Val
 Met
 Arg

 Val
 Pro
 Ala
 Arg
 Ser
 Arg
 Gly
 Arg
 Trp
 Arg
 Arg
 Arg
 Arg
 Arg
 Arg
 Ilo
 Ilo
 Ilo
 Inc
 In

Trp Met

- (2) INFORMATION FOR SEQ ID NO: 2664:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 93 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..93
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601600
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

Ser Pro Ser Pro Ser Leu Pro Leu Ser Ser Leu Ser Ser Ala Pro Met
1 5 10 15

Ala Asp Ala Asp Ala Lys Ser Gln Pro Pro Asp Ala Ala Ser Pro
20 25 30

Asp Ala Ser Ile Ser Ser Pro Ser Ser Leu Gly Gly Gly Gly Asp

Ala Ala Asp Ala Asp Ala Xaa Arg Glu Ala Ala Arg Arg Pro Gly His

Arg Arg Arg Trp Val Pro Arg Ala Ile Gly Met Gly Arg Trp Pro
65 70 75 80

Arg Thr Ser Pro His Pro Gly Arg Cys Pro Cys Arg Arg 85 90

- (2) INFORMATION FOR SEQ ID NO: 2665:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..78
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601601
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

Met Ala Asp Ala Asp Ala Lys Ser Gln Pro Pro Asp Ala Ala Ser
1 5 10 15

Pro Asp Ala Ser Ile Ser Ser Pro Ser Ser Leu Gly Gly Gly Gly 25

Asp Ala Ala Asp Ala Asp Ala Xaa Arg Glu Ala Ala Arg Arg Pro Gly 35 40 45

His Arg Arg Arg Trp Val Pro Arg Ala Ile Gly Met Gly Arg Trp 50 55 60

Pro Arg Thr Ser Pro His Pro Gly Arg Cys Pro Cys Arg Arg 70

- (2) INFORMATION FOR SEQ ID NO:2666:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 289 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..289
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601602
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

  ccccaaageg gatcaaaccc tagatetegt ettgtegeee egtteeteeg ateceateet 60
  atecgateet catggattee teetmwgtee ageeteagee ageageeega gttegaetae 120
  ctetteaage tactyettat eggegaetee ggegteggea agageageet eeteeteege 180
  tteaeegeeg acteettega tgacetetee eetaecatag gtgttgaett caaggtgaag 240
  atggttagea ttggtggeaa aaaaaactea agettgeeat etgggaeae
- (2) INFORMATION FOR SEQ ID NO:2667:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601603
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:
- Pro Gln Ser Gly Ser Asn Pro Arg Ser Arg Leu Val Ala Pro Phe Leu 1 5 10 15
- Arg Ser His Pro Ile Arg Ser Ser Trp Ile Pro Pro Xaa Ser Ser Leu 20 25 30
- Ser Gln Gln Pro Glu Phe Asp Tyr Leu Phe Lys Leu Xaa Leu Ile Gly 35 40 45
- Asp Ser Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ala Asp 50 55 60
- Ser Phe Asp Asp Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys 65 70 75 80
- Met Val Ser Ile Gly Gly Lys Lys Asn Ser Ser Leu Pro Ser Gly Thr 85 90 95
- (2) INFORMATION FOR SEQ ID NO: 2668:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 72 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..72
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601604
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:
- Pro Lys Ala Asp Gln Thr Leu Asp Leu Val Leu Ser Pro Arg Ser Ser 1 5 10 15
- Asp Pro Ile Leu Ser Asp Pro His Gly Phe Leu Xaa Xaa Pro Ala Ser
- Ala Ser Ser Pro Ser Ser Thr Thr Ser Ser Ser Tyr Xaa Leu Ser Ala 35 40 45
- Thr Pro Ala Ser Ala Arg Ala Ala Ser Ser Ser Ala Ser Pro Pro Thr 50 55 60
- Pro Ser Met Thr Ser Pro Leu Pro
- 65 70
- (2) INFORMATION FOR SEQ ID NO:2669:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 489 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..489
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601605
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

accacgetgt geetgtgagt gacteggteg catetteece attetecate gacgeaeegg 60 cggcggcgca agtgaagcga agaggaaagg aagctacgag atgtcggcga ccactgcagc 120 ggtgcccttc tggcgggcgg cggggatgac ctacatcggc tactccaaca tctgcgctgc 180 240 gctggtccgg aactgcctca aggagccctt caagtctgag gccgcgtccc gcgagaaggt 300 tcatttctcc atctccaagt ggacggatgg caagcaggag aagcccactg tccgcacaga atcggatgac taagggctgg cgcgccatgg cgacatagtc cttcccacag atgatttgaa 360 gcgtcgttgc aagtttctga gacttgttat ttagttggct tgatttgtaa tcaatgctga 420 agaataaata ctttttgcga caatggtctt tttacaatgt cgtgttgttt tcgttgctaa 480 ttgcacttg

- (2) INFORMATION FOR SEQ ID NO:2670:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 48 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..48
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601606
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

His Ala Val Pro Val Ser Asp Ser Val Ala Ser Ser Pro Phe Ser Ile
1 10 15

Asp Ala Pro Ala Ala Ala Gln Val Lys Arg Arg Gly Lys Glu Ala Thr 20 25 30

Arg Cys Arg Arg Pro Leu Gln Arg Cys Pro Ser Gly Gly Arg Arg Gly 35 40 45

- (2) INFORMATION FOR SEQ ID NO:2671:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..70
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601607
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn Cys 20 25 30

Leu Lys Glu Pro Phe Lys Ser Glu Ala Ala Ser Arg Glu Lys Val His  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr Val 50 55 60

Arg Thr Glu Ser Asp Asp

```
70
65
(2) INFORMATION FOR SEQ ID NO:2672:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 55 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..55
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601608
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:
Met Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn
                                    10
                5
Cys Leu Lys Glu Pro Phe Lys Ser Glu Ala Ala Ser Arg Glu Lys Val
                                25
His Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr
                            40
Val Arg Thr Glu Ser Asp Asp
                        55
(2) INFORMATION FOR SEQ ID NO:2673:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 455 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
           (B) LOCATION: 1..455
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601609
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:
gtctagatcg ctcgtccggt gtggtctctg gacttgcttg ccgttcactt ctcttcagcg
gcagcgtggc aaggcaacga gagcaacgaa gagtattcaa accgaaaaca atggatccgg
                                                                        120
tgcggaagag cgtgtgcgtg accggcgctg gcggcttcgt cgcgtcggag ctggtgaagc
                                                                        180
tectectete eeggggeeaa tacgeggtee geggeacegt gegegaeeet ggtgetagea
                                                                        240
agaatgccca tctcaaggtg ctggaaggag ctgaggaaag gttgcagctt ctcaaggctg
                                                                        300
atctgatgga ctacgacagc attgcatcag cagttgccgg ctgtgagggt gtcttccatg
                                                                        360
tagctagece tgteetttee categaceet ceaaceetga ggtggaggte atageteeeg
                                                                        420
 ctgtaatagg tacaaccaat gtgttaaagg cttgc
 (2) INFORMATION FOR SEQ ID NO:2674:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 78 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..78
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601610
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:
 Ser Arg Ser Leu Val Arg Cys Gly Leu Trp Thr Cys Leu Pro Phe Thr
                                                          15
                                      10
 Ser Leu Gln Arg Gln Arg Gly Lys Ala Thr Arg Ala Thr Lys Ser Ile
                                                      30
             20
 Gln Thr Glu Asn Asn Gly Ser Gly Ala Glu Glu Arg Val Arg Asp Arg
                              40
                                                  45
 Arg Trp Arg Leu Arg Arg Val Gly Ala Gly Glu Ala Pro Pro Leu Pro
                                              60
     50
```

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Gly Pro Ile Arg Gly Pro Arg His Arg Ala Arg Pro Trp Cys 65 70 75
```

- (2) INFORMATION FOR SEQ ID NO:2675:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 151 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..151
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601611
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

Leu Asp Arg Ser Ser Gly Val Val Ser Gly Leu Ala Cys Arg Ser Leu

1 5 10 15

Leu Phe Ser Gly Ser Val Ala Arg Gln Arg Glu Gln Arg Arg Val Phe 20 25 30

Lys Pro Lys Thr Met Asp Pro Val Arg Lys Ser Val Cys Val Thr Gly 35 40 45 .

Ala Gly Gly Phe Val Ala Ser Glu Leu Val Lys Leu Leu Ser Arg 50 60

Gly Gln Tyr Ala Val Arg Gly Thr Val Arg Asp Pro Gly Ala Ser Lys
65 70 75 80

Asn Ala His Leu Lys Val Leu Glu Gly Ala Glu Glu Arg Leu Gln Leu 85 90 95

Leu Lys Ala Asp Leu Met Asp Tyr Asp Ser Ile Ala Ser Ala Val Ala 100 105 110

Gly Cys Glu Gly Val Phe His Val Ala Ser Pro Val Leu Ser His Arg \$115\$ \$120\$ \$125\$

Pro Ser Asn Pro Glu Val Glu Val Ile Ala Pro Ala Val Ile Gly Thr
130 135 140

Thr Asn Val Leu Lys Ala Cys

145 150

- (2) INFORMATION FOR SEQ ID NO: 2676:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 115 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..115
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601612
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Met Asp Pro Val Arg Lys Ser Val Cys Val Thr Gly Ala Gly Gly Phe 1 5 10 15

Val Ala Ser Glu Leu Val Lys Leu Leu Ser Arg Gly Gln Tyr Ala
20 25 30

Val Arg Gly Thr Val Arg Asp Pro Gly Ala Ser Lys Asn Ala His Leu
35 40 45

Lys Val Leu Glu Gly Ala Glu Glu Arg Leu Gln Leu Lys Ala Asp

Leu Met Asp Tyr Asp Ser Ile Ala Ser Ala Val Ala Gly Cys Glu Gly
65 70 75 80

Val Phe His Val Ala Ser Pro Val Leu Ser His Arg Pro Ser Asn Pro 85 90 95

Glu Val Glu Val Ile Ala Pro Ala Val Ile Gly Thr Thr Asn Val Leu 100 105 110

Lys Ala Cys

- (2) INFORMATION FOR SEQ ID NO:2677:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 513 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..513
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601616
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677: aataatctac tactaccgcc cccatggagg ccggggggca gttttctctc tcgctcgctc

- (2) INFORMATION FOR SEQ ID NO:2678:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 171 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..171
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601617
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

Asn Asn Leu Leu Pro Pro Pro Trp Arg Pro Gly Gly Ser Phe Leu
1 5 10 15

Ser Arg Ser Leu Ser Ser Arg Leu Leu Gln Lys Leu Val Phe Leu Ala 20 25 30

Leu Pro Ser Ser Leu Ser Leu Ser Leu Thr Thr Lys Leu Ser Pro Trp  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Pro Lys Ala His Ala Ser Tyr Ala Pro Ala Ala Ser Pro Ala Pro Ala 50 55 60

Pro Ser Pro Ala Thr Cys Ala Pro Thr Pro Trp Pro Pro Gln Ser Arg
65 70 75 80

Arg Ser His Arg Pro Arg Arg Leu Arg His Pro Ser Arg Leu Ala Ala 85 90 95

Ser Thr Pro Thr Arg Ser Ala Ala Pro Ser Gly Gly Thr Arg Cys Gly
100 105 110

Arg Ile Pro Ser Ala Ala Ala Ser Thr Thr Arg Ile Ala Arg Ala 115 120 125

Arg Arg Arg Thr Thr Leu Arg Arg Arg Thr Pro Ser Ala Arg Thr 130 135 140

Pro Asp Arg Gly Thr Arg Ser Pro Val Ser Ser Val Ser Asp Ala Ala 145 150 155 160

Thr Pro Glu Glu Asp Val Ala Leu Xaa Leu Met 165 170

- (2) INFORMATION FOR SEQ ID NO:2679:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..124
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Met Ala Lys Ser Thr Cys Lys Leu Cys Ser Arg Arg Phe Ala Ser Pro  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Arg Ala Leu Ala Gly His Met Arg Ala His Ser Met Ala Ser Ala Lys 20 25 30

Ser Gln Ile Ser Ser Ala Ser Ser Ala Ser Thr Ser Ile Thr Ala Ser 35 40 45

Gly Ile Asp Ala Asp Lys Lys Arg Gly Pro Val Arg Gly His Ala Leu 50 55 60

Arg Glu Asn Pro Lys Arg Arg Gly Arg Leu Asp Asp Ser Asp Arg Glu 65 70 75 80

Ser Glu Thr Thr Asp Tyr Tyr Ser Pro Ser Pro Asp Ala Lys Arg Ser 85 90 95

His Ala Gly Ser Gly Asp Ala Glu Pro Gly Glu Leu Gly Leu Arg Arg 100 105 110

Gly His Ala Gly Gly Gly Arg Arg Ala Val Xaa Asp 115 120

- (2) INFORMATION FOR SEQ ID NO:2680:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..102
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601619
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

Met Arg Ala His Ser Met Ala Ser Ala Lys Ser Gln Ile Ser Ser Ala 1 5 10 15

Ser Ser Ala Ser Thr Ser Ile Thr Ala Ser Gly Ile Asp Ala Asp Lys 20 25 30

Lys Arg Gly Pro Val Arg Gly His Ala Leu Arg Glu Asn Pro Lys Arg 35 40 45

Arg Gly Arg Leu Asp Asp Ser Asp Arg Glu Ser Glu Thr Thr Asp Tyr 50 55 60

Tyr Ser Pro Ser Pro Asp Ala Lys Arg Ser His Ala Gly Ser Gly Asp 70 75 80

Ala Glu Pro Gly Glu Leu Gly Leu Arg Arg Gly His Ala Gly Gly 85 90 95

Arg Arg Ala Val Xaa Asp

100

- (2) INFORMATION FOR SEQ ID NO: 2681:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 413 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..413
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601636
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

accgcaaacg ccaccacgc cacgcctcgc cgcgcaccac atctgaaacc tccagcccga 60 cgccggcgcc ggcgccgctg ctcgcctgct cgtcacattt cctggtgccc gccaagcccc 120 gcgacctggg ctccccagct ccatccatca accgcctgca gccgcggaaa tggcagcgcc 180 gacgacgctg cgctcggcgg cggcgcggg gcgcgcggcg gcagcggag ctcgtgaaggg 240 gcggtggccg cagcggcgt tggggacgac gtccgcggcg gagacggaga gcaaaaagaa 300 taacggaag gaggaggag gcgacgtcac gcaccgcgc ctcctcgtcg acg

- (2) INFORMATION FOR SEQ ID NO:2682: (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..100
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601637
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

Thr Ala Asn Ala Thr Thr Pro Thr Pro Arg Arg Ala Pro His Leu Lys
1 10 15

Pro Pro Ala Arg Arg Arg Arg Arg Arg Cys Ser Pro Ala Arg His  $20 \\ 25 \\ 30$ 

Ile Ser Trp Cys Pro Pro Ser Pro Ala Thr Trp Ala Pro Gln Leu His  $35 \hspace{1cm} 40 \hspace{1cm} 45 \hspace{1cm}$ 

Pro Ser Thr Ala Cys Ser Arg Gly Asn Gly Ser Ala Asp Asp Ala Ala 50 55 60

Leu Gly Gly Gly Ala Gly Ala Arg Ala Arg Ser Gly Ala Arg Glu Arg 65 70 75 80

Ala Val Ala Ala Ala Ser Gly Asp Asp Val Arg Gly Gly Asp Gly
85 90 95

Glu Gln Lys Glu

100

- (2) INFORMATION FOR SEQ ID NO: 2683:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 77 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..77
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Arg Lys Arg His His Ala His Ala Ser Pro Arg Thr Thr Ser Glu Thr 1 5 10 15

Phe Leu Val Pro Ala Lys Pro Arg Asp Leu Gly Ser Pro Ala Pro Ser 35 40 45

Ile Asn Arg Leu Gln Pro Arg Lys Trp Gln Arg Arg Arg Cys Ala 50 55 60

Arg Arg Arg Gly Arg Ala Arg Ala Gln Arg Ser Ser 65 70 75

- (2) INFORMATION FOR SEQ ID NO: 2684:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..81
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

Arg Ala Ala Glu Leu Val Arg Gly Arg Trp Pro Gln Arg Arg Leu Gly  $20 \\ 25 \\ 30$ 

Thr Thr Ser Ala Ala Glu Thr Glu Ser Lys Lys Asn Lys Glu Glu 35  $\phantom{000}40\phantom{000}$  45

Glu Glu Gly Ala Gly Trp Glu Leu Ser Ala Ala Arg Glu Tyr Tyr Asp 50 55 60

Tyr Arg Lys Ser Ile Tyr Gly Asp Val Thr His Arg Ala Leu Leu Val 65 70 75 80 Asp

- (2) INFORMATION FOR SEQ ID NO: 2685:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..433
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601640
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685: aaaaaaaaac cttagcaggs caagggcaag gacaatcgca gccagcagcc tcatcccctt

aaaaaaaaac cttagcaggs caagggcaag gacaatcgca gccagcagcc tcatccctt 60 gcccacttct acagccctc tgctgcagca agaaggaaag aagctagcgc ttatagcttg 120 tcagccatgg ccaccgcgc cgcgtctagc ctcctcaagt cctccttcgc gggctcccgg 180 ctcccggcgg ccaccgggac cacaccggcg tccctcgtgg tggccacggc ccgcgcggcg 240 ccggcgcggg gcccatctgc gcgtccatgt ccatgtcctc ctccaacccg ccctacgacc 300 tgacgtcytt ccggttcagc cccatcaagg agtccatcgt gtctccgcga gatgacccgt 360 cgctacatga cggacatgat cacctacgcs gacaccgacg tcgtcatcgt gggcgccggc 420 tccgcqqqqc tgt

- (2) INFORMATION FOR SEQ ID NO: 2686:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..117
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601641
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:

Leu Ile Pro Leu Pro Thr Ser Thr Ala Pro Leu Leu Gln Gln Glu Gly  $20 \ \ 25 \ \ 30$ 

Lys Lys Leu Ala Leu Ile Ala Cys Gln Pro Trp Pro Pro Pro Pro Arg
35 40 45

Leu Ala Ser Ser Pro Pro Ser Arg Ala Pro Gly Ser Arg Pro Pro

50 55 60

Arg Gly Pro His Arg Arg Pro Ser Trp Trp Pro Arg Pro Ala Arg Arg
65 70 75 80

Arg Arg Gly Ala His Leu Arg Val His Val Leu Leu Gln Pro

90 Ala Leu Arg Pro Asp Val Xaa Pro Val Gln Pro His Gln Gly Val His Arg Val Ser Ala Arg 115 (2) INFORMATION FOR SEO ID NO:2687: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..58 (D) OTHER INFORMATION: / Ceres Seq. ID 1601642 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687: Met Ala Thr Ala Ala Ala Ser Ser Leu Leu Lys Ser Ser Phe Ala Gly 5 10 Ser Arg Leu Pro Ala Ala Thr Arg Thr Thr Pro Ala Ser Leu Val Val 20 25 Ala Thr Ala Arg Ala Ala Pro Ala Arg Gly Pro Ser Ala Arg Pro Cys 40 Pro Cys Pro Pro Pro Thr Arg Pro Thr Thr 50 55 (2) INFORMATION FOR SEQ ID NO: 2688: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..465 (D) OTHER INFORMATION: / Ceres Seq. ID 1601653 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688: agtttetteg cegtegettt gegagtgtgg aegggaegga taeatgaggg agaaeggege cqccaqqqac qaqqqcccq ccttqtqcaa qqccqctgcg gcggacqgqq qcggqqatgt 120 qqqcqccqcc tccqccqcc qccqccqccq qctcqqqcqt gccacqqaqg ggcctgctcc 180 gacgaagaga atccggtcgg ggtcgcagag gtcgccgtac gactcgtctc tggagacggc 240 gacqqacqqc tgctqctqqc cgqcqccct atcqcatqqc gccqtgtcqq tgatcqqqcq 300 gcggaggag atggaggacg cgttcgccgt cgcgctctcg ttcctggcct cggaggcggt 360 gggcggcgag caggagcagg agctggactt cttcgccgtg tacgatggcc acggcggtgc 420 aagggtggcg gaggcgtgcc gggagcggat tgcacgtggt gctgg (2) INFORMATION FOR SEQ ID NO: 2689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..155 (D) OTHER INFORMATION: / Ceres Seq. ID 1601654 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689: Ser Phe Phe Ala Val Ala Leu Arg Val Trp Thr Gly Arg Ile His Glu 10 Gly Glu Arg Arg Arg Gln Gly Arg Gly Pro Arg Leu Val Gln Gly Arg

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Cys Gly Gly Arg Gly Arg Gly Cys Gly Arg Arg Leu Arg Pro Pro Pro 35 40 45
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Pro Pro Ala Arg Ala Cys His Gly Gly Ala Cys Ser Asp Glu Glu Asn 50  $\,$  55  $\,$  60

Pro Val Gly Val Ala Glu Val Ala Val Arg Leu Val Ser Gly Asp Gly 65 70 75 80

Asp Gly Arg Leu Leu Ala Gly Ala Pro Ile Ala Trp Arg Val85  $\phantom{0}90$   $\phantom{0}95$ 

Gly Asp Arg Ala Ala Glu Gly Asp Gly Gly Arg Val Arg Arg Arg Ala
100 105 110

Leu Val Pro Gly Leu Gly Gly Gly Gly Arg Arg Ala Gly Ala Gly Ala 115 120 125

Gly Leu Leu Arg Arg Val Arg Trp Pro Arg Arg Cys Lys Gly Gly 130 135 140

Gly Val Pro Gly Ala Asp Cys Thr Trp Cys Trp 145 150 155

- (2) INFORMATION FOR SEQ ID NO: 2690:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 154 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..154
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601655
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Val Ser Ser Pro Ser Leu Cys Glu Cys Gly Arg Asp Gly Tyr Met Arg 1 5 10 15

Glu Asn Gly Ala Ala Arg Asp Glu Gly Pro Ala Leu Cys Lys Ala Ala 20 25 30

Ala Ala Asp Gly Gly Asp Val Gly Ala Ala Ser Ala Arg Arg Arg 35 40 45

Arg Arg Leu Gly Arg Ala Thr Glu Gly Pro Ala Pro Thr Lys Arg Ile 50 55 60

Arg Ser Gly Ser Gln Arg Ser Pro Tyr Asp Ser Ser Leu Glu Thr Ala 65 70 75 80 Thr Asp Gly Cys Cys Trp Pro Ala Arg Leu Ser His Gly Ala Val Ser

85 90 95
Val Ile Gly Arg Arg Glu Met Glu Asp Ala Phe Ala Val Ala Leu
100 105 110

Ser Phe Leu Ala Ser Glu Ala Val Gly Gly Glu Gln Glu Glu Leu 115 120 125

Asp Phe Phe Ala Val Tyr Asp Gly His Gly Gly Ala Arg Val Ala Glu 130 135 140

Ala Cys Arg Glu Arg Ile Ala Arg Gly Ala 145 150

- (2) INFORMATION FOR SEQ ID NO:2691:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601656
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

Met Arg Glu Asn Gly Ala Ala Arg Asp Glu Gly Pro Ala Leu Cys Lys

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10
Ala Ala Ala Asp Gly Gly Gly Asp Val Gly Ala Ala Ser Ala Arg
           20
                               25
Arg Arg Arg Leu Gly Arg Ala Thr Glu Gly Pro Ala Pro Thr Lys
                           40
Arg Ile Arg Ser Gly Ser Gln Arg Ser Pro Tyr Asp Ser Ser Leu Glu
                       55
Thr Ala Thr Asp Gly Cys Cys Trp Pro Ala Arg Leu Ser His Gly Ala
                   70
                                      75
Val Ser Val Ile Gly Arg Arg Glu Met Glu Asp Ala Phe Ala Val
               85
                                   90
Ala Leu Ser Phe Leu Ala Ser Glu Ala Val Gly Gly Glu Gln Glu Gln
           100 -
                              105
Glu Leu Asp Phe Phe Ala Val Tyr Asp Gly His Gly Gly Ala Arg Val
                        120
      115
Ala Glu Ala Cys Arg Glu Arg Ile Ala Arg Gly Ala
                      135
    130
(2) INFORMATION FOR SEQ ID NO:2692:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 409 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..409
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601657
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:
ctaatcqaaa aaaaacacga gcgagcacaa aaaaaaaatc ccaatatccg caacggcaat
gtotocgotg coccgoateg tgotoctogo cgtcgccgcc gccgccgccg cagcggtcac
                                                                     120
ggcgtcagcc acgtcgctca gcggcgcggc gaacgaccta ctccccaagt acggcctccc
                                                                     180
gaaggggete atcceggact cegtegeete etacagette gaegaggeea egggegeett
                                                                    240
cgagatccac ctcgccggca cctgctacgt ccacttcggc tcccacctcg tctactacga
                                                                     300
gaggaccata accggcaagc totocaaggg cgccatotog gacctotocg gegtecagge
                                                                     360
caaqaaactc ttcctctggg tctacgtcac gggatggtcg cgcaccccg
(2) INFORMATION FOR SEQ ID NO: 2693:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 136 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..136
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601658
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:
Leu Ile Glu Lys Lys His Glu Arg Ala Gln Lys Lys Asn Pro Asn Ile
                                   10
Arg Asn Gly Asn Val Ser Ala Ala Pro His Arg Ala Pro Arg Arg
            20
                               25
Arg Arg Arg Arg Ser Gly His Gly Val Ser His Val Ala Gln Arg
                           40
Arg Gly Glu Arg Pro Thr Pro Gln Val Arg Pro Pro Glu Gly Ala His
                       5.5
```

Pro Gly Leu Arg Arg Leu Leu Gln Leu Arg Arg Gly His Gly Arg Leu

Arg Asp Pro Pro Arg Arg His Leu Leu Arg Pro Leu Arg Leu Pro Pro

Arg Leu Leu Arg Glu Asp His Asn Arg Gln Ala Leu Gln Gly Arg His

75

90

70

110 105 100 Leu Gly Pro Leu Arg Arg Pro Gly Gln Glu Thr Leu Pro Leu Gly Leu 115 120 Arg His Gly Met Val Ala His Pro 135 130 (2) INFORMATION FOR SEQ ID NO:2694: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..102 (D) OTHER INFORMATION: / Ceres Seq. ID 1601659 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694: Asn Arg Lys Lys Thr Arg Ala Ser Thr Lys Lys Ser Gln Tyr Pro 10 5 Gln Arg Gln Cys Leu Arg Cys Pro Ala Ser Cys Ser Ser Pro Ser Pro 30 25 20 Pro Pro Pro Pro Gln Arg Ser Arg Arg Gln Pro Arg Arg Ser Ala Ala 40 Arg Arg Thr Thr Tyr Ser Pro Ser Thr Ala Ser Arg Arg Gly Ser Ser 55 Arg Thr Pro Ser Pro Pro Thr Ala Ser Thr Arg Pro Arg Ala Pro Ser 75 70 Arg Ser Thr Ser Pro Ala Pro Ala Thr Ser Thr Ser Ala Pro Thr Ser 90 Ser Thr Thr Arg Gly Pro 100 (2) INFORMATION FOR SEQ ID NO: 2695: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..117 (D) OTHER INFORMATION: / Ceres Seq. ID 1601660 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695: Met Ser Pro Leu Pro Arg Ile Val Leu Leu Ala Val Ala Ala Ala 10 5 Ala Ala Ala Val Thr Ala Ser Ala Thr Ser Leu Ser Gly Ala Ala Asn 25 20 Asp Leu Leu Pro Lys Tyr Gly Leu Pro Lys Gly Leu Ile Pro Asp Ser 45 40 Val Ala Ser Tyr Ser Phe Asp Glu Ala Thr Gly Ala Phe Glu Ile His 60 55 Leu Ala Gly Thr Cys Tyr Val His Phe Gly Ser His Leu Val Tyr Tyr 75 70 Glu Arg Thr Ile Thr Gly Lys Leu Ser Lys Gly Ala Ile Ser Asp Leu 95 90 85 Ser Gly Val Gln Ala Lys Lys Leu Phe Leu Trp Val Tyr Val Thr Gly 100 Trp Ser Arg Thr Pro 115

(2) INFORMATION FOR SEQ ID NO:2696:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..460
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601676
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696: atccaattca cacgatecte actcaccaca ccaaccagca agcaaaagte ecceaatect

ctcgtctccg cggcgaagat gtcgggggc ggcaagggcg gcaagggcct gggcaagggc 120 ggcgcgaagc gtcaccggaa ggtgctgcgc gacaacatcc aggggatcac gaagccggcg 180 atccggaggc tggcgcggcg gggcggcgt aacgtcatct cggggctcat ctacgaggag 240 acccgcggcg tgctcaagat cttcctggag aacgtcatcc gcgacgccgt cacctacacc 300 gagcacgcgc gccgtaagac cgtcaccgcc atggacgtcg tctacggct taagcgccag 360 ggccgcaccc tctacggctt cggcggctag gcctgcgcg cgcgcttcgc cgtcgctgcg 420

gttctggtgt tgctgcagtt cgcaagttgt ttgtgtgggc

- (2) INFORMATION FOR SEQ ID NO:2697:
   (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..129
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601677
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

Ser Pro Asn Pro Leu Val Ser Ala Ala Lys Met Ser Gly Arg Gly Lys 20 25 30

Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg His Arg Lys Val\$35\$ 40 45

Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Arg Leu 50 55 60

Ala Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr Glu Glu 65 70 75 80

Thr Arg Gly Val Leu Lys Ile Phe Leu Glu Asn Val Ile Arg Asp Ala

85 90 95
Val Thr Tyr Thr Glu His Ala Arg Arg Lys Thr Val Thr Ala Met Asp

100 105 110

Val Val Tyr Ala Leu Lys Arg Gln Gly Arg Thr Leu Tyr Gly Phe Gly
115 120 125

Gly

- (2) INFORMATION FOR SEQ ID NO: 2698:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 104 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..104
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601678
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

Pro Ile His Thr Ile Leu Thr His His Thr Asn Gln Gln Ala Lys Val

His Leu His Arg Ala Arg Ala Pro 100

- (2) INFORMATION FOR SEQ ID NO:2699:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..103
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala
1 5 10 15

Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys 20 25 30

Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu 50 55 60

Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys 70 75 80

Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg 85 90 95

Thr Leu Tyr Gly Phe Gly Gly 100

- (2) INFORMATION FOR SEQ ID NO:2700:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 440 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..440
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

aagccgattt cgtgtccctg cagccacgge caccgccaat ctccacttet ttatettete cgaggaaagt aggtcgagga tgccccgcag cggcttctcg gggtccttca ggtcgcccaa 120 gatcgacgtc gtcatcgaca tgggaaaccc cttcctcaac cgcaccgtcg acggcttcct 180 caagatcggc gccgtcggcg cctgcaaggt ggctgccgag gagaccttcg agtgcctcca 240 cagggggat gtttcgaage acaaggttga gcatgccctg aggaagatgt gcaaggaggg 300 cgcatattgg ggcactgttg ctggagtta tgtgggcatg gtgtacggcg tggaaagggt 360 ccgtggccgc agtgactgga agaacgcgat gatcggggc gccttgtccg gcgccctgat 420 ctccqqcqcc aqcaacagcg

- (2) INFORMATION FOR SEQ ID NO:2701:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..146
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Ser Arg Phe Arg Val Pro Ala Ala Thr Ala Thr Ala Asn Leu His Phe  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Phe Ile Phe Ser Glu Glu Ser Arg Ser Arg Met Pro Arg Ser Gly Phe 20 25 30

Ser Gly Ser Phe Arg Ser Pro Lys Ile Asp Val Val Ile Asp Met Gly 35 40 45

Asn Pro Phe Leu Asn Arg Thr Val Asp Gly Phe Leu Lys Ile Gly Ala 50 60

Val Gly Ala Cys Lys Val Ala Ala Glu Glu Thr Phe Glu Cys Leu His 65 70 75 80

Arg Gly Asp Val Ser Lys His Lys Val Glu His Ala Leu Arg Lys Met 85 90 95

Cys Lys Glu Gly Ala Tyr Trp Gly Thr Val Ala Gly Val Tyr Val Gly
100 105 110

Met Val Tyr Gly Val Glu Arg Val Arg Gly Arg Ser Asp Trp Lys Asn  $115 \\ \hspace{1.5cm} 120 \\ \hspace{1.5cm} 125$ 

Ala Met Ile Gly Gly Ala Leu Ser Gly Ala Leu Ile Ser Gly Ala Ser 130 135 140

Asn Ser

145

- (2) INFORMATION FOR SEQ ID NO:2702:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: peptide
    - (ix) FEATURE:
      - (A) NAME/KEY: peptide
      - (B) LOCATION: 1..120
      - (D) OTHER INFORMATION: / Ceres Seq. ID 1601686
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

Met Pro Arg Ser Gly Phe Ser Gly Ser Phe Arg Ser Pro Lys Ile Asp 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15

Val Val Ile Asp Met Gly Asn Pro Phe Leu Asn Arg Thr Val Asp Gly
20 25 30

Phe Leu Lys Ile Gly Ala Val Gly Ala Cys Lys Val Ala Ala Glu Glu 35 40 45

Thr Phe Glu Cys Leu His Arg Gly Asp Val Ser Lys His Lys Val Glu 50 60

His Ala Leu Arg Lys Met Cys Lys Glu Gly Ala Tyr Trp Gly Thr Val 65 70 75 80

Ala Gly Val Tyr Val Gly Met Val Tyr Gly Val Glu Arg Val Arg Gly
85 90 95

Arg Ser Asp Trp Lys Asn Ala Met Ile Gly Gly Ala Leu Ser Gly Ala 100 105 110

Leu Ile Ser Gly Ala Ser Asn Ser 115 120

- (2) INFORMATION FOR SEQ ID NO:2703:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 100 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..100
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

Met Gly Asn Pro Phe Leu Asn Arg Thr Val Asp Gly Phe Leu Lys Ile 1  $\phantom{-}5\phantom{+}$  10  $\phantom{-}15\phantom{+}$ 

Gly Ala Val Gly Ala Cys Lys Val Ala Ala Glu Glu Thr Phe Glu Cys 20 25 30

Leu His Arg Gly Asp Val Ser Lys His Lys Val Glu His Ala Leu Arg 35 40 45

Lys Met Cys Lys Glu Gly Ala Tyr Trp Gly Thr Val Ala Gly Val Tyr

Val Gly Met Val Tyr Gly Val Glu Arg Val Arg Gly Arg Ser Asp Trp 65 70 75 80

Lys Asn Ala Met Ile Gly Gly Ala Leu Ser Gly Ala Leu Ile Ser Gly 85 90 95

Ala Ser Asn Ser

100

- (2) INFORMATION FOR SEQ ID NO: 2704:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: DNA (genomic)
    - (ix) FEATURE:
      - (A) NAME/KEY: -
      - (B) LOCATION: 1..488
      - (D) OTHER INFORMATION: / Ceres Seq. ID 1601688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704: aaaacggcgt agcatactgg cttcgataat cacgagaagg gcgccgatct gggaaggcat 60 tgtcttgttg tactttccct tccggcagtg gcctcgattc gcatcccctt ttcccgtcca 120 180 tgcgcgcgcc ggcgggcggt gccagtgcca ccgcgctcgc ggcggccatg aacattaagc 240 ageogetica eggegeateg aegetigtteg egetigetete tetetegetig eteeteetee 300 quetquetcut coquetcogo etggeogoet teogogaego ggogotgtog etccacctgo 360 tggcgcgcct ccgcctccgc cccgtcctcc tctgcctccc ggcagcctgc cacgacggcg qeqceqqeqc eqqeqceace acgetgegeg tetggtgece egccacecca tectceaage 420 480 cgccgctgct cctcctccac ggcttcggcg gggacgccaa gtggacgtgg gcgcgcaacc
- ttcccgcg (2) INFORMATION FOR SEQ ID NO:2705:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..123
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601689
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Met Arg Ala Pro Ala Gly Gly Ala Ser Ala Thr Ala Leu Ala Ala Ala 1 5 10 15

Met Asn Ile Lys Gln Pro Leu His Gly Ala Ser Thr Leu Phe Ala Leu 20 25 30

Leu Ser Leu Leu Leu Leu Arg Leu Leu Arg Leu Arg Leu

```
40
Ala Ala Phe Arg Asp Ala Ala Leu Ser Leu His Leu Leu Ala Arg Leu
                       55
                                           60
Arg Leu Arg Pro Val Leu Leu Cys Leu Pro Ala Ala Cys His Asp Gly
                   70
                                       75
Gly Ala Gly Ala Gly Ala Thr Thr Leu Arg Val Trp Cys Pro Ala Thr
               85
                                   90
Pro Ser Ser Lys Pro Pro Leu Leu Leu His Gly Phe Gly Asp
           100
                              105
Ala Lys Trp Thr Trp Ala Arg Asn Leu Pro Ala
                           120
(2) INFORMATION FOR SEQ ID NO:2706:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 107 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..107
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601690
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:
Met Asn Ile Lys Gln Pro Leu His Gly Ala Ser Thr Leu Phe Ala Leu
           5
                                   10
Leu Ser Leu Ser Leu Leu Leu Arg Leu Leu Leu Arg Leu Arg Leu
          20
                               25
Ala Ala Phe Arg Asp Ala Ala Leu Ser Leu His Leu Leu Ala Arg Leu
                           4.0
Arg Leu Arg Pro Val Leu Cys Leu Pro Ala Ala Cys His Asp Gly
                       55
Gly Ala Gly Ala Gly Ala Thr Thr Leu Arg Val Trp Cys Pro Ala Thr
                                       75
                   70
Pro Ser Ser Lys Pro Pro Leu Leu Leu His Gly Phe Gly Gly Asp
              85 90
Ala Lys Trp Thr Trp Ala Arg Asn Leu Pro Ala
           100
                              105
(2) INFORMATION FOR SEQ ID NO:2707:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 524 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..524
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601691
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:
agattgacgg acatgatgca ccctacgaga agcttccctt tctccttgtc cttgcaaccc
                                                                      60
tecgecettt eggttgtege aatataaact tgeeggggag egtggeggee atttgeeece
                                                                     120
agcagatett gtgaecetee etcageegeg tegegteeca tectaegate caaaggtete
                                                                     180
tctgctcgca gccatggcga agaactaccc gaccgtgagc gccgagtaca gcgaggctgt
                                                                     240
cgagaaggcc aggcgcaagc tccgagccct catcgccgag aagagctgcg ccccgctcat
                                                                     300
geteegeete gegtggeact cegeggggae gttegaegtg tegtegagga eeggeggtee
                                                                     360
atteggeacg atgaageate agteggaatt ggeteacgge getaacgegg ggetggaeat
                                                                     420
cgcggtgcgg ctgctcgagc ccatcaagga ggagttccca atcctctctt acgccgattt
                                                                     480
ctaccagete gegggagttg tggcegtgga ggtcaccggt gggc
(2) INFORMATION FOR SEQ ID NO:2708:
     (i) SEQUENCE CHARACTERISTICS:
```

(A) LENGTH: 110 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..110
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601692
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Met Ala Lys Asn Tyr Pro Thr Val Ser Ala Glu Tyr Ser Glu Ala Val 1 5 10 15

Glu Lys Ala Arg Arg Lys Leu Arg Ala Leu Ile Ala Glu Lys Ser Cys 20 25 30

Ala Pro Leu Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp 35 40 45

Val Ser Ser Arg Thr Gly Gly Pro Phe Gly Thr Met Lys His Gln Ser 50 55 60

Glu Leu Ala His Gly Ala As<br/>n Ala Gly Leu Asp Ile Ala Val Arg Leu  $65 \hspace{1.5cm} 70 \hspace{1.5cm} 75 \hspace{1.5cm} 80$ 

Leu Glu Pro Ile Lys Glu Glu Phe Pro Ile Leu Ser Tyr Ala Asp Phe 85 90 95

Tyr Gln Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly
100 105 110

- (2) INFORMATION FOR SEQ ID NO:2709:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..75
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601693
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp Val Ser Ser 1 10 15

Arg Thr Gly Gly Pro Phe Gly Thr Met Lys His Gln Ser Glu Leu Ala 20 25 30

His Gly Ala Asn Ala Gly Leu Asp Ile Ala Val Arg Leu Leu Glu Pro 35 40 45

Ile Lys Glu Glu Phe Pro Ile Leu Ser Tyr Ala Asp Phe Tyr Gln Leu 50 55 60

Ala Gly Val Val Ala Val Glu Val Thr Gly Gly 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2710:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..505
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601697
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

tttaaactag ctcgcctttc cctccacaaa cacccatcag ccatcccctt ttgctgcaaa 60 tctttctctg aattgtgggt ctccgacaat ggcggcgcta gctccatcca agattctggg cacccagctc aacttcgcgg gctcctcccg ctacgccacc gcagcgccaa ccgcgggggc 180 tcagaagatt gtctcccttt tcagcaagaa gcctgcccag aagcccaagc ccgctgcggt 240

atogtoctot totocagaca toagogacga getegecaag tggtatggte etgacaggag 300 gatetacetg eeggatgge tgttggaceg gteggaggtg eeggagtace teaeeggaga 360 ggtecetgga gaetatgget aegaeeettt tggeetgge aagaageeag aggaettege 420 caagtaceag geetaegage tgateeatge eagatggee atgeteggtg eegetggege 480

- tgtcatccca gaggcctgca acaag (2) INFORMATION FOR SEQ ID NO:2711:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601698
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

Phe Lys Leu Ala Arg Leu Ser Leu His Lys His Pro Ser Ala Ile Pro 1 5 10 15

Phe Cys Cys Lys Ser Phe Ser Glu Leu Trp Val Ser Asp Asn Gly Gly 20 25 30

Ala Ser Ser Ile Gln Asp Ser Gly His Pro Ala Gln Leu Arg Gly Leu 35 40 45

Leu Pro Leu Arg His Arg Ser Ala His Arg Gly Gly Ser Glu Asp Cys 50 55 60

Leu Pro Phe Gln Gln Glu Ala Cys Pro Glu Ala Gln Ala Arg Cys Gly 65 70 75 80

Ile Val Leu Phe Ser Arg His Gln Arg Arg Ala Arg Gln Val Val Trp 85 90 95

Ser

- (2) INFORMATION FOR SEQ ID NO:2712:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..139
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

Met Ala Ala Leu Ala Pro Ser Lys Ile Leu Gly Thr Gln Leu Asn Phe

1 10 15

Ala Gly Ser Ser Arg Tyr Ala Thr Ala Ala Pro Thr Ala Gly Ala Gln 20 25 30

Lys Ile Val Ser Leu Phe Ser Lys Lys Pro Ala Gln Lys Pro Lys Pro 35 40 45

Ala Ala Val Ser Ser Ser Ser Pro Asp Ile Ser Asp Glu Leu Ala Lys
50 55 60

Trp Tyr Gly Pro Asp Arg Arg Ile Tyr Leu Pro Asp Gly Leu Leu Asp 65 70 75 80

Arg Ser Glu Val Pro Glu Tyr Leu Thr Gly Glu Val Pro Gly Asp Tyr
85 90 95

Gly Tyr Asp Pro Phe Gly Leu Gly Lys Lys Pro Glu Asp Phe Ala Lys
100 105 110

Tyr Gln Ala Tyr Glu Leu Ile His Ala Arg Trp Ala Met Leu Gly Ala 115 120 125

Ala Gly Ala Val Ile Pro Glu Ala Cys Asn Lys 130

- (2) INFORMATION FOR SEQ ID NO:2713:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 504 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..504
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601700
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

60 gtgcgctgcg gacgggtcgg atctgagacg agacgatece ececteceet caaceggaac ttgttttacc ccatctcatc ccactgactc cageccaccc accegecege tgcctccgcc 120 gagatetegt eggaetegga teegeeegae caegaceaee eegegeegee geegegeage 180 agcagcagat cagagaagat ggccggactc gacaccttcc tcttcacctc ggagtccgtg 240 aacgagggac accetgacaa getetgegae caggteteag atgetgttet ggaegettge 300 cttgctgagg accetgacag caaggttgct tgcgagacct gcaccaagac caacatggtc 360 atggtetttg gtgagateae caecaaggee aatgtegaet aegagaagat tgteagggag 420 acatgccgca acattggttt cgtgtcgaac gatgtcgggc ttgacgctga ccactgcaag 480 gtgcttgtga acattgagca gcag

- (2) INFORMATION FOR SEQ ID NO:2714:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..79
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601701
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

Cys Ala Ala Asp Gly Ser Asp Leu Arg Arg Asp Asp Pro Pro Leu Pro 1 5 10 15

Ser Thr Gly Thr Cys Phe Thr Pro Ser His Pro Thr Asp Ser Ser Pro 20 25 30

Pro Thr Arg Pro Leu Pro Pro Pro Arg Ser Arg Arg Thr Arg Ile Arg 35 40 45

Pro Thr Thr Thr Pro Arg Arg Arg Ala Ala Ala Ala Asp Gln 50 55 60

Arg Arg Trp Pro Asp Ser Thr Pro Ser Ser Ser Pro Arg Ser Pro 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2715:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..102
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

Met Ala Gly Leu Asp Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu 1 5 10 15

Gly His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp 20 25 30

Ala Cys Leu Ala Glu Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys 35 40 45

Val Asn Ile Glu Gln Gln 100

- (2) INFORMATION FOR SEQ ID NO:2716:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 69 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..69
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601703
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Met Leu Phe Trp Thr Leu Ala Leu Leu Arg Thr Leu Thr Ala Arg Leu  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Leu Ala Arg Pro Ala Pro Arg Pro Thr Trp Ser Trp Ser Leu Val Arg 20 25 30

Ser Pro Pro Arg Pro Met Ser Thr Thr Arg Arg Leu Ser Gly Arg His 35 40 45

Ala Ala Thr Leu Val Ser Cys Arg Thr Met Ser Gly Leu Thr Leu Thr 50 55 60

Thr Ala Arg Cys Leu

55

- (2) INFORMATION FOR SEQ ID NO:2717:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 554 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..554
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601704
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

ctgtggtgtg gactcctgca ctgtgctcct tcgtctcctc ctcccctgcc tgccaccaac 60 tqccaaggtg ccaagcaagt gcagatacct tecetgeete acaaacaacg ccatcagggt 120 cttcaaccag ggcaggttct cttctttcat tcagctatgg gcaacctgtg ctgctgtgtt 180 240 caagttgacc agtcgactgt ggccatcagg gagcagtttg gcaagtttga cagcgtgctt 300 gagccaggat gccactgcat gccttggttc gccggcaagc gtgtagctgg gcatctcaca ctcaggctgc agcaactgga tgtgcgctgt gagacaaaaa caaaggacaa tgtttttgtg 360 aatqtqqtqq catctattca qtaccqcqct ctgqctqaca aagcaagtga cgctttctac 420 aaactgagca acacaaggtc ccagatccaa gcctacgtct ttgacgtgat cagagcaagc 480 gttcccaagc tccatttgga cgatgctttc gagcagaagg acgagatcgc aagggcggtg 540 gaggaagagc tgag

- (2) INFORMATION FOR SEQ ID NO:2718:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 184 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide

- (B) LOCATION: 1..184
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

Leu Trp Cys Gly Leu Leu His Cys Ala Pro Ser Ser Pro Pro Pro Leu 1 5 10 15

Pro Ala Thr Asn Cys Gln Gly Ala Lys Gln Val Gln Ile Pro Ser Leu 20 25 30

Pro His Lys Gln Arg His Gln Gly Leu Gln Pro Gly Gln Val Leu Phe 35 40

Phe His Ser Ala Met Gly Asn Leu Cys Cys Cys Val Gln Val Asp Gln 50 55 60

Ser Thr Val Ala Ile Arg Glu Gln Phe Gly Lys Phe Asp Ser Val Leu 65 70 75 80

Glu Pro Gly Cys His Cys Met Pro Trp Phe Ala Gly Lys Arg Val Ala 85 90 95

Gly His Leu Thr Leu Arg Leu Gln Gln Leu Asp Val Arg Cys Glu Thr  $100 \,$   $105 \,$   $110 \,$ 

Lys Thr Lys Asp Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr \$115\$ \$120\$

Arg Ala Leu Ala Asp Lys Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn 130 135 140

Thr Arg Ser Gln Ile Gln Ala Tyr Val Phe Asp Val Ile Arg Ala Ser 145 150 155 160

Val Pro Lys Leu His Leu Asp Asp Ala Phe Glu Gln Lys Asp Glu Ile \$165\$ \$170\$ \$175\$

Ala Arg Ala Val Glu Glu Glu Leu 180

- (2) INFORMATION FOR SEQ ID NO:2719:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..132
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601706
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

Met Gly Asn Leu Cys Cys Cys Val Gl<br/>n Val Asp Gl<br/>n Ser Thr Val Ala 1 5 10 15

Ile Arg Glu Gln Phe Gly Lys Phe Asp Ser Val Leu Glu Pro Gly Cys 20 25 30

His Cys Met Pro Trp Phe Ala Gly Lys Arg Val Ala Gly His Leu Thr 35 40 45

Leu Arg Leu Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp 50 55 60

Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala 65 70 75 80

Asp Lys Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn Thr Arg Ser Gln
85 90 95

Ile Gl<br/>n Ala Tyr Val Phe Asp Val Ile Arg Ala Ser Val Pro Lys Leu<br/>  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$ 

His Leu Asp Asp Ala Phe Glu Gln Lys Asp Glu Ile Ala Arg Ala Val 115 120 125

Glu Glu Glu Leu

130

- (2) INFORMATION FOR SEQ ID NO:2720:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..98
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601707
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

Leu Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp Asn Val 20 25 30

Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala Asp Lys 35 40 45

Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn Thr Arg Ser Gln Ile Gln 50 55 60

Ala Tyr Val Phe Asp Val Ile Arg Ala Ser Val Pro Lys Leu His Leu 65 70 75 80

Asp Asp Ala Phe Glu Gln Lys Asp Glu Ile Ala Arg Ala Val Glu Glu 85 90 95

Glu Leu

- (2) INFORMATION FOR SEQ ID NO:2721:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 533 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..533
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601719
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721: atctaaaaaa cacctagegg aaaaagaaaa ggaaaaaagt cgcccctccg ttgggaccta attcaggggt ttgagggtc ctcccatttc gtcggcttcg ttgtcgtcg tcgtaagctg

atteacgegt tteagggete eteccattee gteggetteg ttegtegteg tegtaagetg 120 cagetagtgt ggactggaga teeaccaete eaccagteeg gtecatetge tggacetega 180 ttggtttett ettacetagg aacateeggg gatgtegaet eetgegagga agaggetgat 240 gagggatte aageggtga tgeaggaee teeggeegge ataagtggeg eecegeagga 300 taacaacata atgetgtga atgetgteat atttggaeet gatgatacee egtgggatgg 360 aggtacgttt aagetgaete teeagtttaa tgaagaatat eeaaacaaae eaceaaetgt 420 gegatttgtt tetaggatgt teeateetaa eatttatget gatggaagea tatgettaga 480 tateetgeag aateagtgga gteeegatat atgatgtage tgegataete aeg

- (2) INFORMATION FOR SEQ ID NO:2722:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 100 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..100
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601720
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

Met Ser Thr Pro Ala Arg Lys Arg Leu Met Arg Asp Phe Lys Arg Leu

1 5 10 15

Met Gln Asp Pro Pro Ala Gly Ile Ser Gly Ala Pro Gln Asp Asn Asn 20 25 30

Ile Met Leu Trp Asn Ala Val Ile Phe Gly Pro Asp Asp Thr Pro Trp
35 40 45

Asp Gly Gly Thr Phe Lys Leu Thr Leu Gln Phe Asn Glu Glu Tyr Pro 50 60

Asn Lys Pro Pro Thr Val Arg Phe Val Ser Arg Met Phe His Pro Asn 65 70 75 80

Ile Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Gln Trp
85 90 95

Ser Pro Asp Ile

100

- (2) INFORMATION FOR SEQ ID NO:2723:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 91 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..91
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601721
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

Met Arg Asp Phe Lys Arg Leu Met Gln Asp Pro Pro Ala Gly Ile Ser 1 5 10 15

Gly Ala Pro Gln Asp Asn Asn Ile Met Leu Trp Asn Ala Val Ile Phe  $20 \\ 25 \\ 30$ 

Gly Pro Asp Asp Thr Pro Trp Asp Gly Gly Thr Phe Lys Leu Thr Leu  $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$ 

Gln Phe Asn Glu Glu Tyr Pro Asn Lys Pro Pro Thr Val Arg Phe Val 50 60

Ser Arg Met Phe His Pro Asn Ile Tyr Ala Asp Gly Ser Ile Cys Leu 65 70 75 80

Asp Ile Leu Gln Asn Gln Trp Ser Pro Asp Ile 85 90

- (2) INFORMATION FOR SEQ ID NO:2724:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 84 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..84
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601722
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

Met Gln Asp Pro Pro Ala Gly Ile Ser Gly Ala Pro Gln Asp Asn Asn 1 5 10 15

Ile Met Leu Trp Asn Ala Val Ile Phe Gly Pro Asp Asp Thr Pro Trp
20 25 30

Asp Gly Gly Thr Phe Lys Leu Thr Leu Gln Phe Asn Glu Glu Tyr Pro  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Asn Lys Pro Pro Thr Val Arg Phe Val Ser Arg Met Phe His Pro Asn 50 55 60

Ile Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Gln Trp65707580

Ser Pro Asp Ile

- (2) INFORMATION FOR SEQ ID NO: 2725:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 523 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..523
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601731
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725: 60 qqttccatta ctqqtcccta qcaqqaaqca qqatqqaqtt qqcqctcaqc ttqqqqqaqa ccatggcgga tgccggaagg gacctcatgc tggggcttgg gatgggggtc ggggtgcgga 120 180 qqqaqqaqqa aqcqcaqaqa qqqaqqaqqq acaqqqaqqt gagqcgggag ctggagttca 240 eggegaggag egeceggteg tegeeggage eggeggtgeg acteacecte etgeaeggee 300 teggectece gtggeegeeg eegeegtegt eegagaceaa eeggeacetg gaggegtegg 360 egegtggett egaegtgaae egggegeegt egetgteege ggeeggtgge geegeggagg aggacgagga gcaggacgag gcggcggcgg cggcggcatc gtcgtcgccc aacaacagcg 420 480 cqaqctcctt cccgacgqac ttctccgcgc agggccaggt ggcgcccggc gccgaccgcg
- (2) INFORMATION FOR SEQ ID NO:2726:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 174 amino acids

cgtgctcccg cgccagcgac gaggacgacg gcggctccgc gcg

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..174
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601732
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:
- Val Pro Leu Leu Val Pro Ser Arg Lys Gln Asp Gly Val Gly Ala Gln 1 5 10 15
- Leu Gly Gly Asp His Gly Gly Cys Arg Lys Gly Pro His Ala Gly Ala 20 25 30
- Trp Asp Gly Gly Arg Gly Ala Glu Gly Gly Gly Ser Ala Glu Arg Glu
  35 40 45
- Glu Gly Gln Gly Glu Glu Ala Gly Ala Gly Val His Gly Glu Glu Arg
  50 55 60
- Pro Val Val Ala Gly Ala Gly Gly Ala Thr His Pro Pro Ala Arg Pro 65 70 75 80
- Arg Pro Pro Val Ala Ala Ala Val Val Arg Asp Gln Pro Ala Pro 85 90 95
- Gly Gly Val Gly Ala Trp Leu Arg Arg Glu Pro Gly Ala Val Ala Val 100 105 110
- Arg Gly Arg Trp Arg Arg Gly Gly Gly Arg Gly Ala Gly Arg Gly Gly 115 120 125
- Gly Gly Gly Ile Val Val Ala Gln Gln Arg Glu Leu Leu Pro 130 135 140
- Asp Gly Leu Leu Arg Ala Gly Pro Gly Gly Ala Arg Arg Pro Arg 145 150 155 160
- Val Leu Pro Arg Gln Arg Arg Gly Arg Arg Arg Leu Arg Ala 165 170
- (2) INFORMATION FOR SEQ ID NO:2727:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 173 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..173
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727: Phe His Tyr Trp Ser Leu Ala Gly Ser Arg Met Glu Leu Ala Leu Ser 10 Leu Gly Glu Thr Met Ala Asp Ala Gly Arg Asp Leu Met Leu Gly Leu 25 Gly Met Gly Val Gly Val Arg Arg Glu Glu Glu Ala Gln Arg Gly Arg Arg Asp Arg Glu Val Arg Arg Glu Leu Glu Phe Thr Ala Arg Ser Ala 55 Arg Ser Ser Pro Glu Pro Ala Val Arg Leu Thr Leu Leu His Gly Leu 70 75 Gly Leu Pro Trp Pro Pro Pro Pro Ser Ser Glu Thr Asn Arg His Leu 90 85 Glu Ala Ser Ala Arg Gly Phe Asp Val Asn Arg Ala Pro Ser Leu Ser 105 100 Ala Ala Gly Gly Ala Ala Glu Glu Asp Glu Glu Gln Asp Glu Ala Ala 120 140

Ala Ala Ala Ser Ser Ser Pro Asn Asn Ser Ala Ser Ser Phe Pro 135

Thr Asp Phe Ser Ala Gln Gly Gln Val Ala Pro Gly Ala Asp Arg Ala 150 155

Cys Ser Arg Ala Ser Asp Glu Asp Asp Gly Gly Ser Ala 165 170

- (2) INFORMATION FOR SEQ ID NO:2728:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 163 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..163
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601734
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

Met Glu Leu Ala Leu Ser Leu Gly Glu Thr Met Ala Asp Ala Gly Arg 10 Asp Leu Met Leu Gly Leu Gly Met Gly Val Gly Val Arg Arg Glu Glu

25

Glu Ala Gln Arg Gly Arg Arg Asp Arg Glu Val Arg Arg Glu Leu Glu 40

Phe Thr Ala Arg Ser Ala Arg Ser Ser Pro Glu Pro Ala Val Arg Leu 55 Thr Leu Leu His Gly Leu Gly Leu Pro Trp Pro Pro Pro Pro Ser Ser

70 75 Glu Thr Asn Arg His Leu Glu Ala Ser Ala Arg Gly Phe Asp Val Asn

90 Arq Ala Pro Ser Leu Ser Ala Ala Gly Gly Ala Ala Glu Glu Asp Glu

105 Glu Gln Asp Glu Ala Ala Ala Ala Ala Ala Ser Ser Pro Asn Asn

125 120

Ser Ala Ser Ser Phe Pro Thr Asp Phe Ser Ala Gln Gly Gln Val Ala 130 135 140

Pro Gly Ala Asp Arg Ala Cys Ser Arg Ala Ser Asp Glu Asp Asp Gly 150 155 145 Gly Ser Ala

- (2) INFORMATION FOR SEQ ID NO:2729:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 511 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..511
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729: 60 aacttegete egteeceae acaetgteae tgeeageete eeettegett egettagete geogteacea tggegacete eacettetet eegegeeeeg ceaceeteaa geoeetgegg 120 180 geacgegeea ageoegeegg cetecagete caceteetee cetteeegeg cetecgegte gcctgcgcca ccgcgccggg gaggcgccgc ccgttgagca gcgggacgag gtggagccgg 240 cctccgccgc ggcatccaac gggactgccg tcaaggtcga ggcgcccgcc gcgaagcccg 300 agteccegee egegeeegeg eeegegeeeg egeeggteee ggeetteege gaegeeaggt 360 gggtcaacgg cacctgggac ctcaccaagt tcgacaaggg cggcggcgtc gactgggacg 420 ccgtcatcqa cgccgaggcc aggagaagga aatggctcga aagactaccc ggaggcgacg
- agcacwgacg atgccgtcgt cttcgacacc t (2) INFORMATION FOR SEQ ID NO:2730:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 169 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..169
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601754
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:
- Leu Arg Ser Val Pro His Thr Leu Ser Leu Pro Ala Ser Pro Ser Leu 1 5 10 15
- Arg Leu Ala Arg Arg His His Gly Asp Leu His Leu Leu Ser Ala Pro 20 25 30
- Arg His Pro Gln Ala Pro Ala Gly Thr Arg Gln Ala Arg Arg Pro Pro 35 40 45
- Ala Pro Pro Pro Pro Leu Pro Ala Pro Pro Arg Arg Leu Arg His Arg 50 55 60
- Ala Gly Glu Ala Pro Pro Val Glu Gln Arg Asp Glu Val Glu Pro Ala 65 70 75 80
- Ser Ala Ala Ser Asn Gly Thr Ala Val Lys Val Glu Ala Pro Ala 85 90 95
- Ala Lys Pro Glu Ser Pro Pro Ala Pro Ala Pro Ala Pro Ala Pro Val 100 105 110
- Pro Ala Phe Arg Asp Ala Arg Trp Val Asn Gly Thr Trp Asp Leu Thr 115 120 125
- Lys Phe Asp Lys Gly Gly Gly Val Asp Trp Asp Ala Val Ile Asp Ala 130 135 140
- Glu Ala Arg Arg Arg Lys Trp Leu Glu Arg Leu Pro Gly Gly Asp Glu 145 150 155 160
- His Xaa Arg Cys Arg Arg Leu Arg His 165
- (2) INFORMATION FOR SEQ ID NO:2731:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1601755 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731: Met Ala Thr Ser Thr Phe Ser Pro Arg Pro Ala Thr Leu Lys Pro Leu 10 5 Arg Ala Arg Ala Lys Pro Ala Gly Leu Gln Leu His Leu Leu Pro Phe 2.0 25 Pro Arg Leu Arg Val Ala Cys Ala Thr Ala Pro Gly Arg Arg Pro 40 Leu Ser Ser Gly Thr Arg Trp Ser Arg Pro Pro Pro Arg His Pro Thr 55 60 Gly Leu Pro Ser Arg Ser Arg Arg Pro Pro Arg Ser Pro Ser Pro Arg 70 7.5 Pro Arg Pro Arg Pro Arg Arg Ser Arg Pro Ser Ala Thr Pro 85 90 Gly Gly Ser Thr Ala Pro Gly Thr Ser Pro Ser Ser Thr Arg Ala Ala 110 100 105 Ala Ser Thr Gly Thr Pro Ser Ser Thr Pro Arg Pro Gly Glu Gly Asn 120 125 Gly Ser Lys Asp Tyr Pro Glu Ala Thr Ser Xaa Asp Asp Ala Val Val 130 135 Phe Asp Thr

145

- (2) INFORMATION FOR SEQ ID NO:2732:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..477
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601760
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732: actocatoco tgotocgtog togogtgoca tootagggtt totttoccog toggegooto cccagatttg gacgctgccg ccgccgccgc tgacccaggt tgtcttgatg gcgcccgctg 120 tagaagccgt gaaggagaca ggcaccttcc agaaggttcc tgccatgaac gaaaggatac 180 240 tgtcatccat gtccaggagg tctgttgctg cacacccttg gcatgatctg gagataggtc ctggtgctcc aaccatattc aactgcgtca ttgagatacc aaggggcagc aaggttaaat 300 360 atgaacttga caagaaaact ggactgatca aggtggaccg ggtgttgtat tcatcagttg tttaccctca caactatgga ttcattcctc gcacgctttg tgaagacagt gatcctttgg 420 atgtactggt tataatgcag gagcctgtta tcccaggctg tttcctacgt gcgaagg
- (2) INFORMATION FOR SEQ ID NO:2733: (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 158 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..158
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601761
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:
- Ser Ile Pro Ala Pro Ser Ser Arg Ala Ile Leu Gly Phe Leu Ser Pro 10
- Ser Ala Pro Pro Gln Ile Trp Thr Leu Pro Pro Pro Pro Leu Thr Gln 20 25
- Val Val Leu Met Ala Pro Ala Val Glu Ala Val Lys Glu Thr Gly Thr 40
- Phe Gln Lys Val Pro Ala Met Asn Glu Arg Ile Leu Ser Ser Met Ser

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50
                     55
                                        60
Arg Arg Ser Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro
                  70
                                   75
Gly Ala Pro Thr Ile Phe Asn Cys Val Ile Glu Ile Pro Arg Gly Ser
                                90
Lys Val Lys Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys Val Asp
                            105
Arg Val Leu Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly Phe Ile
           120 125
Pro Arg Thr Leu Cys Glu Asp Ser Asp Pro Leu Asp Val Leu Val Ile
                    135 140
Met Gln Glu Pro Val Ile Pro Gly Cys Phe Leu Arg Ala Lys
                 150
                                   155
(2) INFORMATION FOR SEQ ID NO:2734:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 123 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..123
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601762
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:
Met Ala Pro Ala Val Glu Ala Val Lys Glu Thr Gly Thr Phe Gln Lys
1 5
                              10
Val Pro Ala Met Asn Glu Arg Ile Leu Ser Ser Met Ser Arg Arg Ser
                            25
    20
Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Gly Ala Pro
                        40
Thr Ile Phe Asn Cys Val Ile Glu Ile Pro Arg Gly Ser Lys Val Lys
                                       60
                     55
Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys Val Asp Arg Val Leu
                                   75
               70
Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly Phe Ile Pro Arg Thr
             85 90 95
Leu Cys Glu Asp Ser Asp Pro Leu Asp Val Leu Val Ile Met Gln Glu
        100 105
Pro Val Ile Pro Gly Cys Phe Leu Arg Ala Lys
      115 120
(2) INFORMATION FOR SEQ ID NO:2735:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 104 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..104
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601763
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:
Met Asn Glu Arg Ile Leu Ser Ser Met Ser Arg Arg Ser Val Ala Ala
                                 10
His Pro Trp His Asp Leu Glu Ile Gly Pro Gly Ala Pro Thr Ile Phe
                             25
Asn Cys Val Ile Glu Ile Pro Arg Gly Ser Lys Val Lys Tyr Glu Leu
                        40
Asp Lys Lys Thr Gly Leu Ile Lys Val Asp Arg Val Leu Tyr Ser Ser
```

Val Val Tyr Pro His Asn Tyr Gly Phe Ile Pro Arg Thr Leu Cys Glu 65
Asp Ser Asp Pro Leu Asp Val Leu Val Ile Met Gln Glu Pro Val Ile 85
Pro Gly Cys Phe Leu Arg Ala Lys

Pro Gly Cys Phe Leu Arg Ala Lys 100

- (2) INFORMATION FOR SEQ ID NO:2736:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..497
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601773

gatggtctac agectegeet teetgeegee caecetgeee aggeagaaeg acaaeggeaa

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736:

  agcagcacac aacctaccac actegcattg cattgeattg catteettea gtteagtagt 60
  gtgetetgac agtgagatgg egagegtgaa ggtttteggg teacecacet eggeggaggt 120
  egeoegegtg eteatgtgee tettegagaa ggaggtggag tteeagetga teegegtega 180
  egeetacege ggeaceaage geatgeecea gtaceteaag etgeageege aaggegagge 240
  geteacette gaggaegag geeteaceet eteegactee agggggatee teegeecacat 300
  eteecacaag taegegaage agggeaacee gtacetgatt ggeacggge egetggageg 360
  ggegteeate gageagtgge tgeagaegga ggegeagage ttegaegege ceagegeega 420
- (2) INFORMATION FOR SEQ ID NO: 2737:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 165 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

cggcggcgcg ttcaacg

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601774
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2737:
- Ala Ala His Asn Leu Pro His Ser His Cys Ile Ala Leu His Ser Phe 1 5 10 15 Ser Ser Val Val Cys Ser Asp Ser Glu Met Ala Ser Val Lys Val Phe
- 20 25 30

  Gly Ser Pro Thr Ser Ala Glu Val Ala Arg Val Leu Met Cys Leu Phe
- 35 40 45 Arg Val Clu Pho Clu Lou Tlo Arg Val Arg Tur Arg Clu
- Glu Lys Glu Val Glu Phe Gln Leu Ile Arg Val Asp Ala Tyr Arg Gly 50 55 60

  Thr Lys Arg Met Pro Gln Tyr Leu Lys Leu Gln Pro Gln Gly Glu Ala
- 65 70 75 80 Leu Thr Phe Glu Asp Glu Ser Leu Thr Leu Ser Asp Ser Arg Gly Ile
- 85 90 95 Leu Arg His Ile Ser His Lys Tyr Ala Lys Gln Gly Asn Pro Tyr Leu
- 100 105 110 Ile Gly Thr Gly Ala Leu Glu Arg Ala Ser Ile Glu Gln Trp Leu Gln
- 115 120 125 Thr Glu Ala Gln Ser Phe Asp Ala Pro Ser Ala Glu Met Val Tyr Ser
- Gly Gly Ala Phe Asn

- (2) INFORMATION FOR SEQ ID NO:2738:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601775
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2738:

Arg Val Leu Met Cys Leu Phe Glu Lys Glu Val Glu Phe Gln Leu Ile 20 25 30

Arg Val Asp Ala Tyr Arg Gly Thr Lys Arg Met Pro Gln Tyr Leu Lys 35 40 45

Leu Gln Pro Gln Gly Glu Ala Leu Thr Phe Glu Asp Glu Ser Leu Thr 50 55 60

Leu Ser Asp Ser Arg Gly Ile Leu Arg His Ile Ser His Lys Tyr Ala 65 70 75 80

Lys Gln Gly Asn Pro Tyr Leu Ile Gly Thr Gly Ala Leu Glu Arg Ala 85 90 95

Ser Ile Glu Gln Trp Leu Gln Thr Glu Ala Gln Ser Phe Asp Ala Pro  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$ 

Ser Ala Glu Met Val Tyr Ser Leu Ala Phe Leu Pro Pro Thr Leu Pro 115 120 125

Arg Gln Asn Asp Asn Gly Asn Gly Gly Ala Phe Asn 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2739:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 121 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..121
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601776
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2739:

Met Cys Leu Phe Glu Lys Glu Val Glu Phe Gln Leu Ile Arg Val Asp 1 5 10 15

Ala Tyr Arg Gly Thr Lys Arg Met Pro Gln Tyr Leu Lys Leu Gln Pro 20 25 30

Gln Gly Glu Ala Leu Thr Phe Glu Asp Glu Ser Leu Thr Leu Ser Asp 35 40 45

Ser Arg Gly Ile Leu Arg His Ile Ser His Lys Tyr Ala Lys Gln Gly 50 60

Asn Pro Tyr Leu Ile Gly Thr Gly Ala Leu Glu Arg Ala Ser Ile Glu
65 70 75 80

Gln Trp Leu Gln Thr Glu Ala Gln Ser Phe Asp Ala Pro Ser Ala Glu 85 90 95

Met Val Tyr Ser Leu Ala Phe Leu Pro Pro Thr Leu Pro Arg Gln Asn 100 105 110

Asp Asn Gly Asn Gly Gly Ala Phe Asn 115 120

- (2) INFORMATION FOR SEQ ID NO:2740:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 479 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..479
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601777
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740:

ategecteca acttgttett cegetgeaag acageagtee egagetgtag cetgetaeeg 60 teettgteta gtegtettee eeggeaagee geggeggteg ttgeeeete gtataateta 120 ctegeggeat cettgteate geegattega ttgggttgat acagagggga geegegaggg 180 ggeggagatg eegacgetga egaagetgta eageatggag gaggetgese teeacaacac 240 geegacgae tgetgggtea tegtegaegg caagattat gatgtgaeea agtatttgga 300 agaceateet geagggeaea geaggatgee eagagateea eteetgagatg etacagaaga 360 atttgaegat ttggaeeaa eteetgaeat teetgagatg gaggtttea ggaaggage

- (2) INFORMATION FOR SEQ ID NO:2741:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 159 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..159
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601778
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741:

Ser Pro Pro Thr Cys Ser Ser Ala Ala Arg Gln Gln Ser Arg Ala Val 1 5 10 15

Ala Cys Tyr Arg Ser Cys Leu Val Val Phe Pro Gly Lys Pro Arg Arg 20 25 30

Ser Leu Pro Pro Arg Ile Ile Tyr Ser Arg His Pro Cys His Arg Arg
35
40
45

Phe Asp Trp Val Asp Thr Glu Gly Ser Arg Glu Gly Ala Glu Met Pro
50 55 60

Thr Leu Thr Lys Leu Tyr Ser Met Glu Glu Ala Xaa Leu His Asn Thr 65 70 75 80
Pro Asp Asp Cys Trp Val Ile Val Asp Gly Lys Ile Tyr Asp Val Thr

85 90 95
Lys Tyr Leu Glu Asp His Pro Gly Gly Ala Asp Val Leu Leu Glu Ala

100 105 110

Thr Gly Lys Asp Ala Thr Glu Glu Phe Asp Asp Ala Gly His Ser Lys
115 120 125

Ser Ala Lys Asp Leu Met Gln Asp Tyr Phe Ile Gly Glu Leu Asp Leu
130 135 140

Asp Pro Thr Pro Asp Ile Pro Glu Met Glu Val Phe Arg Lys Glu 145 150 155

- (2) INFORMATION FOR SEQ ID NO:2742:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601779
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742:

Met Pro Thr Leu Thr Lys Leu Tyr Ser Met Glu Glu Ala Xaa Leu His 10 5 Asn Thr Pro Asp Asp Cys Trp Val Ile Val Asp Gly Lys Ile Tyr Asp 30 20 25 Val Thr Lys Tyr Leu Glu Asp His Pro Gly Gly Ala Asp Val Leu Leu 40 Glu Ala Thr Gly Lys Asp Ala Thr Glu Glu Phe Asp Asp Ala Gly His 55 Ser Lys Ser Ala Lys Asp Leu Met Gln Asp Tyr Phe Ile Gly Glu Leu 75 70 Asp Leu Asp Pro Thr Pro Asp Ile Pro Glu Met Glu Val Phe Arg Lys 90 8.5

Glu

- (2) INFORMATION FOR SEQ ID NO:2743:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..88
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601780
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743:

Met Glu Glu Ala Xaa Leu His Asn Thr Pro Asp Asp Cys Trp Val Ile 10 5

Val Asp Gly Lys Ile Tyr Asp Val Thr Lys Tyr Leu Glu Asp His Pro 30 25 20

Gly Gly Ala Asp Val Leu Leu Glu Ala Thr Gly Lys Asp Ala Thr Glu 45 40

Glu Phe Asp Asp Ala Gly His Ser Lys Ser Ala Lys Asp Leu Met Gln 55 60

Asp Tyr Phe Ile Gly Glu Leu Asp Leu Asp Pro Thr Pro Asp Ile Pro 75 70

Glu Met Glu Val Phe Arg Lys Glu 85

- (2) INFORMATION FOR SEQ ID NO: 2744:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..476
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601792
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744:

atttccgcac cacgcccagt cgcccacgca gccggcccaa gcccaaaaac ctttctccat 60 cetetactet catececacg atggeogecg ecgecaccac geogeactee etecteetee 120 agegegeege gateceggee gegeegtega gggegteege geegeetete eegteegeet 180 cccggtccgc gccgccagga tetcgtgcgc ggcggtggcg gcgccgtccc cggccgcagc 240 cgccgcggcg gacgaggtgg agcgcggcgt ctacaacttc gcggcgggtc ccgcgacgct 300 360 ccctctctcc gtgctcaagc gggcgcaggc ggagctggtg gactaccacg gctccgggat gagcatcatg gagatgagcc accgcgggaa ggagttcgac gccgccatca agaaggccga 420 gteegacetg egegegetee tegeggtgee tgacacecae geegtgetet teetee

- (2) INFORMATION FOR SEQ ID NO:2745:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 150 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..150
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601793
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2745:
- Ile Ser Ala Pro Arg Pro Val Ala His Ala Ala Gly Pro Ser Pro Lys
  1 10 15
- Thr Phe Leu His Pro Leu Leu Ser Ser Pro Arg Trp Pro Pro Pro 20 25 . 30
- Pro Arg Arg Thr Pro Ser Ser Ser Ser Ala Pro Arg Ser Arg Pro Arg 35 40 45
- Arg Arg Gly Arg Pro Arg Arg Leu Ser Arg Pro Pro Pro Gly Pro Arg
- Arg Gln Asp Leu Val Arg Gly Gly Gly Gly Ala Val Pro Gly Arg Ser 70 75 80
- Arg Arg Gly Gly Arg Gly Gly Ala Arg Arg Leu Gln Leu Arg Gly Gly 85 90 95
- Ser Arg Asp Ala Pro Ser Leu Arg Ala Gln Ala Gly Ala Gly Gly Ala
  100 105 110
- Gly Gly Leu Pro Arg Leu Arg Asp Glu His His Gly Asp Glu Pro Pro 115 120 125
- Arg Glu Gly Val Arg Arg His Gln Glu Gly Arg Val Arg Pro Ala 130 135 140
- Arg Ala Pro Arg Gly Ala 145 150
- (2) INFORMATION FOR SEQ ID NO:2746:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..158
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601794
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2746:
- Phe Pro His His Ala Gln Ser Pro Thr Gln Pro Ala Gln Ala Gln Lys
  1 5 10 15
- Pro Phe Ser Ile Leu Tyr Ser His Pro His Asp Gly Arg Arg Arg His 20 25 30
- His Ala Ala Leu Pro Pro Pro Pro Ala Arg Arg Asp Pro Gly Arg Ala 35 40 45
- Val Glu Gly Val Arg Ala Ala Ser Pro Val Arg Leu Pro Val Arg Ala 50 55 60
- Ala Arg Ile Ser Cys Ala Ala Val Ala Ala Pro Ser Pro Ala Ala Ala 65 70 70 75 80 Ala Ala Ala Asp Glu Val Glu Arg Gly Val Tyr Asn Phe Ala Ala Gly
- 85 90 95
  Pro Ala Thr Leu Pro Leu Ser Val Leu Lys Arg Ala Gln Ala Glu Leu
- 100 105 110 Met Clu Met Ser His Arg
- Val Asp Tyr His Gly Ser Gly Met Ser Ile Met Glu Met Ser His Arg 115 120 125
- Gly Lys Glu Phe Asp Ala Ala Ile Lys Lys Ala Glu Ser Asp Leu Arg 130 135 140
- Ala Leu Leu Ala Val Pro Asp Thr His Ala Val Leu Phe Leu 145 150 155

- (2) INFORMATION FOR SEQ ID NO:2747:
  (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..119
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601795
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2747:

Phe Arg Thr Thr Pro Ser Arg Pro Arg Ser Arg Pro Lys Pro Lys Asn 1 5 10 15

Leu Ser Pro Ser Ser Thr Leu Ile Pro Thr Met Ala Ala Ala Thr 20 25 30

Thr Pro His Ser Leu Leu Gln Arg Ala Ala Ile Pro Ala Ala Pro  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Ser Arg Ala Ser Ala Pro Pro Leu Pro Ser Ala Ser Arg Ser Ala Pro 50 55 60

Pro Gly Ser Arg Ala Arg Arg Trp Arg Arg Arg Pro Arg Pro Gln Pro 65 70 75 80

Pro Arg Arg Thr Arg Trp Ser Ala Ala Ser Thr Thr Ser Arg Arg Val

Pro Arg Arg Ser Leu Ser Pro Cys Ser Ser Gly Arg Arg Arg Ser Trp
100 105 110

Trp Thr Thr Ala Pro Gly
115

- (2) INFORMATION FOR SEQ ID NO:2748:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601800
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2748:

agagagagaa ggtgagtgct ttgacaaggg gaaaaaaccc aggtctgtgt gtgtgtgtgc gagagagaga gagagagaga gagagagag

(2) INFORMATION FOR SEQ ID NO:2749:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..32
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601801
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2749:

Glu Arg Glu Gly Glu Cys Phe Asp Lys Gly Lys Lys Pro Arg Ser Val 1 5 10 15

Cys Val Cys Ala Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu 20 25 30

(2) INFORMATION FOR SEQ ID NO:2750:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 31 amino acids(B) TYPE: amino acid(C) STRANDEDNESS:
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide

(D) TOPOLOGY: linear

- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601802
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2750:

Arg Glu Lys Val Ser Ala Leu Thr Arg Gly Lys Asn Pro Gly Leu Cys 1 5 10 15

Val Cys Val Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu 20 25 30

- (2) INFORMATION FOR SEQ ID NO:2751:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..435
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601803
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751:

  aacetgatte etteegeett gteagegeag egatecagae ecacengage caacaaceca 60
  tggeegeege gaegeeget eteetgeteg eggtegeggg eetcaceete geegteeteg 120
  cegeegegt etegeegtet etggeggegg ggeegeeggt getgeaggae eeggeggake 180
  teetgegeet tgeeaaggag eeggeetteg eggaetggat ggteggggtg eggeggegga 240
  teeaegagta aceeggaget gggataegag gagtteeaga eeagegaget egtgegeegg 300
  gageteeaeg eeatggggat eeeetaeagg eaeeeetteg eegteaeegg egtggtagea 360
  acagteggaa eeggeggtee geeettegtt getetgeggg eggaeatgga eggetgeee 420
- (2) INFORMATION FOR SEQ ID NO:2752:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 145 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

ttqcaqqqaa agtgt

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752:

Asn Leu Ile Pro Ser Ala Leu Ser Ala Gln Arg Ser Arg Pro Thr Xaa 1 5 10 15

Ala Asn Asn Pro Trp Pro Pro Arg Arg Arg Val Ser Cys Ser Arg Ser 20 25 30

Arg Ala Ser Pro Ser Pro Ser Ser Pro Pro Arg Ser Arg Arg Leu Trp  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Arg Arg Gly Arg Cys Cys Arg Thr Arg Arg Xaa Ser Cys Ala Leu 50 60

Pro Arg Ser Arg Pro Ser Arg Thr Gly Trp Ser Gly Cys Gly Gly 65 70 75 80

Ser Thr Ser Asn Pro Glu Leu Gly Tyr Glu Glu Phe Gln Thr Ser Glu 85 90 95

Leu Val Arg Arg Glu Leu His Ala Met Gly Ile Pro Tyr Arg His Pro 100 105 110

Phe Ala Val Thr Gly Val Val Ala Thr Val Gly Thr Gly Gly Pro Pro 120 115 Phe Val Ala Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Gln Gly Lys 140 135 130 Cys 145 (2) INFORMATION FOR SEQ ID NO:2753: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..82 (D) OTHER INFORMATION: / Ceres Seq. ID 1601805 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2753: Pro Asp Ser Phe Arg Leu Val Ser Ala Ala Ile Gln Thr His Xaa Ser 10 5 Gln Gln Pro Met Ala Ala Ala Thr Pro Arg Leu Leu Ala Val Ala 25 . 30 Gly Leu Thr Leu Ala Val Leu Ala Ala Ala Val Ser Pro Ser Leu Ala 40 45 Ala Gly Pro Pro Val Leu Gln Asp Pro Ala Xaa Leu Leu Arg Leu Ala 60 55 Lys Glu Pro Ala Phe Ala Asp Trp Met Val Gly Val Arg Arg Ile 75 70 His Glu (2) INFORMATION FOR SEQ ID NO:2754: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 261 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..261 (D) OTHER INFORMATION: / Ceres Seq. ID 1601806 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2754: atttctttga agtcaaggct gtgaaagaaa ttgagcctgc acttaagaag cagctcatca tetecacegt cetgatgact tttggtattg etetaateag etggttggee ettecageta agttcaccat ctacaacttc ggtactcaga aggaggtttc caactggggt ttgttcttct 180 gtgtttcaat tggtctgtgg gctggtttga ttattggttt tgtcacagaa tactacacta gcaatgcata cagtcctgtg c (2) INFORMATION FOR SEQ ID NO:2755: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..86 (D) OTHER INFORMATION: / Ceres Seq. ID 1601807 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2755: Phe Phe Glu Val Lys Ala Val Lys Glu Ile Glu Pro Ala Leu Lys Lys

10

5

(C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

> (A) NAME/KEY: peptide (B) LOCATION: 1..48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2758:

(D) OTHER INFORMATION: / Ceres Seq. ID 1601817

(ix) FEATURE:

```
Page 1357
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Gln Leu Ile Ile Ser Thr Val Leu Met Thr Phe Gly Ile Ala Leu Ile
                                25
            20
Ser Trp Leu Ala Leu Pro Ala Lys Phe Thr Ile Tyr Asn Phe Gly Thr
                            40
        35
Gln Lys Glu Val Ser Asn Trp Gly Leu Phe Phe Cys Val Ser Ile Gly
                       55
                                             60
Leu Trp Ala Gly Leu Ile Ile Gly Phe Val Thr Glu Tyr Tyr Thr Ser
                                         75
                    70
Asn Ala Tyr Ser Pro Val
                85
(2) INFORMATION FOR SEQ ID NO: 2756:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 62 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..62
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601808
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2756:
Met Thr Phe Gly Ile Ala Leu Ile Ser Trp Leu Ala Leu Pro Ala Lys
                                    10
                5
Phe Thr Ile Tyr Asn Phe Gly Thr Gln Lys Glu Val Ser Asn Trp Gly
                                                     30
            20
                                 25
Leu Phe Phe Cys Val Ser Ile Gly Leu Trp Ala Gly Leu Ile Ile Gly
                             40
Phe Val Thr Glu Tyr Tyr Thr Ser Asn Ala Tyr Ser Pro Val
                        55
    50
 (2) INFORMATION FOR SEQ ID NO:2757:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 400 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (ix) FEATURE:
           (A) NAME/KEY: -
           (B) LOCATION: 1..400
           (D) OTHER INFORMATION: / Ceres Seq. ID 1601816
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2757:
 acctcccttc ccccactctc ttctctcccc gcggcccgtg actcatccac ccacagtcca
                                                                         60
 ctcgccactc cccccggaac ggcggcggcg gcgacggcgg aggagtaacg caagatggcg
                                                                        120
 aggaaacctc tcgactacga ggagctgaac gagaacgtca agagggtgca gtacgcggtg
                                                                        180
 cgcggggagc tgtacctccg cgcctccgag ctgcagaagg agggcaagaa gatcatcttc
                                                                        240
                                                                        300
 accaacgtcg gcaacccgca cgccctcggc cagaaaccgc tcaccttccc gcgccaggtg
 gtggcgctgt gccaggctcc gttcctcctc gacgatcccc acgtcggcct catgttcccg
                                                                        360
 geggaegeea tegetaggge caageaetat etegeeatgg
 (2) INFORMATION FOR SEQ ID NO:2758:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 48 amino acids
            (B) TYPE: amino acid
```

 Pro
 Pro
 Phe
 Pro
 His
 Ser
 Leu
 Leu
 Ser
 Pro
 Arg
 Pro
 Val
 Thr
 His
 Pro
 10
 10
 15
 15
 15
 15
 17
 Pro
 Pro

- (2) INFORMATION FOR SEQ ID NO:2759:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..95
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601818
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759:

Met Ala Arg Lys Pro Leu Asp Tyr Glu Glu Leu Asn Glu Asn Val Lys
1 5 10 15

Arg Val Gln Tyr Ala Val Arg Gly Glu Leu Tyr Leu Arg Ala Ser Glu 20 25 30

Leu Gln Lys Glu Gly Lys Lys Ile Ile Phe Thr Asn Val Gly Asn Pro 35 40 45

His Ala Leu Gly Gln Lys Pro Leu Thr Phe Pro Arg Gln Val Val Ala 50 55 60

Leu Cys Gln Ala Pro Phe Leu Leu Asp Asp Pro His Val Gly Leu Met 65 70 75 80

Phe Pro Ala Asp Ala Ile Ala Arg Ala Lys His Tyr Leu Ala Met 85 90 95

- (2) INFORMATION FOR SEQ ID NO:2760:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..492
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601823
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760:

aaacctcatc ttctctcctt ttgctcggaa cgcacacaca gcccggtccc cgatctccga tecectegte gatecaagat geagatette gteaagaeee teaetggaaa gaetateaee 120 ctcgaggtgg agtcttctga caccattgac aacgtcaagg ccaagaatcc aggacaagga 180 gggcattece ceggaceage ageggeteat ettegetgge aageageteg aggaceggeg 240 300 cacacttgcc gactacaaca tecagaagga gagcaceete cacettgtte teegeeteag gggaggcatg cagatetteg teaagaceet caetggaaag actateacee tegaggtgga 360 gtettetgae accategaea aegteaagge caagatetag gaeaaggagg geatecetee 420 ggaccagcag cggctcattt ttgctggcaa gcagctcgag gacgggcgca cgcctggccg 480 actacaacat tc

- (2) INFORMATION FOR SEQ ID NO:2761:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 122 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2761:

Lys Pro His Leu Leu Ser Phe Cys Ser Glu Arg Thr His Ser Pro Val 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15

Pro Asp Leu Arg Ser Pro Arg Arg Ser Lys Met Gln Ile Phe Val Lys  $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30 \hspace{1.5cm}$ 

Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr 35 40 45

Ile Asp Asn Val Lys Ala Lys Asn Pro Gly Gln Gly Gly His Ser Pro 50 55 60

Gly Pro Ala Ala Ala His Leu Arg Trp Gln Ala Ala Arg Gly Arg Ala 65 70 75 80

His Thr Cys Arg Leu Gln His Pro Glu Gly Glu His Pro Pro Pro Cys 85 90 95

Ser Pro Pro Gln Gly Arg His Ala Asp Leu Arg Gln Asp Pro His Trp 100 105 110

Lys Asp Tyr His Pro Arg Gly Gly Val Phe 115 120

- (2) INFORMATION FOR SEQ ID NO:2762:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..132
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601825
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2762:

Asn Leu Ile Phe Ser Pro Phe Ala Arg Asn Ala His Thr Ala Arg Ser 1 5 10 15

Pro Ile Ser Asp Pro Leu Val Asp Pro Arg Cys Arg Ser Ser Arg 20 25 30

Pro Ser Leu Glu Arg Leu Ser Pro Ser Arg Trp Ser Leu Leu Thr Pro 35 40 45

Leu Thr Thr Ser Arg Pro Arg Ile Gln Asp Lys Glu Gly Ile Pro Pro 50 55 60

Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg 65 70 75 80

Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val 85 90 95

Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly

100 105 110

Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val

115 120 Lys Ala Lys Ile

130

- (2) INFORMATION FOR SEQ ID NO:2763:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601826

 (xi) SEQUENCE DESCRIPTION: SEQ ID No:2763:

 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu

 1
 5
 10
 15

 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Asn Pro Gly
 20
 30

 Gln Gly Gly His Ser Pro Gly Pro Ala Ala Ala His Leu Arg Trp Gln
 40
 45

 Ala Ala Arg Gly Arg Ala His Thr Cys Arg Leu Gln His Pro Glu Gly
 50
 60

 Glu His Pro Pro Pro Cys Ser Pro Pro Gln Gly Arg His Ala Asp Leu
 65
 70

 Arg Gln Asp Pro His Trp Lys Asp Tyr His Pro Arg Gly Gly Val Phe
 26

## (2) INFORMATION FOR SEQ ID NO:2764:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..531
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764: aacaqcttgc gtggtctgtg gtctcatctc actcacactc tctctctctc tcggcgacgt 60 ctacgccgag tgcccaggca ttcttcaggc gcaggtcgct ggctcgctgc cgccctacac 120 180 caqqtqcccc qqtcttcttc cqtcccttcg ccggcgacga gcactgccag gacagtatag cqqatqqctt cqtcqqtqcq qqcqccatcq qqqtcqqtqa tcqccqtqqc atcqtcctct 240 tectcaqcaq ccqcqqccqq qqtqtqcqqc acgggctccc gtgcgccqcq tgcaagttcc 300 tgcgtcgcaa gtgccagccg gactgcgtgt tcgcgcccta cttcccaccg gacaacccgc 360 agaagttogt gcgcgtgcac cgcgtcttcg gcgcgagcaa cgtgaccaag ctgatgaacg 420 aaatccaccc gttgcagcgc gaggacgcca tgaactcgct cgcctacgag gccgacatgc 480 gaattegega eecegtetae ggetgegtgg gegteatete cateeteeag e
- (2) INFORMATION FOR SEQ ID NO:2765:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 176 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..176
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601841
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765:

Gln Leu Ala Trp Ser Val Val Ser Ser His Ser His Ser Leu Ser Leu  $1 ag{15}$ 

Ser Ala Thr Ser Thr Pro Ser Ala Gln Ala Phe Phe Arg Arg Ser 20 25 30

Leu Ala Arg Cys Arg Pro Thr Pro Gly Ala Pro Val Phe Phe Arg Pro 35 40 45

Phe Ala Gly Asp Glu His Cys Gln Asp Ser Ile Ala Asp Gly Phe Val 50 60

Gly Ala Gly Ala Ile Gly Val Gly Asp Arg Arg Gly Ile Val Leu Phe 65 70 75 80

Leu Ser Ser Arg Gly Arg Gly Val Arg His Gly Leu Pro Cys Ala Ala 85 90 95

Cys Lys Phe Leu Arg Arg Lys Cys Gln Pro Asp Cys Val Phe Ala Pro

- (2) INFORMATION FOR SEQ ID NO:2766:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..497
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601858
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2766: agagecacce ggttgeteet cattteeact tteeactetg ceteegetge egategeegt 60 ccccgaccgc agcgcaggtg aggatccaac cccaacaaac ttccaggcga cggactgagg 120 atgagtgaag aggataaggc tgctgcttct gctgagcagc ctaagagggc ccctaagctc 180 aatgaaagga toototooto totgtocagg aggtocgtag otgotoatoo atggoatgat 240 ctcgagatcg gtcctggtgc tcctgctgta ttcaatgttg ttgttgagat cacaaaggga 300 agcaaagtca aatacgagct tgacaagaaa actggactga ttaaggttga tcgagtcctt 360 tactcatcag ttgtataccc tcacaattat ggtttcattc caaggactct ttgtgaagac 420 aatgacccaa tggatgtgtt ggtcctgatg caggagcctg ttgttcctgg ttcgttcctg 480
- (2) INFORMATION FOR SEQ ID NO:2767:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

agagctagag caattgg

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601859
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2767:

Met Ser Glu Glu Asp Lys Ala Ala Ala Ser Ala Glu Gln Pro Lys Arg 1 5 10 15

Ala Pro Lys Leu Asn Glu Arg Ile Leu Ser Ser Leu Ser Arg Arg Ser 20 25 30

Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Gly Ala Pro 35 40 45

Ala Val Phe Asn Val Val Val Glu Ile Thr Lys Gly Ser Lys Val Lys 50 55 60

Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys Val Asp Arg Val Leu 65 70 75 80

Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly Phe Ile Pro Arg Thr 85 90 95

Leu Cys Glu Asp Asn Asp Pro Met Asp Val Leu Val Leu Met Gln Glu
100 105 110

Pro Val Val Pro Gly Ser Phe Leu Arg Ala Arg Ala Ile 115 120 125

(2) INFORMATION FOR SEQ ID NO:2768:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 523 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..523
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601860
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768: acaagtttcg cttctcgtcg cgacgactgg gcgagaccgc cgccgccgcc tgagttctgt agaaatggct gatggtgagg acatccagcc tcttgtctgc gacaatggca ctggaatggt 120 caaggctggt tttgctggcg acgatgcacc aagggctgtt ttccctagta ttgttggccg 180 240 tectegecae actggtgtta tggtagggat gggacagaag gatgegtatg ttggegaega 300 ggcacagtcc aagagaggta ttctcacgct caagtatccg atcgagcatg gtattgtgag 360 caactgggat gacatggaga aaatctggca tcacactttc tacaacgagc ttcgtgttgc cccagaggag caccetgtgt tgctcactga ggctcetttg aacccaaagg ccaacaggga 420 gaagatgacc cagattatgt tcgagacttt caatgttcct gccatgtacg ttgcaattca 480
- agcagtgctg tcactctatg ccagtggacg tactactggt att (2) INFORMATION FOR SEQ ID NO:2769:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 174 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..174
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601861
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769:
- Gln Val Ser Leu Leu Val Ala Thr Thr Gly Arg Asp Arg Arg Arg 1 10 15
- Leu Ser Ser Val Glu Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val 20 25 30
- Cys Asp Asn Gly Thr Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp 35 40 45
- Ala Pro Arg Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Thr 50 55 60
- Gly Val Met Val Gly Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu 65 70 75 80
  Ala Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His
- 85 90 95
  Gly Ile Val Ser Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr
- 100 105 110

  Phe Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu
  115 120 125
- Thr Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln
  130 135 140
- Ile Met Phe Glu Thr Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln
  145 150 155 160
- Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile 165 170
- (2) INFORMATION FOR SEQ ID NO:2770:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 153 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..153
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601862
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2770:
- Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val Cys Asp Asn Gly Thr 1 5 10
- Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val 20 25 30
- Phe Pro Ser Ile Val Gly Arg Pro Arg His Thr Gly Val Met Val Gly 35 40 45
- Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg 50 55 60
- Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Ser Asn 65 70 75 80
- Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu 85 90 95
- Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu 100 105 110
- Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr 115 120 125
- Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu 130 135 140
- Tyr Ala Ser Gly Arg Thr Thr Gly Ile 145 150
- (2) INFORMATION FOR SEQ ID NO:2771:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..136
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601863
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771:
- Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe 1 5 10 15
- Pro Ser Ile Val Gly Arg Pro Arg His Thr Gly Val Met Val Gly Met
  20 25 30
- Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly 35  $\phantom{-}40\phantom{+}45\phantom{+}$
- Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Ser Asn Trp 50 55 60
- Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg 65 70 75 80
- Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn 85 90 95
- Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe 100 105 110
- Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr 115 120 125
- Ala Ser Gly Arg Thr Thr Gly Ile 130 135
- (2) INFORMATION FOR SEQ ID NO:2772:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 494 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..494
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601864

tgcggaagcg gtgcggccag atcctcagca ggctgcgcaa ggacaagcgc agcgtgtggt

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772:

  acctgcatec tecetetet tetecegete ecgtgetete tecetetece caggatega 60
  attgccageg caccagtega getegeggga cetegeegge geeggegatg geeteeteec 120
  ttttggccgg acggggaggg ggccaccace acaactgggg ggagacgege geecegeteg 180
  agcccatace ecceaaceet agteccagee ageeceacee geggegegae gggtecaagt 240
  ccaageegge ggeggegee ggetacgtga agtteegee ggegteeteg ggeaecegeg 300
  aggecegege geteegggae egcetegegg tggagetegg ecaggteete geeteetet 360
  ecegcatega cacetggeag eageaggree egeegeegeg egeggteete egeggggega 420
- (2) INFORMATION FOR SEQ ID NO:2773:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

tcaacgcgcc cgtc

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601865
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773:
- Thr Cys Ile Leu Pro Leu Ser Leu Pro Leu Pro Cys Ser Leu Pro Leu 1 5 10 15
- Pro Arg Ile Arg Ile Ala Ser Ala Pro Val Glu Leu Ala Gly Pro Arg 20 25 30
- Arg Arg Arg Trp Pro Pro Pro Phe Trp Pro Asp Gly Glu Gly Ala 35 40 45
- Thr Thr Thr Gly Gly Arg Arg Ala Pro Arg Ser Ser Pro Tyr Pro 50 55 60
- Pro Thr Leu Val Pro Ala Ser Pro Thr Arg Ala Pro Thr Gly Pro Ser 65 70 75 80
- Pro Ser Arg Gly Arg Arg Pro Ala Thr 85
- (2) INFORMATION FOR SEQ ID NO:2774:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..164
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601866
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774:
- Leu His Pro Pro Ser Leu Ser Pro Ala Pro Val Leu Ser Pro Ser Pro 1 5 10 15
- Gln Asp Pro Asn Cys Gln Arg Thr Ser Arg Ala Arg Gly Thr Ser Pro
- Ala Pro Ala Met Ala Ser Ser Leu Leu Ala Gly Arg Gly Gly His 35 40 45
- His His Asn Trp Gly Glu Thr Arg Ala Pro Leu Glu Pro Ile Pro Pro 50 55 60
- Asn Pro Ser Pro Ser Gln Pro His Pro Arg Ala Asp Gly Ser Lys Ser 65 70 75 80

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Lys Pro Arg Ala Ala Ala Gly Tyr Val Lys Phe Arg Pro Ala Ser Leu
                                   90
Gly His Arg Glu Ala Arg Ala Leu Arg Asp Arg Leu Ala Val Glu Leu
                              105
                                                  110
           100
Gly Gln Val Arg Ala Leu Leu Ser Arg Ile Asp Thr Trp Gln Gln
                          120
                                              125
       115
Xaa Pro Pro Pro Arg Ala Val Leu Arg Gly Ala Met Arg Lys Arg Cys
                   135
                                          140
Gly Gln Ile Leu Ser Arg Leu Arg Lys Asp Lys Arg Ser Val Trp Phe
145
                   150
                                      155
Asn Ala Pro Val
```

- (2) INFORMATION FOR SEQ ID NO:2775:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 129 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..129
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601867
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775:

Met Ala Ser Ser Leu Leu Ala Gly Arg Gly Gly His His His Asn 1 5 10 15

Trp Gly Glu Thr Arg Ala Pro Leu Glu Pro Ile Pro Pro Asn Pro Ser 20 25 30

Pro Ser Gln Pro His Pro Arg Ala Asp Gly Ser Lys Ser Lys Pro Arg

Ala Ala Gly Tyr Val Lys Phe Arg Pro Ala Ser Leu Gly His Arg 50 55 60

Glu Ala Arg Ala Leu Arg Asp Arg Leu Ala Val Glu Leu Gly Gln Val 65 70 75 80

Arg Ala Leu Leu Ser Arg Ile Asp Thr Trp Gln Gln Gln Xaa Pro Pro 85 90 95

Pro Arg Ala Val Leu Arg Gly Ala Met Arg Lys Arg Cys Gly Gln Ile 100 105 110

Leu Ser Arg Leu Arg Lys Asp Lys Arg Ser Val Trp Phe Asn Ala Pro 115 120 125

Val

- (2) INFORMATION FOR SEQ ID NO:2776:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 411 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..411
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601868
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2776:

ataacgcaag	caaagcctct	gctgcgtgct	ctgctcctct	ctctcctcca	tttgctgccg	60
	agctcgccct					120
agcctgccct	tagcacgcag	cgccagtgaa	gaaggccgag	ataatggagg	tggagacgat	180
	gacgtgttct					240
cgacgacgag	ggcgcggact	tcgccgccgc	gcagttcatc	cccgccgccg	ccgccgccgc	300
cgcgcccctc	caggggttcg	cgtcgcgcgc	ccatgtgccg	tcgcaggcgt	cgctgctggc	360
gccaccggcc	tacgcgctgt	accactacca	ccacggcgcc	agctacggcg	g	

- (2) INFORMATION FOR SEQ ID NO:2777:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 137 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..137
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601869
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2777:

Ile Thr Gln Ala Lys Pro Leu Leu Arg Ala Leu Leu Leu Ser Leu Leu 1 5 10 15

His Leu Leu Pro Gl<br/>n Leu Ser Glu Leu Ala Leu Ala Ala Ala Ala Ser 20  $\phantom{\bigg|}25\phantom{\bigg|}30\phantom{\bigg|}$ 

Ala Gln His Ser Thr Asp Ser Glu Ser Leu Pro Leu Ala Arg Ser Ala 35 40 45

Ser Glu Glu Gly Arg Asp Asn Gly Gly Gly Asp Asp Ala Gly Arg Arg 50 55

Arg Val Leu Arg Arg Ala Gln Gln Ala Asp Ile Ala Ala His His Arg 65 70 75 80

Arg Arg Arg Gly Arg Gly Leu Arg Arg Arg Ala Val His Pro Arg Arg 85 90 95

Arg Arg Arg Arg Ala Pro Pro Gly Val Arg Val Ala Arg Pro Cys
100 105 110

Ala Val Ala Gly Val Ala Ala Gly Ala Thr Gly Leu Arg Ala Val Pro 115 120 125

Leu Pro Pro Arg Arg Gln Leu Arg Arg 130 135

(2) INFORMATION FOR SEQ ID NO:2778:

- (i) SEQUENCE CHARACTERISTICS:
  - I) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..82
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778:

Met Glu Val Glu Thr Met Leu Asp Asp Val Phe Phe Ala Glu Leu 1 5 10 15

Ser Lys Arg Ile Ser Leu Leu Ile Thr Asp Asp Asp Glu Gly Ala Asp 20 25 30

Phe Ala Ala Ala Gln Phe Ile Pro Ala Ala Ala Ala Ala Ala Pro 35 40 45

Leu Gln Gly Phe Ala Ser Arg Ala His Val Pro Ser Gln Ala Ser Leu 50 55 60

Leu Ala Pro Pro Ala Tyr Ala Leu Tyr His Tyr His His Gly Ala Ser 65 70 75 80

Tyr Gly

- (2) INFORMATION FOR SEQ ID NO:2779:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 77 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..77
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601871
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2779:
- Met Leu Asp Asp Val Phe Phe Ala Glu Leu Ser Lys Arg Ile Ser 1 5 10 15
- Leu Leu Ile Thr Asp Asp Glu Gly Ala Asp Phe Ala Ala Gln 20 25 30
- Phe Ile Pro Ala Ala Ala Ala Ala Ala Pro Leu Gln Gly Phe Ala 35 40 45
- Ser Arg Ala His Val Pro Ser Gln Ala Ser Leu Leu Ala Pro Pro Ala 50 55 60
- Tyr Ala Leu Tyr His Tyr His His Gly Ala Ser Tyr Gly 65 70 75
- (2) INFORMATION FOR SEQ ID NO:2780:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..364
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601872
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2780:
- catteetet etecetete aeggeecaeg eceaeegee eatecaeee gaaaceetag 60 eggategteg ecatggeege ggeegegete ettegeega teeeegeege gegggeeeeg 120 geeaeeggeet teatggegge geaeeeggte teegatteea eggeggeget eaceategag acatetgtee ettteaeete eeaeetegte gaeeegeet eggeggeget eaceaeee 240 geegaeteee tetataagge eaageteate egegggttet geeaeeteta egaeggeeag 300 gagg
- (2) INFORMATION FOR SEQ ID NO:2781:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 121 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..121
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601873
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2781:
- Ile Pro Pro Leu Pro Leu His Gly Pro Arg Pro Pro Pro His Pro Pro 1 5 10 15
- Arg Asn Pro Ser Gly Ser Ser Pro Trp Pro Arg Pro Arg Ser Phe Ala 20 25 30
- Ala Ser Pro Pro Arg Gly Pro Arg Pro Arg Pro Ser Trp Arg Arg Thr 35 40 45
- Arg Ser Pro Ile Pro Arg Arg Arg Ser Pro Ser Arg His Leu Ser Leu 50 55 60
- Ser Pro Pro Thr Ser Ser Thr Arg Pro Arg Ala Met Ser Pro Pro 65 70 75 80
- Pro Pro Ser Ser Pro Ser Ser Ala Thr Cys Pro Ser Cys Ala Ala 85 90 95
- Trp Arg Ser Leu Pro Thr Pro Ser Ile Arg Pro Ser Ser Ser Ala Gly
  100 105 110
- Ser Ala Thr Ser Thr Thr Ala Arg Arg

- (2) INFORMATION FOR SEQ ID NO:2782:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 104 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..104
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601874
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2782:

Phe Leu Leu Ser Leu Ser Thr Ala His Ala His Arg Pro Ile His Pro 1 5 10 15

Glu Thr Leu Ala Asp Arg Arg His Gly Arg Gly Arg Ala Pro Ser Pro  $20 \\ 25 \\ 30$ 

His Pro Arg Arg Ala Gly Pro Gly His Gly Leu His Gly Gly Ala Pro  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gly Leu Arg Phe His Gly Gly Ala His His Arg Asp Ile Cys Pro Phe 50 55 60

His Leu Pro Pro Arg Arg Pro Ala Leu Ala Arg Cys His His Pro 65 70 75 80

Arg Arg Ala Arg His Leu Leu Pro Arg His Val Pro His Ala Pro His 85 90 95

- Gly Asp Arg Cys Arg Leu Pro Leu 100
- (2) INFORMATION FOR SEQ ID NO:2783:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601875
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2783:

Met Ala Ala Ala Leu Leu Arg Arg Ile Pro Ala Ala Arg Ala Pro 1 5 10 15

Ala Thr Ala Phe Met Ala Ala His Pro Val Ser Asp Ser Thr Ala Ala 20 25 30

Leu Thr Ile Glu Thr Ser Val Pro Phe Thr Ser His Leu Val Asp Pro 35 40 45

Pro Ser Arg Asp Val Thr Thr Thr Pro Ala Glu Leu Val Thr Phe Phe 50 55 60

Arg Asp Met Ser Leu Met Arg Arg Met Glu Ile Ala Ala Asp Ser Leu 65 70 75 80

Tyr Lys Ala Lys Leu Ile Arg Gly Phe Cys His Leu Tyr Asp Gly Gln 85 90 95

Glu

- (2) INFORMATION FOR SEQ ID NO:2784:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 174 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601883
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784: aaggeeteea eteatteetg eeceegacae teecaetgee accagteete teacegeeag gegecageca cageggeaca atgeageege etactaceet tetecegeta ggegeegteg 120 tggtcgccat cctcctgctc gccaccgccc cgagccccgc cgtctcccgt aacc
- (2) INFORMATION FOR SEQ ID NO:2785:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..36
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601884
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2785:

Lys Ala Ser Thr His Ser Cys Pro Arg His Ser His Cys His Gln Ser 10 5

Ser His Arg Gln Ala Pro Ala Thr Ala Ala Gln Cys Ser Arg Leu Leu 20 25

Pro Phe Ser Arg 35

- (2) INFORMATION FOR SEQ ID NO:2786:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 56 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..56
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2786:

Arg Pro Pro Leu Ile Pro Ala Pro Asp Thr Pro Thr Ala Thr Ser Pro 10 5 Leu Thr Ala Arg Arg Gln Pro Gln Arg His Asn Ala Ala Ala Tyr Tyr

25 30

Pro Ser Pro Ala Arg Arg Arg Gly Arg His Pro Pro Ala Arg His

Arg Pro Glu Pro Arg Arg Leu Pro

- (2) INFORMATION FOR SEQ ID NO:2787:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..57
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601886
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2787:

Gly Leu His Ser Phe Leu Pro Pro Thr Leu Pro Leu Pro Pro Val Leu 10

Ser Pro Pro Gly Ala Ser His Ser Gly Thr Met Gln Pro Pro Thr Thr 30 20 25

Leu Leu Pro Leu Gly Ala Val Val Ala Ile Leu Leu Ala Thr 40 Ala Pro Ser Pro Ala Val Ser Arg Asn 55 50 (2) INFORMATION FOR SEQ ID NO:2788: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..241
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601890
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788: aggacaggtt gcatttgcat ctgagttcct gatcgttgta ttccagtttc ttccgtgagt 60 120 tttgtgggat cgcgaggaag aaggatgtcg tgcygcggar gcaactgcgg gtgcggccc ggctgcaagt gcggcagcgg ctgcggaggg tgccgcaccc gcatttccat cctgtcgtgg 180 gatcccagcc accgccgcta gaagaagagc tcggcgattc ccaggtcccg cgagaatatg 240
- (2) INFORMATION FOR SEQ ID NO:2789:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 38 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..38
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601891
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789:

Met Ser Cys Xaa Gly Xaa Asn Cys Gly Cys Gly Ala Gly Cys Lys Cys 10 5 Gly Ser Gly Cys Gly Cys Arg Thr Arg Ile Ser Ile Leu Ser Trp 25 20

Asp Pro Ser His Arg Arg 35

- (2) INFORMATION FOR SEQ ID NO:2790:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..437
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601892
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790: acctetectt ecetecacee gegeegtege etegeetate egatetgeea eetecteeeg 60 totogcacgt toottoccaa otocgcagog tagoototoc goggogogat ccagatocag 120 gtttttcagc atgggcctgg tgaaggaagg catcgacatg gaggagggaa cccttgagat 180 cggcatggag tacaggactg tatctggtgt tgctgggcct ctggtcatat tggataaagt 240 300 aaagggccca aagtaccaag aaattgtaaa catccgactt ggagatggca ccaatcgccg 360 tggtcaagtc ctggaagttg atggcgaaaa agctgttgtg caggtctttg aaggaacttc 420 tggaatagac racaaataca caaccgtgca gtttacaggc gaggttttga aaactcctgt ctcacttgat atgcttg
- (2) INFORMATION FOR SEQ ID NO:2791:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..145
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601893
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2791:

Pro Leu Leu Pro Ser Thr Arg Ala Val Ala Ser Pro Ile Arg Ser Ala
1 5 10 15

Thr Ser Ser Arg Leu Ala Arg Ser Phe Pro Thr Pro Gln Arg Ser Leu 20 25 30

Ser Ala Ala Arg Ser Arg Ser Arg Phe Phe Ser Met Gly Leu Val Lys 35 40 45

Glu Gly Ile Asp Met Glu Glu Gly Thr Leu Glu Ile Gly Met Glu Tyr 50 60

Arg Thr Val Ser Gly Val Ala Gly Pro Leu Val Ile Leu Asp Lys Val 65 70 75 80

Thr Asn Arg Arg Gly Gln Val Leu Glu Val Asp Gly Glu Lys Ala Val 100 105 110

Val Gln Val Phe Glu Gly Thr Ser Gly Ile Asp Xaa Lys Tyr Thr Thr 115 120 125

Val Gln Phe Thr Gly Glu Val Leu Lys Thr Pro Val Ser Leu Asp Met 130 135 140

Leu

145

- (2) INFORMATION FOR SEQ ID NO:2792:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..102
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601894
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2792:

Met Gly Leu Val Lys Glu Gly Ile Asp Met Glu Glu Gly Thr Leu Glu 1 5 10 15

Ile Leu Asp Lys Val Lys Gly Pro Lys Tyr Gln Glu Ile Val Asn Ile 35 40 45

Arg Leu Gly Asp Gly Thr Asn Arg Arg Gly Gln Val Leu Glu Val Asp 50 60

Gly Glu Lys Ala Val Val Gln Val Phe Glu Gly Thr Ser Gly Ile Asp 65 70 75 80

Xaa Lys Tyr Thr Thr Val Gln Phe Thr Gly Glu Val Leu Lys Thr Pro85 90 95

Val Ser Leu Asp Met Leu

100

- (2) INFORMATION FOR SEQ ID NO:2793:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 93 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1601895 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2793: Met Glu Glu Gly Thr Leu Glu Ile Gly Met Glu Tyr Arg Thr Val Ser 5 10 Gly Val Ala Gly Pro Leu Val Ile Leu Asp Lys Val Lys Gly Pro Lys 20 25 Tyr Gln Glu Ile Val Asn Ile Arg Leu Gly Asp Gly Thr Asn Arg Arg 40 Gly Gln Val Leu Glu Val Asp Gly Glu Lys Ala Val Val Gln Val Phe 55 Glu Gly Thr Ser Gly Ile Asp Xaa Lys Tyr Thr Thr Val Gln Phe Thr 70 75 Gly Glu Val Leu Lys Thr Pro Val Ser Leu Asp Met Leu 85 (2) INFORMATION FOR SEQ ID NO:2794: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..341 (D) OTHER INFORMATION: / Ceres Seq. ID 1601900 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794: gaaaagaaaa gcacgggaga cgggacggga ccgctgggcg cgccgggccg cgccgagccg agggagtegt coacteteca etecqueege cacquecacq coccqtecte gettecqtet cccacaatcc aaggacaccg agcagcaggc ggcggaagca acccgctgtg gggggggggt ggagtccagt tttgctcggc tcgtcgctgg gatccgccgg ccggcgaagc ggggaaggga 240 agaggagcgg agattggaga gtacaagcag gggaagatgt cagacgcgct gatcaacggc 300 ctcgccggcg ccggcggcgg gatcatcgcc cagctcctta c (2) INFORMATION FOR SEQ ID NO:2795: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..113 (D) OTHER INFORMATION: / Ceres Seq. ID 1601901 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795: Glu Lys Lys Ser Thr Gly Asp Gly Thr Gly Pro Leu Gly Ala Pro Gly 10 Arg Ala Glu Pro Ser Glu Ser Ser Thr Leu His Ser Ala Arg His Ala 25 His Ala Pro Ser Ser Leu Pro Ser Pro Thr Ile Gln Gly His Arg Ala Ala Gly Gly Gly Ser Asn Pro Leu Trp Gly Arg Arg Gly Val Gln Phe 55 Cys Ser Ala Arg Arg Trp Asp Pro Pro Ala Gly Glu Ala Gly Lys Gly 70 75

Arg Gly Ala Glu Ile Gly Glu Tyr Lys Gln Gly Lys Met Ser Asp Ala

90

Leu Ile Asn Gly Leu Ala Gly Ala Gly Gly Gly Ile Ile Ala Gln Leu 100 105 110

Leu

- (2) INFORMATION FOR SEQ ID NO:2796:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601902
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796:

Lys Arg Lys Ala Arg Glu Thr Gly Arg Asp Arg Trp Ala Arg Arg Ala 1 5 10 15

Ala Pro Ser Arg Ala Ser Arg Pro Leu Ser Thr Pro Pro Ala Thr Pro 20 25 30

Thr Pro Arg Pro Arg Phe Arg Leu Pro Gln Ser Lys Asp Thr Glu Gln 35 40

Gln Ala Ala Glu Ala Thr Arg Cys Gly Gly Gly Val Glu Ser Ser Phe 50 60

Ala Arg Leu Val Ala Gly Ile Arg Arg Pro Ala Lys Arg Gly Arg Glu 65 70 75 80

Glu Glu Arg Arg Leu Glu Ser Thr Ser Arg Gly Arg Cys Gln Thr Arg
85 90 95

- (2) INFORMATION FOR SEQ ID NO:2797:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..113
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601903
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797:

Lys Glu Lys His Gly Arg Arg Asp Gly Thr Ala Gly Arg Ala Gly Pro

1 5 10 15 Arg Arg Ala Glu Arg Val Val His Ser Pro Leu Arg Pro Pro Arg Pro

20 25 30
Arg Pro Val Leu Ala Ser Val Ser His Asn Pro Arg Thr Pro Ser Ser

Arg Arg Lys Gln Pro Ala Val Gly Ala Ala Trp Ser Pro Val Leu
50 55

4.0

Leu Gly Ser Ser Leu Gly Ser Ala Gly Arg Arg Ser Gly Glu Gly Lys 65 70 75 80

Arg Ser Gly Asp Trp Arg Val Gln Ala Gly Glu Asp Val Arg Arg Ala 85 90 95

Asp Gln Arg Pro Arg Arg Arg Arg Arg Asp His Arg Pro Ala Pro
100 105 110

Tyr

- (2) INFORMATION FOR SEQ ID NO:2798:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 311 base pairs

180

240

300

60

120

180

240

300

360

420

480

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..311 (D) OTHER INFORMATION: / Ceres Seq. ID 1601904 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798: agaggeteca caacggegga geactageag etaggeeacg agacgatgge ggeeeeggeg ceteacgteg eggtggtege egeeggteet geteeteete eegteeetee tegetgtegt cgcgcagacg cccaagggcg ccaaggcttt ctgcattagc cagttcgcca tcgccagcca ggeetgetee atcetgeege egageeeace egacqaqeac caccacqacq atqacqaqqa tgatgacgac aacgacgacg agcaccatga ccgcgaccgt cgcagccacc acqcqqcqqc catgagette t (2) INFORMATION FOR SEQ ID NO:2799: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..100 (D) OTHER INFORMATION: / Ceres Seq. ID 1601905 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799: Arg Leu His Asn Gly Gly Ala Leu Ala Ala Arg Pro Arg Asp Asp Gly 10 Gly Pro Gly Ala Ser Arg Arg Gly Gly Arg Arg Arg Ser Cys Ser Ser 20 25 Ser Arg Pro Ser Ser Leu Ser Ser Arg Arg Pro Arg Ala Pro Arg 40 Leu Ser Ala Leu Ala Ser Ser Pro Ser Pro Ala Arg Pro Ala Pro Ser 55 Cys Arg Arg Ala His Pro Thr Ser Thr Thr Thr Thr Met Thr Arg Met 70 75 Met Thr Thr Thr Thr Ser Thr Met Thr Ala Thr Val Ala Ala Thr 85 90 Thr Arg Arg Pro 100 (2) INFORMATION FOR SEQ ID NO:2800: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800: agtccgagaa gaaaaaggaa actgaagaag agacctcgtc gtctcgtgca gccgcaagca cgaggctgtg agcgagacag ccaaggtgct catcgactcc agccagccgc ccaaaaagcc aggcgcaaat cacaacctcg cctcctgtcc cctcccggc tcctcgttcc cctctcgccg ctcgcctcc cgccgagatc gaggaggcgc caatagcgag agggtttcct cttccctcca cggctccaac gagccccgg ccctccgcc tcaaatccca cgcgcccggt tggccgccccccccgccatg gatgtggatc tgtggatctc caaggtcaag gaaggccagc acctcqccqa

(D) OTHER INFORMATION: / Ceres Seq. ID 1601909

gcacgagett cagtetetet gegaataegt aaaggagate etcategaag agtegaaegt

tcaaccggtg aattagccct gtgacggttt gcggtgacat ccatgggcag ttcatgacct

(B) LOCATION: 1..494

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gatgaagctc ttcq
(2) INFORMATION FOR SEQ ID NO:2801:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 71 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..71
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601910
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801:
Ser Pro Arg Arg Lys Arg Lys Leu Lys Lys Arg Pro Arg Arg Leu Val
               5
                                    10
Gln Pro Gln Ala Arg Gly Cys Glu Arg Asp Ser Gln Gly Ala His Arg
                                25
Leu Gln Pro Ala Ala Gln Lys Ala Arg Arg Lys Ser Gln Pro Arg Leu
                            40
                                                45
Leu Ser Pro Pro Arg Leu Leu Val Pro Leu Ser Pro Leu Ala Ser Pro
                        55
Pro Arg Ser Arg Arg Arg Gln
                    70
(2) INFORMATION FOR SEQ ID NO:2802:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 42 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..42
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601911
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802:
Met Asp Val Asp Leu Trp Ile Ser Lys Val Lys Glu Gly Gln His Leu
               5
                                   10
Ala Glu His Glu Leu Gln Ser Leu Cys Glu Tyr Val Lys Glu Ile Leu
          20
                                25
Ile Glu Glu Ser Asn Val Gln Pro Val Asn
        35
(2) INFORMATION FOR SEQ ID NO:2803:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 476 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..476
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601916
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803:
aacccctttc tttttcttaa ttcctcatcc actcgccgca cgacgaagag ageggctccc
                                                                       60
attocccaco acctactogg accggagoag caggttotog aaccgacogg tgaaacatto
                                                                      120
tegegecaat tgtgggggee atgggegeea acggacaece geeggegage accqteqege
                                                                      180
agaacggatc ccactctggc ggaggcggag gagggggagg gggagtgaac cctagcaacg
                                                                      240
gcggcacggg ggcggctctt cggcacgacc ctggtctggc gcgggagtgg tcgacggagg
                                                                      300
agcaqaccat cetegacgag etgetggtea agtatgeate egatttacce gtegtteget
                                                                      360
atgcaaaagt tgcaatgaag ttgccagaga aaacagttcg ggatgtagcc ttgcqctqca
                                                                      420
gatggatgaa taaaaaggag agcgccaaaa gaaagaaaga ggatcacaac tcgtct
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(2) INFORMATION FOR SEQ ID NO:2804:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 75 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..75
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601917
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2804:
Asn Pro Phe Leu Phe Leu Asn Ser Ser Ser Thr Arg Arg Thr Thr Lys
                                   10
Arg Ala Pro Ile Pro His His Leu Leu Gly Pro Glu Gln Gln Val
          20
                            25
                                                   30
Leu Glu Pro Thr Gly Glu Thr Phe Ser Arg Gln Leu Trp Gly Pro Trp
       35
                          40
                                              4.5
Ala Pro Thr Asp Thr Arg Arg Ala Pro Ser Arg Arg Thr Asp Pro
                       55
Thr Leu Ala Glu Ala Glu Glu Gly Glu Gly Glu
                  70
(2) INFORMATION FOR SEQ ID NO:2805:
   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 77 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
         (A) NAME/KEY: peptide
          (B) LOCATION: 1..77
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601918
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2805:
Thr Pro Phe Phe Leu Ile Pro His Pro Leu Ala Ala Arg Arg Arg
         5
                               10
Glu Arg Leu Pro Phe Pro Thr Thr Tyr Ser Asp Arg Ser Ser Arg Phe
          20
                              25
Ser Asn Arg Pro Val Lys His Ser Arg Ala Asn Cys Gly Gly His Gly
                          40
                                              4.5
Arg Gln Arg Thr Pro Ala Gly Glu His Arg Arg Ala Glu Arg Ile Pro
                    55
Leu Trp Arg Arg Arg Arg Gly Arg Gly Ser Glu Pro
                   70
(2) INFORMATION FOR SEQ ID NO:2806:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 112 amino acids
          (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
          (B) LOCATION: 1..112
         (D) OTHER INFORMATION: / Ceres Seq. ID 1601919
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2806:
Met Gly Ala Asn Gly His Pro Pro Ala Ser Thr Val Ala Gln Asn Gly
              5
                                   10
Ser His Ser Gly Gly Gly Gly Gly Gly Gly Val Asn Pro Ser
                               25
```

Asn Gly Gly Thr Gly Ala Ala Leu Arg His Asp Pro Gly Leu Ala Arg

 Glu
 Trp
 Ser
 Thr
 Glu
 Glu
 Gln
 Thr
 Ile
 Leu
 Asp
 Glu
 Leu
 Leu
 Val
 Lys

 Tyr
 Ala
 Ser
 Asp
 Leu
 Pro
 Val
 Val
 Arg
 Tyr
 Ala
 Lys
 Val
 Ala
 Met
 Lys

 65
 70
 75
 80

 Leu
 Pro
 Glu
 Lys
 Arg
 Asp
 Val
 Ala
 Leu
 Arg
 Cys
 Arg
 Trp
 Met

 Asn
 Lys
 Lys
 Lys
 Lys
 Lys
 Bull
 Asp
 Asp
 Ser
 Ser

 Asn
 Lys
 <td

- (2) INFORMATION FOR SEQ ID NO:2807:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..472
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601928
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2807:

gacgcatgcctagctgggccacaggtggttggaaatcatgtaggctcaaaggttgtagta60cagcactccagctcatagccgagctgcaggagagaagagaagcaccgcaaccctaggttg120ccgcctcttttcctctccactcgtccgcgcgacgcgacgcgacgcgacgacaaccggagg180gttttctgcggggattgtttgtcgccgactcgccagcagccaagatgaggccggtcttc240gtggggaacctggactatgacacccgccactcggaggtcgaccgcctcttctaccgctac300ggcagggtcgagcgcatcgacatgaggtctttgtctactttgaggatgaa360cgtgatgcaatgatgccatacagggttgakcaagctggtagacgtgatgtggcagacgc420aggctttcagtagagtggtcacgggggtgakcaagctggtagacgtgatggc

- (2) INFORMATION FOR SEQ ID NO:2808:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids(B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..37
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601929
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2808:

Arg Met Pro Ser Trp Ala Thr Gly Gly Trp Lys Ser Cys Arg Leu Lys 1 5 10 15

Gly Cys Ser Thr Ala Leu Gln Leu Ile Ala Glu Leu Gln Glu Arg Arg
20 25 30

Glu Ala Pro Gln Pro 35

(2) INFORMATION FOR SEQ ID NO:2809:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..74
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809:

```
Met Arg Pro Val Phe Val Gly Asn Leu Asp Tyr Asp Thr Arg His Ser
                                    10
Glu Leu Asp Arg Leu Phe Tyr Arg Tyr Gly Arg Val Glu Arg Ile Asp
                                25
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Gly
                            40
Asn Asp Ala Ile Gln Ala Leu Asp Gly Tyr Pro Phe Gly Pro Gly Arg
                        55
Arg Arg Leu Ser Val Glu Trp Ser Arg Gly
                    70
(2) INFORMATION FOR SEQ ID NO:2810:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 42 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..42
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601931
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810:
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Gly
                                    10
Asn Asp Ala Ile Gln Ala Leu Asp Gly Tyr Pro Phe Gly Pro Gly Arg
          20
                                25
Arg Arg Leu Ser Val Glu Trp Ser Arg Gly
       35
(2) INFORMATION FOR SEQ ID NO:2811:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 412 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..412
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601940
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2811:
gttegegttg ceegegacte teteegteet ectaetetea eaegettgge gegegegtge
ttccacacgt ccgtcgcctc gcctggctga ttggtttggg acctggctcc agcaatggcg
                                                                      120
gtgcaggcgc attatcacca ccaccaccac caccaccacc gcgagtcccc tttcctcgtc
                                                                      180
ageggeggeg egeeggaggg eageeggttg geggeggega tqqaqetqea teaqqeqeaq
aaggaggeta ctacqqcqca qcaqcacqct ccqcccqact tctcqcatqq aqqttqcqqc
                                                                      300
ggcgggaaga agcggcagcg cgaggcggac cccgtgtccc ggcagctctt gtcgttgcag
                                                                      360
cagcagcaac cacaggcgca ggggcccaag ttcatcaacc tggcgcaact gc
(2) INFORMATION FOR SEQ ID NO:2812:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 137 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..137
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601941
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812:
Phe Ala Leu Pro Ala Thr Leu Ser Val Leu Leu Ser His Ala Trp
                5
                                    10
```

```
Arg Ala Arg Ala Ser Thr Arg Pro Ser Pro Arg Leu Ala Asp Trp Phe 20 25 30 Gly Thr Trp Leu Gln Gln Trp Arg Cys Arg Arg Ile Ile Thr Thr
```

35 40 45

Thr Thr Thr Thr Ala Ser Pro Leu Ser Ser Ser Ala Ala Arg 50 55 60

Arg Arg Ala Ala Gly Trp Arg Arg Trp Ser Cys Ile Arg Arg 65 70 75 80

Arg Arg Leu Leu Arg Arg Ser Ser Thr Leu Arg Pro Thr Ser Arg Met 85 90 95

Glu Val Ala Ala Gly Arg Ser Gly Ser Ala Arg Arg Thr Pro Cys 100 105 110

Pro Gly Ser Ser Cys Arg Cys Ser Ser Ser Asn His Arg Arg Gly  $115 \\ 120 \\ 125$ 

Pro Ser Ser Ser Thr Trp Arg Asn Cys 130 135

- (2) INFORMATION FOR SEQ ID NO:2813:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..136
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601942
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813:

Ser Arg Cys Pro Arg Leu Ser Pro Ser Ser Tyr Ser His Thr Leu Gly  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Ala Arg Val Leu Pro His Val Arg Arg Leu Ala Trp Leu Ile Gly Leu 20 25 30

Gly Pro Gly Ser Ser Asn Gly Gly Ala Gly Ala Leu Ser Pro Pro Pro 35 40 45

Pro Pro Pro Pro Arg Val Pro Phe Pro Arg Gln Arg Arg Ala 50 55 60

Gly Gly Gln Pro Val Gly Gly Gly Asp Gly Ala Ala Ser Gly Ala Glu 65 70 75 80

Gly Gly Tyr Tyr Gly Ala Ala Ala Arg Ser Ala Arg Leu Leu Ala Trp \$85\$ 90 95

Arg Leu Arg Arg Glu Glu Ala Ala Ala Arg Gly Gly Pro Arg Val 100 105 110

Pro Ala Ala Leu Val Val Ala Ala Ala Ala Thr Thr Gly Ala Gly Ala 115 120 125

Gln Val His Gln Pro Gly Ala Thr

- (2) INFORMATION FOR SEQ ID NO:2814:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..99
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601943
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814:

Met Ala Val Gln Ala His Tyr His His His His His His His Arg

1 5 10 15

Glu Ser Pro Phe Leu Val Ser Gly Gly Ala Pro Glu Gly Ser Arg Leu

- (2) INFORMATION FOR SEQ ID NO:2815:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..462
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601947
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2815:

gtgattttct gggtgaattt ttcccggcct ccgctccggc cagatcggcg cgggtgaacc ccggccccta ccgatccgga tccgtccca tcgcctcgtg tgttttccgt cgagtattt 120 agcgagtttg tcatggcgtc taagcgcatc ctcaaggagc tgaaggacct gcagaaagac 180 ccccccacat catgcagtgc aggtcctgct ggtgaggaca tgtttcattg gcaagcaaca 240 attatgggac cacctgacag tccctatgct ggcggtgttt tcttagtgaa cattcattc 300 ccgccagatt accccttcaa acctccaaag gtttctttca agacaaaggt cttccatcct 360 aatatcaaca gcaatggaag tatatgcctt gacattctca aagagcagtg gagccctgct 420 ctgacaattt ctaaggtcct gctcccatc tgctccctgc tg

- (2) INFORMATION FOR SEQ ID NO:2816:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 110 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..110
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601948
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816:

Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp 1 5 10 15

Pro Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Met Phe His 20 25 30

Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly 35 40 45

Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro 50 55 60

Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser 65 70 75 80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala

105

85 90 Ser Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu

(2) INFORMATION FOR SEQ ID NO:2817:

100

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..81
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601949
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr

1 10 15

Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro 20 25 30

Phe Lys Pro Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn 35 40 45

Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp 50 55 60

Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:2818:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..73
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601950
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818:

Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly Val Phe Leu Val Asn 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15

Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe 20 25 30

Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys 50 55 60

Val Leu Leu Ser Ile Cys Ser Leu Leu 65 70

- (2) INFORMATION FOR SEQ ID NO:2819:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..445
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601957
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819:

gaaaagtcaa aagaacccgc agcaggggag actgggagat agagagagga gagggagggt 60 ttcctcaaag agaacccgaa accaaaccca agcagagaac actagcgttc cctcaccagg 120 gcgtccatcc cagcagccat ggcgatggcg tacaagatgg cgacggaggg gatgaacgtg 180 aaggaggagt gccagcgctg gttcatggag atgaagtgga agaaggtgca ccgcttcgtg 240 gtgtacaaga tcgacgagcg gtcgcgccc gtgctggtgg acaaggtggg cggccccggg 300 gaagggtacg aggactcgt ggccgcgctg cccggcgacg actgccgcta cgccgtctc 360 gacttcgact tcgtcaccgt cgacaactgc cagaagagca agatcttctt catcgcctgg 420

tcaccggcgg cgtcgaggat caggg (2) INFORMATION FOR SEQ ID NO:2820: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..147 (D) OTHER INFORMATION: / Ceres Seq. ID 1601958 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2820: Lys Val Lys Arg Thr Arg Ser Arg Gly Asp Trp Glu Ile Glu Arg Gly 5 10 Glu Gly Gly Phe Pro Gln Arg Glu Pro Glu Thr Lys Pro Lys Gln Arg 25 Thr Leu Ala Phe Pro His Gln Gly Val His Pro Ser Ser His Gly Asp 40 Gly Val Gln Asp Gly Asp Gly Asp Glu Arg Glu Gly Gly Val Pro 55 Ala Leu Val His Gly Asp Glu Val Glu Glu Gly Ala Pro Leu Arg Gly 70 75 Val Gln Asp Arg Arg Ala Val Ala Arg Arg Ala Gly Gly Gln Gly Gly 85 90 Arg Pro Arg Gly Arg Val Arg Gly Ala Arg Gly Arg Ala Ala Arg Arg 100 105 Arg Leu Pro Leu Arg Arg Leu Arg Leu Arg Leu Arg His Arg Arg Gln 115 120 Leu Pro Glu Glu Gln Asp Leu Leu His Arg Leu Val Thr Gly Gly Val 135 Glu Asp Gln 145 (2) INFORMATION FOR SEQ ID NO:2821: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..102 (D) OTHER INFORMATION: / Ceres Seq. ID 1601959 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2821: Met Ala Met Ala Tyr Lys Met Ala Thr Glu Gly Met Asn Val Lys Glu 5 10 Glu Cys Gln Arg Trp Phe Met Glu Met Lys Trp Lys Lys Val His Arg 25 Phe Val Val Tyr Lys Ile Asp Glu Arg Ser Arg Ala Val Leu Val Asp 40 Lys Val Gly Gly Pro Gly Glu Gly Tyr Glu Glu Leu Val Ala Ala Leu 55 60 Pro Gly Asp Asp Cys Arg Tyr Ala Val Phe Asp Phe Asp Phe Val Thr 70 75 Val Asp Asn Cys Gln Lys Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro 85 Ala Ala Ser Arg Ile Arg 100 (2) INFORMATION FOR SEQ ID NO:2822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..100 (D) OTHER INFORMATION: / Ceres Seq. ID 1601960 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2822: Met Ala Tyr Lys Met Ala Thr Glu Gly Met Asn Val Lys Glu Glu Cys 5 10 Gln Arg Trp Phe Met Glu Met Lys Trp Lys Lys Val His Arg Phe Val 20 25 Val Tyr Lys Ile Asp Glu Arg Ser Arg Ala Val Leu Val Asp Lys Val 40 Gly Gly Pro Gly Glu Gly Tyr Glu Glu Leu Val Ala Ala Leu Pro Gly 55 60 Asp Asp Cys Arg Tyr Ala Val Phe Asp Phe Asp Phe Val Thr Val Asp 70 75 Asn Cys Gln Lys Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro Ala Ala 85 90 Ser Arg Ile Arg 100 (2) INFORMATION FOR SEQ ID NO:2823: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 407 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..407 (D) OTHER INFORMATION: / Ceres Seq. ID 1601976 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2823: gcggtccaga tcgatcggta tttgcagatt ggtgcgtcca cacgagagtt tacggcggcc 60 caaacccccc aaatccagtt ccatcccaat cgccgagaag gggaagccaa atcgatggcg 120 geggeggegg ceggeggega gaacagegge geggggegg gegegggega gggegagtte tacctgcggt actacgtggg gcacaagggc aagttcgggc acgagttcct cgagttcgag ttccqcccq acqqcaaqct ccqctacqcc aacaactcca actacaaqaa cqacaccatq 300 atccgcaagg aggtcttcgt ctccccctcc qtcctccgcg aggccaggag gatcatccaa ggagtccgat atcatgaagg aggacgacag caactggcct gagcccg (2) INFORMATION FOR SEQ ID NO:2824: (i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 133 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..133 (D) OTHER INFORMATION: / Ceres Seq. ID 1601977 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2824: Ala Val Gln Ile Asp Arg Tyr Leu Gln Ile Gly Ala Ser Thr Arg Glu 10 Phe Thr Ala Ala Gln Thr Pro Gln Ile Gln Phe His Pro Asn Arg Arg 25 30

Glu Gly Glu Ala Lys Ser Met Ala Ala Ala Ala Gly Gly Glu Asn

Ser Gly Ala Gly Ala Gly Ala Gly Glu Gly Glu Phe Tyr Leu Arg Tyr 50 55 60

Tyr Val Gly His Lys Gly Lys Phe Gly His Glu Phe Leu Glu Phe Glu 65 70 75 80

Phe Arg Pro Asp Gly Lys Leu Arg Tyr Ala Asn Asn Ser Asn Tyr Lys 85 90 95

Asn Asp Thr Met Ile Arg Lys Glu Val Phe Val Ser Pro Ser Val Leu 100 105 110

Arg Glu Ala Arg Arg Ile Ile Gln Gly Val Arg Tyr His Glu Gly Gly 115 120 125

Arg Gln Gln Leu Ala

130

- (2) INFORMATION FOR SEQ ID NO:2825:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..99
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601978
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2825:

Arg Ser Arg Ser Ile Gly Ile Cys Arg Leu Val Arg Pro His Glu Ser 1 5 10 15

Leu Arg Arg Pro Lys Pro Pro Lys Ser Ser Ser Ile Pro Ile Ala Glu 20 25 30

Lys Gly Lys Pro Asn Arg Trp Arg Arg Arg Pro Ala Ala Arg Thr
35 40 45

Ala Ala Arg Ala Arg Ala Arg Ala Ser Ser Thr Cys Gly Thr 50 55 60

Thr Trp Gly Thr Arg Ala Ser Ser Gly Thr Ser Ser Ser Ser Ser 65 70 75 80

Ser Ala Pro Thr Ala Ser Ser Ala Thr Pro Thr Thr Pro Thr Thr Arg 85 90 95

Thr Thr Pro

- (2) INFORMATION FOR SEQ ID NO:2826:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..124
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601979
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2826:

Tyr Gly Gly Pro Asn Pro Pro Asn Pro Val Pro Ser Gln Ser Pro Arg
20 25 30

Arg Gly Ser Gln Ile Asp Gly Gly Gly Gly Arg Arg Glu Gln 35 40 45

Arg Arg Gly Arg Gly Arg Gly Arg Val Leu Pro Ala Val Leu 50 55 60

Arg Gly Ala Gln Gly Gln Val Arg Ala Arg Val Pro Arg Val Arg Val
65 70 75 80
Pro Pro Arg Arg Gln Ala Pro Leu Arg Gln Gln Leu Gln Leu Gln Glu

85 90 Arg His His Asp Pro Gln Gly Gly Leu Arg Leu Pro Leu Arg Pro Pro 105 Arg Gly Gln Glu Asp His Pro Arg Ser Pro Ile Ser 115 120 (2) INFORMATION FOR SEQ ID NO:2827: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..474 (D) OTHER INFORMATION: / Ceres Seq. ID 1601980 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2827: atcagacggt ggagagcaac accageteaa aaccetageg tecaaeteat atacetgetg ctegeceega egegeateaa eteeegeege egeceettee teteegtege tegectegeg 120 180 cctacgccac cacctctgcc atggccccga agaaggataa ggccccgccg ccgtcgtcca agccggccaa gtccggaggc gggaagcaga agaagaagaa gtggagcaag ggtaagcaaa 240 aggagaaggt caacaacgct gtgctcttcg accaggccac ctatgacaag ttgctctccg 300 aggtgcccaa gtacaagcag atcaccccat ccgtcctctc cgagcgtctc aggattaatg 360 gatcattykg cacqqaqqqc aatcaaqqat ctqatqqcaa qqqqattcat aagqatqatc 420 totqttcatt ccaqccaqca gatatacacc aggkcaacca acacatqagg gctq (2) INFORMATION FOR SEQ ID NO:2828: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..155 (D) OTHER INFORMATION: / Ceres Seq. ID 1601981 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2828: Ile Arg Arg Trp Arg Ala Thr Pro Ala Gln Asn Pro Ser Val Gln Leu 5 10 Ile Tyr Leu Leu Ala Pro Thr Arg Ile Asn Ser Arg Arg Arg Pro 20 25 Phe Leu Ser Val Ala Arg Leu Ala Pro Thr Pro Pro Pro Leu Pro Trp 45 4.0 Pro Arg Arg Arg Ile Arg Pro Arg Arg Arg Pro Ser Arg Pro Ser 55 Pro Glu Ala Gly Ser Arg Arg Arg Ser Gly Ala Arg Val Ser Lys 75 70 Arg Arg Arg Ser Thr Thr Leu Cys Ser Ser Thr Arg Pro Pro Met Thr 90 85 Ser Cys Ser Pro Arg Cys Pro Ser Thr Ser Arg Ser Pro His Pro Ser 105 100 Ser Pro Ser Val Ser Gly Leu Met Asp His Xaa Ala Arg Arg Ala Ile 115 120 125 Lys Asp Leu Met Ala Arg Gly Phe Ile Arg Met Ile Ser Val His Ser 135 140

- (2) INFORMATION FOR SEQ ID NO:2829:
  - (i) SEQUENCE CHARACTERISTICS:

Ser Gln Gln Ile Tyr Thr Arg Xaa Thr Asn Thr 145 150 155

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide

  - (B) LOCATION: 1..111
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2829:

Met Ala Pro Lys Lys Asp Lys Ala Pro Pro Pro Ser Ser Lys Pro Ala 10 Lys Ser Gly Gly Gly Lys Gln Lys Lys Lys Trp Ser Lys Gly Lys

20 25

Gln Lys Glu Lys Val Asn Asn Ala Val Leu Phe Asp Gln Ala Thr Tyr 40

Asp Lys Leu Leu Ser Glu Val Pro Lys Tyr Lys Gln Ile Thr Pro Ser 55

Val Leu Ser Glu Arg Leu Arg Ile Asn Gly Ser Xaa Xaa Thr Glu Gly 70 75

Asn Gln Gly Ser Asp Gly Lys Gly Ile His Lys Asp Asp Leu Cys Ser 90 85

Phe Gln Pro Ala Asp Ile His Gln Xaa Asn Gln His Met Arg Ala 105 100

- (2) INFORMATION FOR SEQ ID NO:2830:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 390 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..390
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601994
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2830:

60 aaagagaaga taaaggacct gtttgacaaa catggagagg tcacaaaaat cgttctgcct 120 cctgccaagg ctggtcataa gagagacttt ggctttgttc actttgcaga aagatcaagt gcattgaagg cagttaaagg aagtgaaaaa tatgaaatcg atggtcaagt actggaagtg 180 240 tccatggcca aaccattggc agataagaaa cctgatcatt cacacaggcc tggaggaggc cctaattate ecetteetee ctatggtggt ggtggetaea tgggagatee atatggtget 300 360 tatqqtqqtq qcqqtcctqc atacaaccaq ccaatgatat atggcagagg accagcaccg gcaggaatga ggatggtgcc gatggtgctt

- (2) INFORMATION FOR SEQ ID NO:2831:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..130
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601995
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2831:

Lys Glu Lys Ile Lys Asp Leu Phe Asp Lys His Gly Glu Val Thr Lys 5 10

Ile Val Leu Pro Pro Ala Lys Ala Gly His Lys Arg Asp Phe Gly Phe 25

Val His Phe Ala Glu Arg Ser Ser Ala Leu Lys Ala Val Lys Gly Ser 40

Glu Lys Tyr Glu Ile Asp Gly Gln Val Leu Glu Val Ser Met Ala Lys

```
Pro Leu Ala Asp Lys Lys Pro Asp His Ser His Arg Pro Gly Gly
                    70
                                        75
Pro Asn Tyr Pro Leu Pro Pro Tyr Gly Gly Gly Tyr Met Gly Asp
                                    90
                85
Pro Tyr Gly Ala Tyr Gly Gly Gly Pro Ala Tyr Asn Gln Pro Met
           100
                               105
                                                  110
Ile Tyr Gly Arg Gly Pro Ala Pro Ala Gly Met Arg Met Val Pro Met
                                                125
                            120
       115
Val Leu
   130
(2) INFORMATION FOR SEQ ID NO:2832:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..69
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601996
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2832:
Met Ala Lys Pro Leu Ala Asp Lys Lys Pro Asp His Ser His Arg Pro
              5
                                   10
Gly Gly Gly Pro Asn Tyr Pro Leu Pro Pro Tyr Gly Gly Gly Tyr
            20
                               25
                                                    30
Met Gly Asp Pro Tyr Gly Ala Tyr Gly Gly Gly Pro Ala Tyr Asn
                                                45
                           40
Gln Pro Met Ile Tyr Gly Arg Gly Pro Ala Pro Ala Gly Met Arg Met
                        55
Val Pro Met Val Leu
(2) INFORMATION FOR SEQ ID NO:2833:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 390 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..390
          (D) OTHER INFORMATION: / Ceres Seq. ID 1601997
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2833:
                                                                       60
acgggagcgg acggagaaaa ttttgaaacg cgggcgaggc cgccaccacc gcgccaaatc
gagccatcca gattccattc gacggccgga agtcagatcc gtgcatctat aatacttcca
                                                                      120
                                                                      180
ggaattetet ecteteceaa gaeeegeace geaeeaegeg aaateaagte etgeaaaage
                                                                      240
ctcgcggcta cctcacgtgg atcggcgacg gcgatgacgg cgtccttctc ttccgtcgcc
                                                                      300
qaqqtaqcqq ttcccqctqc tqcqqcqqtq atqqcatcaq ctttqccqca gqaqcaqcaq
                                                                      360
caggegege egeggeege geegatgeae getggtggtg gtggtggtgg eggeggegge
qccaatggcc gccaccacgc gtacagccgc
(2) INFORMATION FOR SEQ ID NO:2834:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 130 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
```

(A) NAME/KEY: peptide
(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1601998 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2834: Thr Gly Ala Asp Gly Glu Asn Phe Glu Thr Arg Ala Arg Pro Pro 10 Pro Arg Gln Ile Glu Pro Ser Arg Phe His Ser Thr Ala Gly Ser Gln 20 25 30 Ile Arg Ala Ser Ile Ile Leu Pro Gly Ile Leu Ser Ser Pro Lys Thr 45 40 Arg Thr Ala Pro Arg Glu Ile Lys Ser Cys Lys Ser Leu Ala Ala Thr 55 Ser Arg Gly Ser Ala Thr Ala Met Thr Ala Ser Phe Ser Ser Val Ala 70 75 Glu Val Ala Val Pro Ala Ala Ala Ala Val Met Ala Ser Ala Leu Pro 90 8.5 Gln Glu Gln Gln Ala Arg Pro Arg Pro Arg Pro Met His Ala Gly 105 110 100 Gly Gly Gly Gly Gly Gly Gly Ala Asn Gly Arg His His Ala Tyr 120 115 Ser Arq 130 (2) INFORMATION FOR SEQ ID NO:2835: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 459 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..459 (D) OTHER INFORMATION: / Ceres Seq. ID 1602005 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2835: atctcqqttt tattcaaatg ctcaacacgc ttgtttcccg caggagcgtg gtcagatcct ccacaggttc gcggacctga tcgacgagca cgtggaggag ctggcggcgc tggacacggt 120 ggacgccggc aagctgttcg ccgtgggcaa ggcgcgggac atcccgggcg ccgcgcacct 180 240 gctgcgctac tacgccggcg ccgccgacaa ggtgcacggc gcgacgctca agatggcgca gcggatgcac gggtacacgc tcaaggagcc cgtgggcgtg gtgggccaca tcgtgccctg 300 gaactacccc accaccatgt tcttcttcaa ggtagggccc gcgctcgccg caggctgcgc 360 cgtcgtcgtc aagcccgccg agcagacgcc gctgtccgcg ctcttctacg cgcacctcgc 420 cagggaggcc ggcgtcccgc cggcgtgctc aacgtcgtg (2) INFORMATION FOR SEQ ID NO:2836: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..153 (D) OTHER INFORMATION: / Ceres Seq. ID 1602006 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2836: Ile Ser Val Leu Phe Lys Cys Ser Thr Arg Leu Phe Pro Ala Gly Ala 10 5 Trp Ser Asp Pro Pro Gln Val Arg Gly Pro Asp Arg Arg Ala Arg Gly 25 30 Gly Ala Gly Gly Ala Gly His Gly Gly Arg Arg Gln Ala Val Arg Arg 40 45

Gly Gln Gly Ala Gly His Pro Gly Arg Arg Ala Pro Ala Ala Leu Leu

Arg Arg Arg Arg Gln Gly Ala Arg Arg Asp Ala Gln Asp Gly Ala

55

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75
                   70
65
Ala Asp Ala Arg Val His Ala Gln Gly Ala Arg Gly Arg Gly Gly Pro
                                   90
               85
His Arg Ala Leu Glu Leu Pro His His His Val Leu Leu Gln Gly Arg
                               105
Ala Arg Ala Arg Arg Arg Leu Arg Arg Arg Arg Gln Ala Arg Arg Ala
                         120
       115
Asp Ala Ala Val Arg Ala Leu Leu Arg Ala Pro Arg Gln Gly Gly Arg
                                          140
                       135
Arg Pro Ala Gly Val Leu Asn Val Val
145
                   150
(2) INFORMATION FOR SEQ ID NO:2837:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 152 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..152
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602007
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2837:
Ser Arg Phe Tyr Ser Asn Ala Gln His Ala Cys Phe Pro Gln Glu Arg
                                   10
Gly Gln Ile Leu His Arg Phe Ala Asp Leu Ile Asp Glu His Val Glu
                                                   30
           2.0
                                2.5
Glu Leu Ala Ala Leu Asp Thr Val Asp Ala Gly Lys Leu Phe Ala Val
                            40
Gly Lys Ala Arg Asp Ile Pro Gly Ala Ala His Leu Leu Arg Tyr Tyr
                       55
Ala Gly Ala Ala Asp Lys Val His Gly Ala Thr Leu Lys Met Ala Gln
                                        75
                   70
Arg Met His Gly Tyr Thr Leu Lys Glu Pro Val Gly Val Val Gly His
                85
                                    90
Ile Val Pro Trp Asn Tyr Pro Thr Thr Met Phe Phe Lys Val Gly
                              105
                                                  110
           100
Pro Ala Leu Ala Ala Gly Cys Ala Val Val Lys Pro Ala Glu Gln
                           120
                                   125
Thr Pro Leu Ser Ala Leu Phe Tyr Ala His Leu Ala Arg Glu Ala Gly
                       135
Val Pro Pro Ala Cys Ser Thr Ser
                   150
(2) INFORMATION FOR SEQ ID NO:2838:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 465 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..465
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602032
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2838:
actototage tteccaetee geteggeeae cagetttgae egecteeeet ecceteeget
                                                                      120
cctqttcttc cataccccac tccccqcaq qaqcqqcqcq qcqqcqaa aqqcaaaqqc
                                                                      180
aagatgtteg ggegegeec gaagaagage gacaacacca agtactaega gateeteggg
                                                                      240
qtqcccaagt cggcgtccca ggacgacctc aagaaggcct accgcaaggc cgctatcaag
                                                                      300
aaccaccccg acaagggcgg tgaccccgag aagttcaagg agctcgcaca agcctatgag
gttttgagtg atccagagaa acgtgagatt tatgatcagt atggtgaaga tgcccttaag
                                                                      360
```

gaaggaatgg gtggtggtgg atcccatgct gatccatttg acattttctc atcattcttt 420 ggaccctctt ttggaggagg tggtggaagc agcagggaag aaggc

- (2) INFORMATION FOR SEQ ID NO:2839:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..101
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602033
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2839:

Leu Ser Ser Phe Pro Leu Arg Ser Ala Thr Ser Phe Asp Arg Leu Pro 1.0 5

Ser Pro Pro Leu Leu Phe Phe His Thr Pro Leu Pro Arg Arg Ser Gly 30 25 20

Ala Ala Ala Lys Ala Lys Ala Arg Cys Ser Gly Ala Arg Arg 40 45

Arg Ala Thr Thr Pro Ser Thr Thr Arg Ser Ser Gly Cys Pro Ser Arg 60 55

Arg Pro Arg Thr Thr Ser Arg Pro Thr Ala Arg Pro Leu Ser Arg 75 70

Thr Thr Pro Thr Arg Ala Val Thr Pro Arg Ser Ser Arg Ser Ser His 90 85

Lys Pro Met Arg Phe

100

- (2) INFORMATION FOR SEQ ID NO:2840:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..86
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602034
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2840:

Ser Leu Ala Ser His Ser Ala Arg Pro Pro Ala Leu Thr Ala Ser Pro 5 10 1

Pro Leu Arg Ser Cys Ser Ser Ile Pro His Ser Pro Ala Gly Ala Ala 25

Arg Arg Arg Gln Arg Gln Arg Gln Asp Val Arg Ala Arg Ala Glu Glu 40

Glu Arg Gln His Gln Val Leu Arg Asp Pro Arg Gly Ala Gln Val Gly 55

Val Pro Gly Arg Pro Gln Glu Gly Leu Pro Gln Gly Arg Tyr Gln Glu 70

Pro Pro Arg Gln Gly Arg

- (2) INFORMATION FOR SEQ ID NO:2841:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1602035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2841:

Met Phe Gly Arg Ala Pro Lys Lys Ser Asp Asn Thr Lys Tyr Tyr Glu

1 5 10 15

Ile Leu Gly Val Pro Lys Ser Ala Ser Gln Asp Asp Leu Lys Lys Ala 20 25 30

Tyr Arg Lys Ala Ala Ile Lys Asn His Pro Asp Lys Gly Gly Asp Pro 35 40 45

Glu Lys Phe Lys Glu Leu Ala Gln Ala Tyr Glu Val Leu Ser Asp Pro 50 55 60

Glu Lys Arg Glu Ile Tyr Asp Gln Tyr Gly Glu Asp Ala Leu Lys Glu 65 70 75 80

Gly Met Gly Gly Gly Ser His Ala Asp Pro Phe Asp Ile Phe Ser 85 90 95

Ser Phe Phe Gly Pro Ser Phe Gly Gly Gly Gly Ser Ser Arg Glu 100 105 110

Glu Gly

- (2) INFORMATION FOR SEQ ID NO:2842:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..476
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602039
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2842:

  cagcggcca tggcctccat ggcgttcgcc ctggcggggg ccttcaaggg cctctccctg
  gcgccacca ccaccacct ctccttcccg cgctgcgacc gcgcctcgct ctccgtcgc
  ggcgcagcgg gcgtgccggt gccggtgccg gcgcggcgc tcaccatcca gatggcgcac
  aagaaggggg ccgggagcac caagaacggc cgcgactcca agggccagcg cctcggggtc
  aagatatacg gcgaccagct cgccaagccc ggggccatca tcatccgcca gcgcggcacc
  agggtctatc ctggaaataa cgttggaatg ggcaaggatc acacactctt ttctttgata
  gatggactcg tcaagtttga gaagtatggg ccggacaaga aaaaggtbag tgtttaccca
  tatgagaagg agcctgaaaa cccaaacagt tacagagcaa ggaagagaa gtactt
- (2) INFORMATION FOR SEQ ID NO:2843:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..158
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602040
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2843:
- Gln Arg Pro Met Ala Ser Met Ala Phe Ala Leu Ala Gly Ala Phe Lys
  1 10 15
- Gly Leu Ser Leu Ala Pro Thr Thr Thr Thr Ser Ser Phe Pro Arg Cys
  20 25 30
- Asp Arg Ala Ser Leu Ser Val Gly Gly Ala Ala Gly Val Pro Val Pro 35 40 45
- Val Pro Ala Arg Arg Leu Thr Ile Gln Met Ala His Lys Lys Gly Ala 50 55 60
- Gly Ser Thr Lys Asn Gly Arg Asp Ser Lys Gly Gln Arg Leu Gly Val

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Lys Ile Tyr Gly Asp Gln Leu Ala Lys Pro Gly Ala Ile Ile Ile Arg
                                 90
Gln Arg Gly Thr Arg Val Tyr Pro Gly Asn Asn Val Gly Met Gly Lys
                                                110
          100
                             105
Asp His Thr Leu Phe Ser Leu Ile Asp Gly Leu Val Lys Phe Glu Lys
      115
                         120
Tyr Gly Pro Asp Lys Lys Lys Xaa Ser Val Tyr Pro Tyr Glu Lys Glu
                                       140
   130 135
Pro Glu Asn Pro Asn Ser Tyr Arg Ala Arg Lys Arg Glu Tyr
       150
                                     155
145
(2) INFORMATION FOR SEQ ID NO:2844:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 155 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..155
         (D) OTHER INFORMATION: / Ceres Seq. ID 1602041
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2844:
Met Ala Ser Met Ala Phe Ala Leu Ala Gly Ala Phe Lys Gly Leu Ser
                             10
    5
Leu Ala Pro Thr Thr Thr Ser Ser Phe Pro Arg Cys Asp Arg Ala
                                               30
                             25
Ser Leu Ser Val Gly Gly Ala Ala Gly Val Pro Val Pro Val Pro Ala
                          4.0
                                            45
Arg Arg Leu Thr Ile Gln Met Ala His Lys Lys Gly Ala Gly Ser Thr
                      55
                                        60
Lys Asn Gly Arg Asp Ser Lys Gly Gln Arg Leu Gly Val Lys Ile Tyr
                  70
                                     75
Gly Asp Gln Leu Ala Lys Pro Gly Ala Ile Ile Ile Arg Gln Arg Gly
                                 90
              85
Thr Arg Val Tyr Pro Gly Asn Asn Val Gly Met Gly Lys Asp His Thr
                             105 110
           100
Leu Phe Ser Leu Ile Asp Gly Leu Val Lys Phe Glu Lys Tyr Gly Pro
                         120
                                           125
      115
Asp Lys Lys Lys Xaa Ser Val Tyr Pro Tyr Glu Lys Glu Pro Glu Asn
                   135
Pro Asn Ser Tyr Arg Ala Arg Lys Arg Glu Tyr
                  150
(2) INFORMATION FOR SEQ ID NO:2845:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 152 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
          (B) LOCATION: 1..152
         (D) OTHER INFORMATION: / Ceres Seq. ID 1602042
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2845:
Met Ala Phe Ala Leu Ala Gly Ala Phe Lys Gly Leu Ser Leu Ala Pro
                                 10
       5
Thr Thr Thr Thr Ser Ser Phe Pro Arg Cys Asp Arg Ala Ser Leu Ser
                             25
Val Gly Gly Ala Ala Gly Val Pro Val Pro Val Pro Ala Arg Arg Leu
```

Thr Ile Gln Met Ala His Lys Lys Gly Ala Gly Ser Thr Lys Asn Gly

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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55
Arg Asp Ser Lys Gly Gln Arg Leu Gly Val Lys Ile Tyr Gly Asp Gln
                                        75
                    70
Leu Ala Lys Pro Gly Ala Ile Ile Ile Arg Gln Arg Gly Thr Arg Val
                                    90
               8.5
Tyr Pro Gly Asn Asn Val Gly Met Gly Lys Asp His Thr Leu Phe Ser
           100
                              105
Leu Ile Asp Gly Leu Val Lys Phe Glu Lys Tyr Gly Pro Asp Lys Lys
                           120
                                              125
       115
Lys Xaa Ser Val Tyr Pro Tyr Glu Lys Glu Pro Glu Asn Pro Asn Ser
                       135
                                            140
Tyr Arg Ala Arg Lys Arg Glu Tyr
                    150
(2) INFORMATION FOR SEQ ID NO:2846:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 466 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..466
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602053
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2846:
                                                                       60
aaaaqccctt cccctcctt ttcccccgtt cgagttgctc gagctccgac caaatctcgc
ageggtagea atccccgage ecgaageggg atcagtggag gaegacacce tegattetga
                                                                      120
cctqcqqtcq qcqcqactta cagacaaccq gagatqcaqc agggcqacaq cacqqaqqcq
                                                                      180
caggtgacgt gggaggacca gcagaacatc aaccgcttcg gtcgcctcaa caaccgcctc
                                                                      240
cacgagetee aggacgagat caaactegeg aaggaaacga acgagaacet tgacgatget
                                                                      300
                                                                      360
qqqaacqaac tcatcctqtc qqacqaaqat gtcqtqcqct tccaqatcqq gqaqqtqttt
gctcacatgc cgagggactg acgtcgagac taggctggag cagatgaaag aggatgcggc
                                                                      420
taagaagctg gagaggctag aggaggagaa ggaatccgtc ctcgcc
(2) INFORMATION FOR SEQ ID NO:2847:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 61 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..61
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602054
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2847:
Lys Ala Leu Pro Pro Pro Phe Pro Pro Phe Glu Leu Leu Glu Leu Arg
                                    10
Pro Asn Leu Ala Ala Val Ala Ile Pro Glu Pro Glu Ala Gly Ser Val
            20
                                25
Glu Asp Asp Thr Leu Asp Ser Asp Leu Arg Ser Ala Arg Leu Thr Asp
                            40
        35
Asn Arg Arg Cys Ser Arg Ala Thr Ala Arg Arg Arg
                        55
(2) INFORMATION FOR SEQ ID NO:2848:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 75 amino acids
           (B) TYPE: amino acid
```

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2848:

Met Gln Gln Gly Asp Ser Thr Glu Ala Gln Val Thr Trp Glu Asp Gln 1 5 10 15

Gln Asn Ile Asn Arg Phe Gly Arg Leu Asn Asn Arg Leu His Glu Leu 20 25 30

Gln Asp Glu Ile Lys Leu Ala Lys Glu Thr Asn Glu Asn Leu Asp Asp 35 40 45

Ala Gly Asn Glu Leu Ile Leu Ser Asp Glu Asp Val Val Arg Phe Gln 50 55 60

- Ile Gly Glu Val Phe Ala His Met Pro Arg Asp 65 70 75
- (2) INFORMATION FOR SEQ ID NO:2849:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..57
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602056
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2849:

Met Leu Gly Thr Asn Ser Ser Cys Arg Thr Lys Met Ser Cys Ala Ser

Arg Ser Gly Arg Cys Leu Leu Thr Cys Arg Gly Thr Asp Val Glu Thr 20 25 30

Arg Leu Glu Gln Met Lys Glu Asp Ala Ala Lys Lys Leu Glu Arg Leu 35 40 45

Glu Glu Lys Glu Ser Val Leu Ala 50 55

- (2) INFORMATION FOR SEQ ID NO:2850:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..488
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602060
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2850:

60 cggctcctcc ctctcggatt cccaaacgcc aaaatctcgt tgtcacgccc acgcaccgca 120 tegttegett cetttegtea actecaette tetteteege gteaceteet ettegeegee gccgacgctt cacceggcag ccagccatgg atgaggagta cgacgtgate gtactaggca 180 cggggctcaa ggagtgcatc ctcagcggtc tcctctctgt agacggcctc aaggttttgc 240 atatggacag aaatgactac tatggaggag attccacctc actcaacctt aatcagctct 300 ggaagaggtt tagaggggaa gacaagcccc cagcacatct aggtgcaagc agagactaca 360 atgtggacat ggtgccaaag tttatgatgg caaatgggac attggttcga accctcattc 420 acaccgacgt gacaaagtac ttgtcattca aagctgttga tgggagctat gttttcagca 480 aagggaag

- (2) INFORMATION FOR SEQ ID NO:2851:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 162 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..162
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602061
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2851:

Ala Pro Pro Ser Arg Ile Pro Lys Arg Gln Asn Leu Val Val Thr Pro 1 5 10 15

Thr His Arg Ile Val Arg Phe Leu Ser Ser Thr Pro Leu Leu Phe Ser 20 25 30

Ala Ser Pro Pro Leu Arg Arg Arg Arg Phe Thr Arg Gln Pro Ala 35 40 45

Met Asp Glu Glu Tyr Asp Val Ile Val Leu Gly Thr Gly Leu Lys Glu 50 55 60

Cys Ile Leu Ser Gly Leu Leu Ser Val Asp Gly Leu Lys Val Leu His 65 70 75 80

Met Asp Arg Asn Asp Tyr Tyr Gly Gly Asp Ser Thr Ser Leu Asn Leu 85 90 95

Asn Gln Leu Trp Lys Arg Phe Arg Gly Glu Asp Lys Pro Pro Ala His
100 105 110

Leu Gly Ala Ser Arg Asp Tyr Asn Val Asp Met Val Pro Lys Phe Met 115 120 125

Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly Ser Tyr Val Phe Ser Lys 145 150 155 160

- Gly Lys
- (2) INFORMATION FOR SEQ ID NO:2852:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..114
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602062
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2852:

Met Asp Glu Glu Tyr Asp Val Ile Val Leu Gly Thr Gly Leu Lys Glu 1 5 10 15

Cys Ile Leu Ser Gly Leu Leu Ser Val Asp Gly Leu Lys Val Leu His
20 25 30

Met Asp Arg Asn Asp Tyr Tyr Gly Gly Asp Ser Thr Ser Leu Asn Leu 35 40 45

Asn Gln Leu Trp Lys Arg Phe Arg Gly Glu Asp Lys Pro Pro Ala His
50 55 60

Leu Gly Ala Ser Arg Asp Tyr Asn Val Asp Met Val Pro Lys Phe Met 65 70 75 80

Met Ala Asn Gly Thr Leu Val Arg Thr Leu Ile His Thr Asp Val Thr

Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly Ser Tyr Val Phe Ser Lys
100 105 110

Gly Lys

- (2) INFORMATION FOR SEQ ID NO:2853:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:

120

180

240

300

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..82
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602063
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2853:

Met Asp Arg Asn Asp Tyr Tyr Gly Gly Asp Ser Thr Ser Leu Asn Leu
1 10 15

Asn Gln Leu Trp Lys Arg Phe Arg Gly Glu Asp Lys Pro Pro Ala His
20 25 30

Leu Gly Ala Ser Arg Asp Tyr Asn Val Asp Met Val Pro Lys Phe Met 35 40 45

Met Ala Asn Gly Thr Leu Val Arg Thr Leu Ile His Thr Asp Val Thr 50 55 60

Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly Ser Tyr Val Phe Ser Lys 65 70 75 80 Gly Lys

- (2) INFORMATION FOR SEQ ID NO:2854:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 513 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..513
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602076
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2854:
  actetteyee titteeteet eeteteett eeteteett aggetetagt eetetegeat eegeagette eegageege tagggtitge agatgaegae egeggegee eeeneetggg egeeggeeaa gageageggg geaceegeat etteggeee teeeagaagt teteeteeg egacetegee gegeacacet eeeteaagee aagaaaagae ggteaacaga eecaagaga gttacagaag aggaatetea gggaggaact tgaggaaegt gagegeaage

actactette caaggataag teetatgeeg aagaaagaga eeggeggaaa agetetagee 360 atetactett agaaggttea aagagagaga eagaggataa gatagtteea egagaaateg 420 atgetgatga eteegatgtg gageetaaaa gegatgaega gagegatgaa gatgatgatg 480

- acgacgacac tgaagctcta atggcagagc ttg (2) INFORMATION FOR SEQ ID NO:2855:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602077
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2855:

Met Thr Thr Ala Ala Arg Pro Xaa Trp Ala Pro Ala Lys Gly Gly Asn
1 5 10 15

Glu Gln Gly Gly Thr Arg Ile Phe Gly Pro Ser Gln Lys Phe Ser Ser

Arg Asp Leu Ala Ala His Thr Ser Leu Lys Pro Arg Lys Asp Gly Gln
35 40 45

Gln Thr Gln Glu Glu Leu Gln Lys Arg Asn Leu Arg Glu Glu Leu Glu
50 55 60
Glu Arg Glu Arg Lys His Tyr Ser Ser Lys Asp Lys Ser Tyr Ala Glu

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Client Docket No. 80146.003
                                       75
                   70
65
Glu Arg Asp Arg Arg Lys Ser Ser Ser His Leu Leu Glu Gly Ser
                                   90
               85
Lys Arg Glu Thr Glu Asp Lys Ile Val Pro Arg Glu Ile Asp Ala Asp
                                                  110
                              105
           100
Asp Ser Asp Val Glu Pro Lys Ser Asp Asp Glu Ser Asp Glu Asp Asp
                                              125
                       120
       115
Asp Asp Asp Asp Thr Glu Ala Leu Met Ala Glu Leu
                      135
   130
(2) INFORMATION FOR SEQ ID NO:2856:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 513 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..513
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602078
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2856:
tttgcctttt ctcctgccca ccaccccgcc acaacccttt cccttctctg cttgct
                                                                    120
gctgcagtgc tgcctccccc tcgcccagca gcagggagca gccatgccag ggaaccacgg
                                                                    180
ctccaagggc gacatctcct tcgccggacg cttcacggcc agcgccatag cagcatgctt
                                                                    240
cgcagagata tgtaccatcc cgctcgacac ggccaaggtc aggctccagc tgcagaagaa
                                                                    300
cgtcgtcgcc gccgcgcctc cggggacgcc gcgccagcgc tccccaagta ccgcggcctg
                                                                    360
ctcggaaccg ccgccaccat cgctagggag gaaggggccg cagcgctctg gaagggcatc
                                                                    420
gtcccgggcc tsccaccgac agtgcatcta cgggggggct acgcattggc ctctacgagc
                                                                    480
ctgtcaaatc cttctacgtc ggcaaagacc atg
(2) INFORMATION FOR SEQ ID NO:2857:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 171 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..171
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602079
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2857:
Ile Leu Val Ser Leu Ile Ser Val Arg Arg Arg Arg Arg Pro Ile
                                                       15
                                   10
                5
1
Ser Pro Phe Leu Phe Ala Phe Ser Pro Ala His His Pro Ala Thr Thr
                                                   30
                                25
Leu Ser Leu Leu Cys Leu Leu Ala Ala Ala Val Leu Pro Pro Pro Arg
                                               45
                            40
Pro Ala Ala Gly Ser Ser His Ala Arg Glu Pro Arg Leu Gln Gly Arg
                                           60
                        55
His Leu Leu Arg Arg Thr Leu His Gly Gln Arg His Ser Ser Met Leu
                                       75
                    70
Arg Arg Asp Met Tyr His Pro Ala Arg His Gly Gln Gly Gln Ala Pro
                85
                                    90
Ala Ala Glu Glu Arg Arg Arg Arg Ala Ser Gly Asp Ala Ala Pro
                                105
                                                   110
Ala Leu Pro Lys Tyr Arg Gly Leu Leu Gly Thr Ala Ala Thr Ile Ala
                                               125
        115
 Arg Glu Glu Gly Ala Ala Ala Leu Trp Lys Gly Ile Val Pro Gly Xaa
```

135

Pro Pro Thr Val His Leu Arg Gly Gly Tyr Ala Leu Ala Ser Thr Ser

160 150 145 Leu Ser Asn Pro Ser Thr Ser Ala Lys Thr Met 165 170 (2) INFORMATION FOR SEQ ID NO:2858: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..116 (D) OTHER INFORMATION: / Ceres Seq. ID 1602080 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2858: Met Pro Gly Asn His Gly Ser Lys Gly Asp Ile Ser Phe Ala Gly Arg 10 5 Phe Thr Ala Ser Ala Ile Ala Ala Cys Phe Ala Glu Ile Cys Thr Ile 25 20 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Asn Val Val 45 40 Ala Ala Pro Pro Gly Thr Pro Arg Gln Arg Ser Pro Ser Thr Ala 55 60 Ala Cys Ser Glu Pro Pro Pro Pro Ser Leu Gly Arg Lys Gly Pro Gln 70 75 Arg Ser Gly Arg Ala Ser Ser Arg Ala Xaa His Arg Gln Cys Ile Tyr 90 95 85 Gly Gly Ala Thr His Trp Pro Leu Arg Ala Cys Gln Ile Leu Leu Arg 105 Arg Gln Arg Pro 115 (2) INFORMATION FOR SEQ ID NO:2859: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1602081 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2859: Met Leu Arg Arg Asp Met Tyr His Pro Ala Arg His Gly Gln Gly Gln 10 Ala Pro Ala Ala Glu Glu Arg Arg Arg Arg Ala Ser Gly Asp Ala 25 20 Ala Pro Ala Leu Pro Lys Tyr Arg Gly Leu Leu Gly Thr Ala Ala Thr 40 Ile Ala Arg Glu Glu Gly Ala Ala Ala Leu Trp Lys Gly Ile Val Pro 55 60 Gly Xaa Pro Pro Thr Val His Leu Arg Gly Gly Tyr Ala Leu Ala Ser 70 75 Thr Ser Leu Ser Asn Pro Ser Thr Ser Ala Lys Thr Met 85 (2) INFORMATION FOR SEQ ID NO:2860: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 464 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..464
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602089
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2860: 60 atatattcat gtcccgagaa cttgtcaggc tctcttcctc cctcgccgcg gaacacgcgc cccgtcctcg cccgcccgtg ttcatctctc cattccatac cttgcagtgc aggtgcggtg 120 180 gtagccgagc gctccggcca tggcgttctt ccggggcctc accgcggtct cgaggctgcg atcccgcatg gcgcaggagg ccaccacgct gggtggtgtg agatggctgc agatgcagag 240 cgcgtccgat ctcgatctta agtcccagtt gcaggaattg attccggaac agcaggatcg 300 cctaaagaag cttaaatcag agcatgggaa ggttcagctt ggaaacataa ctgtggatat 360 ggtccttggt ggamtgagag ggatgattgg aatgctttgg gaaacatccc tacttgaccy 420 agaggaggt attcgtttta ggggtctctc gattccagag tgcc
- (2) INFORMATION FOR SEQ ID NO:2861:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..86
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602090
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2861:
- Ile Tyr Ser Cys Pro Glu Asn Leu Ser Gly Ser Leu Pro Pro Ser Pro 1 10 15
- Arg Asn Thr Arg Pro Val Leu Ala Arg Pro Cys Ser Ser Leu His Ser 20 25 30
- Ile Pro Cys Ser Ala Gly Ala Val Val Ala Glu Arg Ser Gly His Gly 35 40 45
- Val Leu Pro Gly Pro His Arg Gly Leu Glu Ala Ala Ile Pro His Gly 50 60
- Ala Gly Gly His His Ala Gly Trp Cys Glu Met Ala Ala Asp Ala Glu 65 70 75 80
- Arg Val Arg Ser Arg Ser 85
- (2) INFORMATION FOR SEQ ID NO:2862:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..108
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602091
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2862:
- Met Ala Phe Phe Arg Gly Leu Thr Ala Val Ser Arg Leu Arg Ser Arg  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$
- Met Ala Gl<br/>n Glu Ala Thr Thr Leu Gly Gly Val Arg Tr<br/>p Leu Gl<br/>n Met 20  $\phantom{000}25\phantom{0}$ 30
- Gln Ser Ala Ser Asp Leu Asp Leu Lys Ser Gln Leu Gln Glu Leu Ile 35 40 45
- Pro Glu Gln Gln Asp Arg Leu Lys Lys Leu Lys Ser Glu His Gly Lys 50 55 60
- Val Gln Leu Gly Asn Ile Thr Val Asp Met Val Leu Gly Gly Xaa Arg 65 70 75 80
- Gly Met Ile Gly Met Leu Trp Glu Thr Ser Leu Leu Asp Xaa Glu Glu

95 90 85 Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys 105 100 (2) INFORMATION FOR SEQ ID NO:2863: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..92 (D) OTHER INFORMATION: / Ceres Seq. ID 1602092 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2863: Met Ala Gln Glu Ala Thr Thr Leu Gly Gly Val Arg Trp Leu Gln Met 10 5 Gln Ser Ala Ser Asp Leu Asp Leu Lys Ser Gln Leu Gln Glu Leu Ile 30 25 Pro Glu Gln Gln Asp Arg Leu Lys Lys Leu Lys Ser Glu His Gly Lys 40 Val Gln Leu Gly Asn Ile Thr Val Asp Met Val Leu Gly Gly Xaa Arg 55 60 Gly Met Ile Gly Met Leu Trp Glu Thr Ser Leu Leu Asp Xaa Glu Glu 70 7.5 Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys 85 (2) INFORMATION FOR SEQ ID NO:2864: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 546 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..546 (D) OTHER INFORMATION: / Ceres Seq. ID 1602093 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2864: accggaacga aacgctgagg cagcatcttc cccgccgtcc tccgccgcct cccattttca 60 cettggctgc agectgcaac acaatectae getteegaet teaaegegeg eceeteecat 120 tttcacctag ccctactcct ttgtacataa aggaagatgg gagcatatgc aacgactggt 180 atgcagatga tagcaacacg cccttccatc ccggcctaca ggcaaatact tggqtcgaca 240 tcagcactat ctgcatttgg aaggtcaatc tgttccagaa ctggctttgc catctcttct 300 aaagccacat cagcaggacc actggtttct tcgaattgca agagggttgt tgtqaqggca 360 atgtcgcaga gaggtgccca aggacttccc attgatctca caggtaaaag agcatttata 420 gctggagttg ctgatgataa tggttatggt tgggcaattg ctaaggctct tgctgctgct 480 540 ggtgctgaga ttcttgttgg tacatgggtg cctgcgttga acatatttga gacaagcttg agacgt (2) INFORMATION FOR SEQ ID NO:2865: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..130 (D) OTHER INFORMATION: / Ceres Seq. ID 1602094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2865:

```
Met Gly Ala Tyr Ala Thr Thr Gly Met Gln Met Ile Ala Thr Arg Pro
                                10
Ser Ile Pro Ala Tyr Arg Gln Ile Leu Gly Ser Thr Ser Ala Leu Ser
                            25
          20
Ala Phe Gly Arg Ser Ile Cys Ser Arg Thr Gly Phe Ala Ile Ser Ser
                         40
Lys Ala Thr Ser Ala Gly Pro Leu Val Ser Ser Asn Cys Lys Arg Val
                    55
Val Val Arg Ala Met Ser Gln Arg Gly Ala Gln Gly Leu Pro Ile Asp
                 70
                                    75
Leu Thr Gly Lys Arg Ala Phe Ile Ala Gly Val Ala Asp Asp Asn Gly
                                90
             8.5
Tyr Gly Trp Ala Ile Ala Lys Ala Leu Ala Ala Gly Ala Glu Ile
                                    110
         100 105
Leu Val Gly Thr Trp Val Pro Ala Leu Asn Ile Phe Glu Thr Ser Leu
       115 120
                                     125
Arg Arg
```

- (2) INFORMATION FOR SEQ ID NO:2866:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 122 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..122
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602095
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2866:

Met Gln Met Ile Ala Thr Arg Pro Ser Ile Pro Ala Tyr Arg Gln Ile 10 1 5

Leu Gly Ser Thr Ser Ala Leu Ser Ala Phe Gly Arg Ser Ile Cys Ser 25

Arg Thr Gly Phe Ala Ile Ser Ser Lys Ala Thr Ser Ala Gly Pro Leu 4.0

Val Ser Ser Asn Cys Lys Arg Val Val Val Arg Ala Met Ser Gln Arg 55

Gly Ala Gln Gly Leu Pro Ile Asp Leu Thr Gly Lys Arg Ala Phe Ile 75

Ala Gly Val Ala Asp Asp Asn Gly Tyr Gly Trp Ala Ile Ala Lys Ala 90

Leu Ala Ala Gly Ala Glu Ile Leu Val Gly Thr Trp Val Pro Ala 105 100

Leu Asn Ile Phe Glu Thr Ser Leu Arg Arg 115

- (2) INFORMATION FOR SEQ ID NO:2867:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..120
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602096
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2867:

Met Ile Ala Thr Arg Pro Ser Ile Pro Ala Tyr Arg Gln Ile Leu Gly 10 5 Ser Thr Ser Ala Leu Ser Ala Phe Gly Arg Ser Ile Cys Ser Arg Thr

360

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20
                                25
Gly Phe Ala Ile Ser Ser Lys Ala Thr Ser Ala Gly Pro Leu Val Ser
                           40
Ser Asn Cys Lys Arg Val Val Val Arg Ala Met Ser Gln Arg Gly Ala
                        55
Gln Gly Leu Pro Ile Asp Leu Thr Gly Lys Arg Ala Phe Ile Ala Gly
                                        75
                    70
Val Ala Asp Asp Asn Gly Tyr Gly Trp Ala Ile Ala Lys Ala Leu Ala
                                    90
               8.5
Ala Ala Gly Ala Glu Ile Leu Val Gly Thr Trp Val Pro Ala Leu Asn
           100 105
                                                   110
Ile Phe Glu Thr Ser Leu Arg Arg
                           120
        115
(2) INFORMATION FOR SEQ ID NO:2868:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 553 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..553
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602104
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2868:
agaccaattc aagcacccca cgggagcgcg tccatcccct tccgccgatc gagccagggc
ccaggccgag caacctggtg ctccgcccct cgccgttaca gcggcgcctc ggcctccggt
                                                                       120
tccacagcgt ctgcctgcct gcgcagccct gtgaccgtga ggcgacacga cgccgagaga
                                                                       180
                                                                       240
tcacccgccc cccgcatcgt gtccgccccg cttgggattg tgaggtaaag cgtgatggca
gegeegeegg egagggeteg ageegactae gactacetaa teaaactget eeteategga
                                                                       300
gacageggeg ttggaaaaag ttgcctcctg ttacggtttt cagatggate attcaccact
agcttcatta ccactattgg cattgacttc aagataagaa ctgttgagtt ggatggcaaa
                                                                       420
aggattaagt tgcagatctg ggatactgca ggccaagaac gtttccgcac aattaccact
gcctactaca ggggagcaat ggggcatctt acttgtgtta tgatgtcmcm gacgagtcat
                                                                       540
ctttcaataa cct
(2) INFORMATION FOR SEQ ID NO:2869:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 75 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..75
           (D) OTHER INFORMATION: / Ceres Seq. ID 1602105
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2869:
 Arg Pro Ile Gln Ala Pro His Gly Ser Ala Ser Ile Pro Phe Arg Arg
                                    10
 Ser Ser Gln Gly Pro Gly Arg Ala Thr Trp Cys Ser Ala Pro Arg Arg
                                 25
             20
 Tyr Ser Gly Ala Ser Ala Ser Gly Ser Thr Ala Ser Ala Cys Leu Arg
                                                 45
 Ser Pro Val Thr Val Arg Arg His Asp Ala Glu Arg Ser Pro Ala Pro
                         55
 Arg Ile Val Ser Ala Pro Leu Gly Ile Val Arg
                     70
```

- (2) INFORMATION FOR SEQ ID NO:2870:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 119 amino acids
    - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..119
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2870:

Thr Asn Ser Ser Thr Pro Arg Glu Arg Val His Pro Leu Pro Pro Ile 1 5 10 15

Glu Pro Gly Pro Arg Pro Ser Asn Leu Val Leu Arg Pro Ser Pro Leu 20 25 30

Gln Arg Arg Leu Gly Leu Arg Phe His Ser Val Cys Leu Pro Ala Gln 35 40 45

Pro Cys Asp Arg Glu Ala Thr Arg Arg Arg Glu Ile Thr Arg Pro Pro 50 55 60

His Arg Val Arg Pro Ala Trp Asp Cys Glu Val Lys Arg Asp Gly Ser 65 70 75 80

Ala Ala Gly Glu Gly Ser Ser Arg Leu Arg Leu Pro Asn Gln Thr Ala 85 90 95

Pro His Arg Arg Gln Arg Arg Trp Lys Lys Leu Pro Pro Val Thr Val
100 105 110

Phe Arg Trp Ile Ile His His 115

- (2) INFORMATION FOR SEQ ID NO:2871:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..106
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602107
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2871:

Met Ala Ala Pro Pro Ala Arg Ala Arg Ala Asp Tyr Asp Tyr Leu Ile 1 5 10 15

Lys Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu 20 25 30

Leu Arg Phe Ser Asp Gly Ser Phe Thr Thr Ser Phe Ile Thr Thr Ile 35 40 45

Gly Ile Asp Phe Lys Ile Arg Thr Val Glu Leu Asp Gly Lys Arg Ile 50 55 60

Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile 70 75 80

Thr Thr Ala Tyr Tyr Arg Gly Ala Met Gly His Leu Thr Cys Val Met 85 90 95

Met Xaa Xaa Thr Ser His Leu Ser Ile Thr 100 105

- (2) INFORMATION FOR SEQ ID NO:2872:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..492
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2872:						
cgcccactac	cctctccaac	tstccgctaa	caaaatctag	aaccctctga	accctccaca	60
ttcctccaga	tcgaataata	acctagetet	gcacaccgcc	cagccaccag	tggcagcagg	120
agcaggggtc	ggaacaagat	ggtggtgacg	gcggccggca	gcgcggagga	ggctgtgcgg	180
cggtgggtgg	acaccaccaa	aggacgcctc	gtcctcgacg	gcgggctggc	cacggagctc	240
gaggccaacg	gcgccgacct	caacqacccq	ctctggagcg	ctaagtgcct	cctctcctcc	300
ccgcacctca	tccgcaaggt	ccacatggac	tatctggaag	ctggcgcaaa	cattataatc	360
acagcatcgt	atcaggccac	tattcaaggg	tttgaatcaa	agggtttttc	aaaagaacag	420
agtgaaaact	tactaacaaa	gagtgtcgag	attgcactgg	aagctcgtga	gatgttcttg	480
aaggaacatc		3 3 3				

- (2) INFORMATION FOR SEQ ID NO:2873:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..118
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602115
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2873:

Met Val Val Thr Ala Ala Gly Ser Ala Glu Glu Ala Val Arg Arg Trp 1 5 10 15

Val Asp Ala Ala Gly Gly Arg Leu Val Leu Asp Gly Gly Leu Ala Thr 20 25 30

Glu Leu Glu Ala Asn Gly Ala Asp Leu Asn Asp Pro Leu Trp Ser Ala 35 40 45

Lys Cys Leu Leu Ser Ser Pro His Leu Ile Arg Lys Val His Met Asp 50 55 60

Tyr Leu Glu Ala Gly Ala Asn Ile Ile Ile Thr Ala Ser Tyr Gln Ala 65 70 75 80

Thr Ile Gln Gly Phe Glu Ser Lys Gly Phe Ser Lys Glu Gln Ser Glu
85
90
95

Asn Leu Leu Thr Lys Ser Val Glu Ile Ala Leu Glu Ala Arg Glu Met 100 105 110

Phe Leu Lys Glu His Leu 115

- (2) INFORMATION FOR SEQ ID NO:2874:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..441
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602137
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2874:

aaccatgatttgcctcaaagccatctcatcccctctccacctcccgaccttccgccgct60caccccacctcctccctcgcgccgcgccgccatgtctcctcctcgtccgcggtcgc120cgccccgatcgagcacttcgtgctcttcaaggcccgcccggaggcggtggcetcgggcgc180cgcggcggcgatggtctcctcgctgcaggcgctggccacgctcgtcccgggcctggcctagaccctcctcgaccggtgctccgcctccgatccccggcgcggaggcgctggccccacgcacctcctccacacccgctacgccaccaaggaggacctggcgtcctacgggggccccacgcggcacgtgtcaacgccgttcctccccaacggctccacatcacccgccgtcgactggtcaacgccgcg

- (2) INFORMATION FOR SEQ ID NO:2875:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 147 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..147
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2875:

Asn His Asp Leu Pro Gln Ser His Leu Ile Pro Ser Pro Pro Pro Asp 1 5 10 15

Leu Pro Pro Pro His Pro His Leu Leu Pro Pro Arg Arg Arg His 20 25 30

Val Leu Leu Leu Val Arg Gly Arg Arg Pro Asp Arg Ala Leu Arg Ala 35 45

Leu Gln Gly Pro Pro Gly Gly Gly Gly Leu Gly Arg Arg Gly Gly Asp 50 55 60

Gly Leu Leu Ala Ala Gly Ala Gly His Ala Arg Pro Gly Pro Gly Leu 65 70 75 80

His Pro Arg Arg Thr Gly Ala Pro Pro Pro Ile Pro Gly Arg Gly Gly 85 90 95

Ala Gly Pro His Ala Pro Pro Pro His Pro Leu Arg His Gln Gly Gly 100 105 110

Pro Gly Val Leu Arg Gly Ala Pro Gly Ala Arg Gly Pro Pro Cys Arg 115 120 125

Gly Thr Ser Ser Pro Thr Arg Ser Thr Ser Pro Ala Val Asp Trp Val 130 135 140

Asn Ala Ala

145

- (2) INFORMATION FOR SEQ ID NO:2876:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..146
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2876:

Thr Met Ile Cys Leu Lys Ala Ile Ser Ser Pro Leu His Leu Pro Thr
1 5 10 15

Phe Arg Arg Leu Thr Pro Thr Ser Ser Leu Arg Ala Ala Ala Met 20 25 30

Ser Ser Ser Ser Ala Val Ala Ala Pro Ile Glu His Phe Val Leu 35 40 45

Phe Lys Ala Arg Pro Glu Ala Val Ala Ser Gly Ala Ala Ala Ala Met 50 55 60

Val Ser Ser Leu Gln Ala Leu Ala Thr Leu Val Pro Gly Leu Ala Tyr 65 70 75 80

Ile His Ala Gly Pro Val Leu Arg Leu Arg Ser Pro Ala Ala Glu Ala 85 90 95

Leu Gly Pro Thr His Leu Leu His Thr Arg Tyr Ala Thr Lys Glu Asp 100 105 110

Leu Ala Ser Tyr Ala Ala His Pro Ala His Val Ala Arg Arg Ala Gly

Ala Arg Pro Pro Gln Arg Ala Arg His His Pro Pro Ser Thr Gly Ser 130

Thr Pro

```
(2) INFORMATION FOR SEQ ID NO:2877:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 145 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
         (A) NAME/KEY: peptide
         (B) LOCATION: 1..145
         (D) OTHER INFORMATION: / Ceres Seq. ID 1602140
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2877:
Met Ile Cys Leu Lys Ala Ile Ser Ser Pro Leu His Leu Pro Thr Phe
                               10
           5
Arg Arg Leu Thr Pro Thr Ser Ser Leu Arg Ala Ala Ala Met Ser
        20
                25
Ser Ser Ser Ser Ala Val Ala Ala Pro Ile Glu His Phe Val Leu Phe
                          40
Lys Ala Arg Pro Glu Ala Val Ala Ser Gly Ala Ala Ala Met Val
                     55
                                         60
Ser Ser Leu Gln Ala Leu Ala Thr Leu Val Pro Gly Leu Ala Tyr Ile
                                  75
                  7.0
His Ala Gly Pro Val Leu Arg Leu Arg Ser Pro Ala Ala Glu Ala Leu
               85
                                 90
Gly Pro Thr His Leu Leu His Thr Arg Tyr Ala Thr Lys Glu Asp Leu
                          105
          100
                                                110
Ala Ser Tyr Ala Ala His Pro Ala His Val Ala Arg Arg Ala Gly Ala
      115 120 125
Arg Pro Pro Gln Arg Ala Arg His His Pro Pro Ser Thr Gly Ser Thr
                      135
130
Pro
145
(2) INFORMATION FOR SEQ ID NO:2878:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 449 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
         (A) NAME/KEY: -
          (B) LOCATION: 1..449
         (D) OTHER INFORMATION: / Ceres Seq. ID 1602141
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2878:
atotoattog cagatogoaa ctogttogac cagaaacaga cotgoacggo tocactocaa
ctcctccca agcccccaac caccttcctt ttccacatcc acaccgcccc gggtttcctc
                                                                   120
acgectecge ceteceaagt cecacecget cactecegte cetatecace gegatggeet
                                                                   180
coegectage egtagoegta geogtagoeg egcaegagta gtatoettaa coeggtagoea
                                                                   240
cogtogococ gococogoto gocotocgoc gaggeotoco gocgaegtgg cacgototoc
gcgccctccc tcgatmccgt ggcgcagccg tcgtgtgcca ggcccarggc ggccaggaca
                                                                   360
cogecateca agttectgat gtgageaaat ceacatggea ateaettgtg gtggagageg
                                                                   420
agetteecgt cetegtteag ttetgggee
(2) INFORMATION FOR SEQ ID NO:2879:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 127 amino acids
          (B) TYPE: amino acid
```

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide

- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602142
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2879:
- Ile Ser Phe Ala Asp Arg Asn Ser Phe Asp Gln Lys Gln Thr Cys Thr
  1 5 10 15
- Ala Pro Leu Gln Leu Pro Pro Lys Pro Pro Thr Thr Phe Leu Phe His 20 25 30
- Ile His Thr Ala Pro Gly Phe Leu Thr Pro Pro Pro Ser Gln Val Pro 35  $\phantom{\bigg|}40\phantom{\bigg|}45\phantom{\bigg|}$
- Pro Ala His Ser Arg Pro Tyr Pro Pro Arg Trp Pro Pro Ala Ser Pro 50 55 60
- Ser Pro Ser Pro Ser Pro Arg Pro Arg Arg Leu Leu Pro Arg Ser Pro 65 70 75 80
- Pro Ser Pro Arg Pro Ala Ser Pro Ser Ala Glu Ala Ser Arg Arg Arg 85 90 95
- Gly Thr Leu Ser Ala Pro Ser Leu Asp Xaa Val Ala Gln Pro Ser Cys 100 105 110
- Ala Arg Pro Xaa Ala Ala Arg Thr Pro Pro Ser Lys Phe Leu Met 115 120 125
- (2) INFORMATION FOR SEQ ID NO:2880:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..125
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602143
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2880:
- Leu His Ser Asn Ser Leu Pro Ser Pro Gln Pro Pro Ser Phe Ser Thr 20 25 30
- Ser Thr Pro Pro Arg Val Ser Ser Arg Leu Arg Pro Pro Lys Ser His 35 40 45
- Pro Leu Thr Pro Val Pro Ile His Arg Asp Gly Leu Pro Pro Arg Arg 50 55 60
- Arg Arg Arg Arg Arg Ala Arg Val Val Ser Phe Pro Gly Arg His
  65 70 75 80
- Arg Arg Pro Ala Pro Arg Arg Pro Pro Pro Arg Pro Pro Ala Asp Val 85 90 95
- Ala Arg Ser Pro Arg Pro Pro Ser Xaa Pro Trp Arg Ser Arg Arg Val 100 105 110
- Pro Gly Pro Xaa Arg Pro Gly His Arg His Pro Ser Ser 115 120 125
- (2) INFORMATION FOR SEQ ID NO:2881:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 149 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..149
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602144
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2881:
- Leu Ile Arg Arg Ser Gln Leu Val Arg Pro Glu Thr Asp Leu His Gly
  1 5 10 15

```
Ser Thr Pro Thr Pro Ser Gln Ala Pro Asn His Leu Pro Phe Pro His
                                25
            2.0
Pro His Arg Pro Gly Phe Pro His Ala Ser Ala Leu Pro Ser Pro Thr
                                                45
                           40
Arg Ser Leu Pro Ser Leu Ser Thr Ala Met Ala Ser Arg Leu Ala Val
                                            60
                        5.5
Ala Val Ala Val Ala Ala Pro Ala Ser Ser Pro Ser Pro Val Ala Thr
                                        75
                    70
Val Ala Pro Pro Arg Val Ala Leu Arg Arg Gly Leu Pro Pro Thr Trp
                                    90
                                                        95
               85
His Ala Leu Arg Ala Leu Pro Arg Xaa Arg Gly Ala Ala Val Val Cys
                               105
                                                    110
           100
Gln Ala Xaa Gly Gly Gln Asp Thr Ala Ile Gln Val Pro Asp Val Ser
                           120
                                               125
Lys Ser Thr Trp Gln Ser Leu Val Val Glu Ser Glu Leu Pro Val Leu
                                            140
                        135
Val Gln Phe Trp Ala
145
(2) INFORMATION FOR SEQ ID NO:2882:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 426 base pairs
```

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..426
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602152
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2882: 60 aatccccacc cgcaacaaac caaacccaac cgcaactgca acacagagge atctctctcc geetecaege egeegeece agaeceteet sgatecageg gtssattege egggeteeeg 120 rrcccggcca tggatttgct ggcgtccttg gccgccgagg agcggtggct gttcccggcg 180 240 ttccctcgcc atgtacgccg ccatctactg cgccggccag ctcgtcgtgt tccggcggtg ggcgccgcgg cagaggctcg acggcgccag ctgcctcatc tcgctattcc acggcacccc 300 egecgegetg geegeegegg gggecateet egegetteee geggagteee geteettege 360 cgcgcccaac gcgcgcctcc aggaccacgt cctcgactac agcgtcgcct acttcaccat 420 ggacct
- (2) INFORMATION FOR SEQ ID NO:2883:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..142
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602153
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2883:
- Asn Pro His Pro Gln Gln Thr Lys Pro Asn Arg Asn Cys Asn Thr Glu

  1 10 15
- Ala Ser Leu Ser Ala Ser Thr Pro Pro Pro Pro Asp Pro Pro Xaa Ser 20 25 30
  Ser Gly Xaa Phe Ala Gly Leu Pro Xaa Pro Ala Met Asp Leu Leu Ala
- 35 40 45
  Ser Leu Ala Ala Glu Glu Arg Trp Leu Phe Pro Ala Phe Pro Arg His
- Ser Leu Ala Ala Glu Glu Arg Trp Leu Phe Pro Ala Phe Plo Alg His 50 55 60
- Val Arg Arg His Leu Leu Arg Arg Pro Ala Arg Arg Val Pro Ala Val 65 70 75 80
- Gly Ala Ala Ala Glu Ala Arg Arg Arg Gln Leu Pro His Leu Ala Ile

90 85 Pro Arg His Pro Arg Arg Ala Gly Arg Arg Gly Gly His Pro Arg Ala 100 105 Ser Arg Gly Val Pro Leu Leu Arg Arg Ala Gln Arg Ala Pro Pro Gly 115 120 125 Pro Arg Pro Arg Leu Gln Arg Arg Leu Leu His His Gly Pro 130 135 140 (2) INFORMATION FOR SEQ ID NO:2884: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..141 (D) OTHER INFORMATION: / Ceres Seq. ID 1602154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2884: Ile Pro Thr Arg Asn Lys Pro Asn Pro Thr Ala Thr Ala Thr Gln Arg 10 5 His Leu Ser Pro Pro Pro Arg Arg Pro Gln Thr Leu Xaa Asp Pro 25 Ala Xaa Xaa Ser Pro Gly Ser Xaa Xaa Arg Pro Trp Ile Cys Trp Arg 40 Pro Trp Pro Pro Arg Ser Gly Gly Cys Ser Arg Arg Ser Leu Ala Met 60 55 Tyr Ala Ala Ile Tyr Cys Ala Gly Gln Leu Val Val Phe Arg Arg Trp 75 70 Ala Pro Arg Gln Arg Leu Asp Gly Ala Ser Cys Leu Ile Ser Leu Phe 90 His Gly Thr Pro Ala Ala Leu Ala Ala Ala Gly Ala Ile Leu Ala Leu 100 105 110 Pro Ala Glu Ser Arg Ser Phe Ala Ala Pro Asn Ala Arg Leu Gln Asp 120 125 His Val Leu Asp Tyr Ser Val Ala Tyr Phe Thr Met Asp 135 (2) INFORMATION FOR SEQ ID NO:2885: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..141 (D) OTHER INFORMATION: / Ceres Seq. ID 1602155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2885: Ser Pro Pro Ala Thr Asn Gln Thr Gln Pro Gln Leu Gln His Arg Gly 10 Ile Ser Leu Arg Leu His Ala Ala Ala Pro Arg Pro Ser Xaa Ile Gln 25 Arg Xaa Ile Arg Arg Ala Pro Xaa Pro Gly His Gly Phe Ala Gly Val 40 Leu Gly Arg Arg Gly Ala Val Ala Val Pro Gly Val Pro Ser Pro Cys 60 55 Thr Pro Pro Ser Thr Ala Pro Ala Ser Ser Ser Cys Ser Gly Gly 70 75 Arg Arg Gly Arg Gly Ser Thr Ala Pro Ala Ala Ser Ser Arg Tyr Ser

Thr Ala Pro Pro Pro Arg Trp Pro Pro Arg Gly Pro Ser Ser Arg Phe
100 105 110

Pro Arg Ser Pro Ala Pro Ser Pro Arg Pro Thr Arg Ala Ser Arg Thr 115 120 125

Thr Ser Ser Thr Thr Ala Ser Pro Thr Ser Pro Trp Thr 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2886:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 469 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..469
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2886: 60 aaccacatcg catatcaaag accagaaagc tcaaaccaag accggcgtgc gcggacgaag cacagatcca tcggagtgac agcgagcgag cgagagcgag agcgagagag acagagagat 120 tatcogogog toaccgacto coggogaaga cgatggggaa ggggttogca toctacctgg 180 cgatgaagac ggggccggag ggcggcgacg cggcggcggc gcagcaggct ctgatcgacg 240 eggacetgeg ggagetegge gtegeegge ggaagetege caaccaegea ttegteeteg 300 geggeggget ggggttegge acctecttee teaaatgget ggeetteete geegeagtgt 360 atctcttgat attggatcgc acaaattgga agaccaacat gctgacagct ctcttggttc 420 cttacatttt cttcaccctg cctaatgtgc tgttttctct gatcagagg
- (2) INFORMATION FOR SEQ ID NO:2887:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 155 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..155
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602157
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2887:
- Pro His Arg Ile Ser Lys Thr Arg Lys Leu Lys Pro Arg Pro Ala Cys

  10
  15
  10
  15
- Ala Asp Glu Ala Gln Ile His Arg Ser Asp Ser Glu Arg Ala Arg Ala
  20 25 30
- Arg Ala Arg Glu Thr Glu Arg Leu Ser Ala Arg His Arg Leu Pro Ala 35
- Lys Thr Met Gly Lys Gly Phe Ala Ser Tyr Leu Ala Met Lys Thr Gly 50 55
- Pro Glu Gly Gly Asp Ala Ala Ala Ala Gln Gln Ala Leu Ile Asp Ala 65 70 75 80 Asp Leu Arg Glu Leu Gly Val Ala Ala Arg Lys Leu Ala Asn His Ala
- 85 90 95
  Phe Val Leu Gly Gly Leu Gly Phe Gly Thr Ser Phe Leu Lys Trp
- Leu Ala Phe Leu Ala Ala Val Tyr Leu Leu Ile Leu Asp Arg Thr Asn
- Trp Lys Thr Asn Met Leu Thr Ala Leu Leu Val Pro Tyr Ile Phe Phe 130 135 140
- Thr Leu Pro Asn Val Leu Phe Ser Leu Ile Arg
- (2) INFORMATION FOR SEQ ID NO:2888:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..105
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602158
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2888:

Met Gly Lys Gly Phe Ala Ser Tyr Leu Ala Met Lys Thr Gly Pro Glu 10 5

Gly Gly Asp Ala Ala Ala Gln Gln Ala Leu Ile Asp Ala Asp Leu 30 20 25

Arg Glu Leu Gly Val Ala Ala Arg Lys Leu Ala Asn His Ala Phe Val 40

Leu Gly Gly Gly Leu Gly Phe Gly Thr Ser Phe Leu Lys Trp Leu Ala 55

Phe Leu Ala Ala Val Tyr Leu Leu Ile Leu Asp Arg Thr Asn Trp Lys 75 70

Thr Asn Met Leu Thr Ala Leu Leu Val Pro Tyr Ile Phe Phe Thr Leu 90 85

Pro Asn Val Leu Phe Ser Leu Ile Arg 100

- (2) INFORMATION FOR SEQ ID NO:2889:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..95
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602159
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2889:

Met Lys Thr Gly Pro Glu Gly Gly Asp Ala Ala Ala Ala Gln Gln Ala 5 10 1

Leu Ile Asp Ala Asp Leu Arg Glu Leu Gly Val Ala Ala Arg Lys Leu 30 25 20

Ala Asn His Ala Phe Val Leu Gly Gly Gly Leu Gly Phe Gly Thr Ser 40

Phe Leu Lys Trp Leu Ala Phe Leu Ala Ala Val Tyr Leu Leu Ile Leu 55 60

Asp Arg Thr Asn Trp Lys Thr Asn Met Leu Thr Ala Leu Leu Val Pro 75 70

Tyr Ile Phe Phe Thr Leu Pro Asn Val Leu Phe Ser Leu Ile Arg 85

- (2) INFORMATION FOR SEQ ID NO:2890:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..441
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602160
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2890:

attettettt eteegteett teeateeeag gtegeeaceg egteteegee etteeeteet ceccaccate tteageacga ggeageacge geggaegtee etecegaeae ggagaaceee

- (2) INFORMATION FOR SEQ ID NO:2891:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..79
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602161
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2891:

Ile Leu Leu Ser Pro Ser Phe Pro Ser Gln Val Ala Thr Ala Ser Pro 1 5 10 15

Pro Phe Pro Pro Pro His His Leu Gln His Glu Ala Ala Arg Ala Asp 20 25 30

Val Pro Pro Asp Thr Glu Asn Pro Ala Pro Arg Ala Arg Ile His Arg 35 40 45

Ala Ala Thr Gln Val Pro Ala Gly Arg Ala Pro Ala Pro Pro Arg Arg 50 60

Arg Pro Cys His Ala Ala Ala Gly Arg Asp Gly Gly Pro His 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2892:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..146
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602162
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2892:

Phe Phe Leu Arg Pro Phe His Pro Arg Ser Pro Pro Arg Leu Arg
1 5 10 15

Pro Ser Leu Leu Pro Thr Ile Phe Ser Thr Arg Gln His Ala Arg Thr 20 25 30

Ser Leu Pro Thr Arg Arg Thr Pro Leu Arg Ala Leu Ala Phe Ile Ala

Pro Pro Pro Arg Ser Gln Pro Ala Ala Arg Pro Arg Pro Pro Ala Ala 50 55 60

Gly Arg Ala Met Pro Arg Arg Gly Glu Thr Ala Val Val Pro Ile Asp 65 70 75 80

Val Ala Ser Ala Gly Gly Gly Arg Gly Asp Glu Arg Pro Lys Arg Glu 85 90 95

Arg His Arg Ser His Gly Xaa Gly Arg His Gly Pro His Arg Ser Arg

Pro Pro Pro Xaa Pro Pro Pro Ala Phe Arg Pro Phe Arg Arg Trp Phe 115 120 125

Pro Phe Leu Val Pro Leu Phe Ile Val Ala Asn Ile Val Leu Phe Val 130 135 140

Leu Thr

145

(2) INFORMATION FOR SEQ ID NO:2893:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..146
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602163
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2893:

Ser Ser Phe Ser Val Leu Ser Ile Pro Gly Arg His Arg Val Ser Ala 1 5 10 15

Leu Pro Ser Ser Pro Pro Ser Ser Ala Arg Gly Ser Thr Arg Gly Arg 20 25 30

Pro Ser Arg His Gly Glu Pro Arg Ser Ala Arg Ser His Ser Ser Arg 35 40 45

Arg His Pro Gly Pro Ser Arg Pro Arg Ala Arg Ala Pro Pro Pro 50 55 60

Ala Val Pro Cys Arg Gly Gly Ala Arg Arg Arg Trp Ser Pro Leu Thr 65 70 75 80

Trp Arg Pro Pro Ala Ala Gly Glu Ala Met Ser Gly Pro Arg Glu Ser 85 90 95

Ala Thr Gly Ala Thr Xaa Pro Ala Ala Thr Val Arg Thr Gly Val Ala
100 105 110

Arg Arg Pro Xaa Pro Arg Arg Ser Gly Arg Ser Gly Gly Ser 115 120 125

Arg Ser Leu Cys Arg Tyr Ser Ser Ser Leu Thr Ser Ser Ser Ser Cys 130 135

Ser Pro

145

- (2) INFORMATION FOR SEQ ID NO:2894:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..505
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602172
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2894:

qaaaacatag tgcagcaagc aactgcaaag cagcaagctc tactcttctt ctgtactgaa cgtgtgacta gataarcaat aagcgtgaac catggcggac gagtacggcc gcagcggcta 120 eggeaggtee ggegeeggeg acgaetaega cageggetae aacagcaagt eeggeactga 180 240 tgactacggc cgtggcgaag gtggctacaa caagtcgggc ggcgatgacg actacggccg 300 caqcqqcqqc qatqqqtacq gcaqgtccqq cqqcqacqac tacqqccqtq gcaccqqcqq tgqtqqctac aacaaqtccg qcqqcqqcga cqactacggc cgcagcqgcg gcgatgggta 360 tggaaggtcc ggcggcgacg actacggccg tggcaccggc gscggcgggt acaacaagtc 420 cggcaacgac ggctacgaca gcgggtacaa cagatcgggc accaccaacg acgacgaata 480 cggccgtggc accggcggcg ggtac

- (2) INFORMATION FOR SEQ ID NO:2895:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1602173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2895:

Met Ala Asp Glu Tyr Gly Arg Ser Gly Tyr Gly Arg Ser Gly Ala Gly
1 5 10 15

Asp Asp Tyr Asp Ser Gly Tyr Asn Ser Lys Ser Gly Thr Asp Asp Tyr 20 25 30

Gly Arg Gly Glu Gly Gly Tyr Asn Lys Ser Gly Gly Asp Asp Asp Tyr 35 40 45

Gly Arg Ser Gly Gly Asp Gly Tyr Gly Arg Ser Gly Gly Asp Asp Tyr
50 55 60

Gly Arg Gly Thr Gly Gly Gly Gly Tyr Asn Lys Ser Gly Gly Gly Asp 65 70 75 80

Asp Tyr Gly Arg Ser Gly Gly Asp Gly Tyr Gly Arg Ser Gly Gly Asp 85 90 95

Asp Tyr Gly Arg Gly Thr Gly Xaa Gly Gly Tyr Asn Lys Ser Gly Asn 100 105 110

Asp Gly Tyr Asp Ser Gly Tyr Asn Arg Ser Gly Thr Thr Asn Asp Asp 115 120 125

Glu Tyr Gly Arg Gly Thr Gly Gly Gly Tyr 130 135

- (2) INFORMATION FOR SEQ ID NO:2896:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..108
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2896:

Thr Thr Thr Ala Ala Ala Ala Ala Met Gly Thr Ala Gly Pro Ala Ala Ala Thr Thr Thr Ala Val Ala Pro Ala Val Val Ala Thr Thr Ser Pro Ala

35 40 45
Ala Ala Thr Thr Ala Ala Ala Ala Ala Met Gly Met Glu Gly Pro

50 55 60 Ala Ala Thr Thr Ala Val Ala Pro Ala Xaa Ala Gly Thr Thr Ser

Ala Ala Thr Thr Ala Val Ala Pro Ala Ala Ala Gry III III Ser

65 70 75 80

Pro Ala Thr Thr Ala Thr Thr Ala Gly Thr Thr Asp Arg Ala Pro Pro 85 90 95

Thr Thr Thr Asn Thr Ala Val Ala Pro Ala Ala Gly 100 105

- (2) INFORMATION FOR SEQ ID NO:2897:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 93 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..93
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2897:
Met Thr Thr Ala Ala Ala Ala Ala Met Gly Thr Ala Gly Pro Ala
1 10 15

Ala Thr Thr Ala Val Ala Pro Ala Val Val Ala Thr Thr Ser Pro
20 25 30

Ala Ala Ala Thr Thr Thr Ala Ala Ala Ala Ala Met Gly Met Glu Gly 35 40 45

Pro Ala Ala Thr Thr Thr Ala Val Ala Pro Ala Xaa Ala Gly Thr Thr 50 55 60

Ser Pro Ala Thr Thr Ala Thr Thr Ala Gly Thr Thr Asp Arg Ala Pro 65 70 75 80

Pro Thr Thr Thr Asn Thr Ala Val Ala Pro Ala Ala Gly 85 90

- (2) INFORMATION FOR SEQ ID NO:2898:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 427 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..427
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2898: ateggtttet gaettattee ggggeatttt ttttttettg tttegageet gtgagtetga 60 ttccattttg acccatggcg geggeggegg eggeggttca tgageeggag gtgateegeg 120 acaaggegge gatgegege tggtegegee geegeegege ggagggaaag geegtegett 180 tagtccccac gatgggcttc ctccacgagg gacacctctc gctcatctcc gcggccgtgg 240 eggeeteege eggeeceate geegtegteg tetecateta egteaacece ageeagtteg 300 ccccaccga ggacctcgcc acctacccct ccgacttcgc cggcgacctc cgcaagctgg 360 ccgccaccgg ggtcgtcgcc gcagtatttt gtcccccaga cctctacgtc cgcggcagcg 420 ctgatcg
- (2) INFORMATION FOR SEQ ID NO:2899:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..117
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602184
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2899:

Met Ala Ala Ala Ala Ala Val His Glu Pro Glu Val Ile Arg Asp 1 5 10 15

Lys Ala Ala Met Arg Ala Trp Ser Arg Arg Arg Arg Ala Glu Gly Lys
20 25 30

Ala Val Ala Leu Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu 35 40 45

Ser Leu Ile Ser Ala Ala Val Ala Ala Ser Ala Gly Pro Ile Ala Val 50 55 60

Val Val Ser Ile Tyr Val Asn Pro Ser Gln Phe Ala Pro Thr Glu Asp
65 70 75 80

Leu Ala Thr Tyr Pro Ser Asp Phe Ala Gly Asp Leu Arg Lys Leu Ala 85 90 95

Ala Thr Gly Val Val Ala Ala Val Phe Cys Pro Pro Asp Leu Tyr Val 100 105 110

Arg Gly Ser Ala Asp

- (2) INFORMATION FOR SEQ ID NO:2900:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 98 amino acids

- (B) TYPE: amino acid (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..98
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602185
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2900:

Met Arg Ala Trp Ser Arg Arg Arg Ala Glu Gly Lys Ala Val Ala 10

Leu Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu Ser Leu Ile 30 25 2.0

Ser Ala Ala Val Ala Ala Ser Ala Gly Pro Ile Ala Val Val Ser 40

Ile Tyr Val Asn Pro Ser Gln Phe Ala Pro Thr Glu Asp Leu Ala Thr 55

Tyr Pro Ser Asp Phe Ala Gly Asp Leu Arg Lys Leu Ala Ala Thr Gly 75 70

Val Val Ala Ala Val Phe Cys Pro Pro Asp Leu Tyr Val Arg Gly Ser 90

Ala Asp

- (2) INFORMATION FOR SEQ ID NO:2901:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..78
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2901:

Met Gly Phe Leu His Glu Gly His Leu Ser Leu Ile Ser Ala Ala Val 10

Ala Ala Ser Ala Gly Pro Ile Ala Val Val Val Ser Ile Tyr Val Asn 30 25 20

Pro Ser Gln Phe Ala Pro Thr Glu Asp Leu Ala Thr Tyr Pro Ser Asp 45 4.0

Phe Ala Gly Asp Leu Arg Lys Leu Ala Ala Thr Gly Val Val Ala Ala 55

Val Phe Cys Pro Pro Asp Leu Tyr Val Arg Gly Ser Ala Asp 70

- (2) INFORMATION FOR SEQ ID NO:2902:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 480 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..480
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602187
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2902:

tecegteceg agagttetga ategaaaceg teggeeacga gageagtgeg aggegeecae cgcgatggct cgaaccaagc accaggccgt gaggaagacg gcggagaagc ccaagaagaa gctccagttc gagcgctcag gtggtgcgag tacctcggcg acgccggaaa gggctgctgg gaccggggga agagcggcgt ctggaggtga ctcagttaag aagacgaaac cacgccaccg

60 120

180

ctggcggccagggactgtagcgctgcgggagatcaggaagtaccagaagtccactgaacc300gctcatccctttgcgcctttcgtccgtgtggtgagggagttaaccaatttcgtaacaaa360cgggaaagtagagcgctataccgcagaagccctccttgcgctgcaagaggcagcagaatt420ccacttgatagaactgtttgaaatggcgaatctgtgtgccatccatgccaagcgtgtcac480

- (2) INFORMATION FOR SEQ ID NO:2903:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 159 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..159
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602188
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2903:
- Pro Val Pro Arg Val Leu Asn Arg Asn Arg Arg Pro Arg Glu Gln Cys
  1 5 10 15
- Glu Ala Pro Thr Ala Met Ala Arg Thr Lys His Gln Ala Val Arg Lys
  20 25 30
- Thr Ala Glu Lys Pro Lys Lys Leu Gln Phe Glu Arg Ser Gly Gly 35 40 45
- Ala Ser Thr Ser Ala Thr Pro Glu Arg Ala Ala Gly Thr Gly Gly Arg 50 55 60
- Ala Ala Ser Gly Gly Asp Ser Val Lys Lys Thr Lys Pro Arg His Arg 65 70 75 80
- Trp Arg Pro Gly Thr Val Ala Leu Arg Glu Ile Arg Lys Tyr Gln Lys 85 90 95
- Ser Thr Glu Pro Leu Ile Pro Phe Ala Pro Phe Val Arg Val Val Arg
  100 105 110
- Glu Leu Thr Asn Phe Val Thr Asn Gly Lys Val Glu Arg Tyr Thr Ala 115 120 125
- Glu Ala Leu Leu Ala Leu Gln Glu Ala Ala Glu Phe His Leu Ile Glu 130 135 140
- (2) INFORMATION FOR SEQ ID NO:2904:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..138
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602189
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2904:
- Met Ala Arg Thr Lys His Gln Ala Val Arg Lys Thr Ala Glu Lys Pro

  1 5 10 15
- Lys Lys Leu Gln Phe Glu Arg Ser Gly Gly Ala Ser Thr Ser Ala 20 25 30
- Thr Pro Glu Arg Ala Ala Gly Thr Gly Gly Arg Ala Ala Ser Gly Gly 35 40 45
- Asp Ser Val Lys Lys Thr Lys Pro Arg His Arg Trp Arg Pro Gly Thr 50 55 60
- Val Ala Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Pro Leu 65 70 75 80
- Ile Pro Phe Ala Pro Phe Val Arg Val Val Arg Glu Leu Thr Asn Phe
  85 90 95

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Val Thr Asn Gly Lys Val Glu Arg Tyr Thr Ala Glu Ala Leu Leu Ala
                                105
           100
Leu Gln Glu Ala Ala Glu Phe His Leu Ile Glu Leu Phe Glu Met Ala
                                               125
      115
                         120
Asn Leu Cys Ala Ile His Ala Lys Arg Val
    130
                       135
(2) INFORMATION FOR SEQ ID NO:2905:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 486 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..486
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602190
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2905:
                                                                       60
taatgagaaa atcacaaaag cagtggttac agtcccagca tatttcaatg attcacaaag
gacagcaact aaagatgctg gccgcattgc aggactggaa gttctccgta ttattaatga
                                                                      120
accaactgct gcatcgttgg cctatggttt cgagaagaaa aataatgaaa caattctagt
                                                                      180
gtttgatttg ggaggcggaa cctttgatgt atctgtattg gaagttggtg atggtgtt
                                                                      240
tgaggtgctt tccacatctg gtgacacaca ccttggtggt gatgacttcg ataagagaat
                                                                      300
agtagattgg cttgctagca acttcaagaa agatgaacgt attgatcttc tgaaggataa
                                                                      360
acaagccctt cagaggctta ctgaggcagc agagaaagct aagatggaac tgtcaacgct
                                                                       420
gacacaggca aatattagcc taccattcat tactgctact gctgatgggc caaaacacat
                                                                       480
cgaggc
(2) INFORMATION FOR SEQ ID NO:2906:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 161 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..161
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602191
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2906:
Asn Glu Lys Ile Thr Lys Ala Val Val Thr Val Pro Ala Tyr Phe Asn
                                    10
Asp Ser Gln Arg Thr Ala Thr Lys Asp Ala Gly Arg Ile Ala Gly Leu
                                25
Glu Val Leu Arg Ile Ile Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr
                                                 45
                            40
 Gly Phe Glu Lys Lys Asn Asn Glu Thr Ile Leu Val Phe Asp Leu Gly
                        55
                                             60
Gly Gly Thr Phe Asp Val Ser Val Leu Glu Val Gly Asp Gly Val Phe
                    70
                                        75
 Glu Val Leu Ser Thr Ser Gly Asp Thr His Leu Gly Gly Asp Asp Phe
```

105 110

125

155

140

Asp Lys Arg Ile Val Asp Trp Leu Ala Ser Asn Phe Lys Lys Asp Glu

Arg Ile Asp Leu Leu Lys Asp Lys Gln Ala Leu Gln Arg Leu Thr Glu

Ile Ser Leu Pro Phe Ile Thr Ala Thr Ala Asp Gly Pro Lys His Ile

120 Ala Ala Glu Lys Ala Lys Met Glu Leu Ser Thr Leu Thr Gln Ala Asn

135

150

85

145 Glu

120

180 240

300

360

- Attorney Docket No. 2750-1237P Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:2907: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..451 (D) OTHER INFORMATION: / Ceres Seq. ID 1602192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2907: gtgttgaagc cgtctaaact tccattttat cgagtgtgtc gtgtttcata atgccaataa tototocgca googactogo eccggtgggg ctgactgago tocggtccgc etcgaccego ggccgtacgc cccggagctc cacccgtcgc gccgcgtcgg agctcgtcgc cggcgatggc ttccqcqqtq qqcqcttcqa ccqccacqcq gttcctcccg cggctcccgg acccgtggcg geogegtegt gegegegeg egeteeegee geteaegtgg eggeeteeeg eggteaeggt ggccgcggcg tcgccccgac ctggggaagc ggaaggtagg cggcgggaga ggacgcggag gcggcgcgcc agggggccgg ggcaagagga aggcgtctcg ctaagctctg aaaaggagac gctaaattct actccacgtg ctcaaaccaa c (2) INFORMATION FOR SEQ ID NO:2908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..92 (D) OTHER INFORMATION: / Ceres Seq. ID 1602193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2908: Met Ala Ser Ala Val Gly Ala Ser Thr Ala Thr Arg Phe Leu Pro Arg 10 5

  - Leu Pro Asp Pro Trp Arg Pro Arg Arg Ala Arg Ala Ala Leu Pro Pro

20 25 Leu Thr Trp Arg Pro Pro Ala Val Thr Val Ala Ala Ala Ser Pro Arg

45 40 Pro Gly Glu Ala Glu Gly Arg Arg Arg Glu Arg Thr Arg Arg Arg

55 60 Ala Arg Gly Pro Gly Gln Glu Glu Gly Val Ser Leu Ser Ser Glu Lys

75

Glu Thr Leu Asn Ser Thr Pro Arg Ala Gln Thr Asn 85

- (2) INFORMATION FOR SEQ ID NO:2909:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..467
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602198
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2909:

· /	~					
ctccacttgc	agaggttcgc	gactcgcgac	gcctccgcag	ccccagcccc	agccccacgc	60
cccqcqatcc	aaaccctagc	cccctccacc	gtaccgccac	cgtcatggcc	gaaccatccg	120
	caccgcagct					180
					cggctggtgg	240
taccaatact	caaggtcgga	agcataatcg	aacaaaaaaa	cgagctcatc	aagcgccttg	300

tcgaggggac caaggccaga gtccgcatcc tcgagggccc cgtcggcgcc accgagcgta 360 tcgttttggt ttctggaaaa gaagatccag gcttggagct atctccagcc atggatgett 420 ctcatgagag tttttaagcg tgtcattggg ataacagatg gagctgc

(2) INFORMATION FOR SEQ ID NO:2910:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 88 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..88
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602199
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2910:

Leu His Leu Gln Arg Phe Ala Thr Arg Asp Ala Ser Ala Ala Pro Ala 1 10 15

Pro Ala Pro Arg Pro Ala Ile Gln Thr Leu Ala Pro Ser Thr Val Pro 20 25 30

Pro Pro Ser Trp Pro Asn His Pro Pro Pro Pro Ser Pro Gln Leu Arg 35 40 45

Ser Gly Arg Ser Pro Met Pro Pro Arg Trp Arg Arg Ser Arg Arg Pro 50 55 60

Arg Arg Gly Gly Arg Gly Gly Pro Gly Thr Ala Cys Ser Gly Trp Trp 65 70 75 80

Cys Gln Cys Ser Arg Ser Glu Ala 85

(2) INFORMATION FOR SEQ ID NO:2911:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..144
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602200
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2911:

Pro Leu Ala Glu Val Arg Asp Ser Arg Arg Leu Arg Ser Pro Ser Pro 1 5 10 15

Ser Pro Thr Pro Arg Asp Pro Asn Pro Ser Pro Leu His Arg Thr Ala
20 25 30

Thr Val Met Ala Glu Pro Ser Ala Ala Ala Val Thr Ala Ala Glu Val 35 40 45

Gly Glu Glu Ser Asp Ala Ala Ala Met Glu Glu Val Ala Ala Ala Ala 50 55 60

Lys Arg Trp Pro Gly Trp Pro Gly Asp Ser Val Phe Arg Leu Val Val 65 70 75 80
Pro Val Leu Lys Val Gly Ser Ile Ile Gly Arg Lys Gly Glu Leu Ile

85 . 90 95

Lys Arg Leu Val Glu Gly Thr Lys Ala Arg Val Arg Ile Leu Glu Gly

100 105 110

Pro Val Gly Ala Thr Glu Arg Ile Val Leu Val Ser Gly Lys Glu Asp

115 120 125
Pro Gly Leu Glu Leu Ser Pro Ala Met Asp Ala Ser His Glu Ser Phe
130 135 140

## (2) INFORMATION FOR SEQ ID NO:2912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..110 (D) OTHER INFORMATION: / Ceres Seq. ID 1602201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2912: Met Ala Glu Pro Ser Ala Ala Ala Val Thr Ala Ala Glu Val Gly Glu 10 5 Glu Ser Asp Ala Ala Ala Met Glu Glu Val Ala Ala Ala Lys Arg 25 2.0 Trp Pro Gly Trp Pro Gly Asp Ser Val Phe Arg Leu Val Val Pro Val 45 4.0 Leu Lys Val Gly Ser Ile Ile Gly Arg Lys Gly Glu Leu Ile Lys Arg 60 55 Leu Val Glu Gly Thr Lys Ala Arg Val Arg Ile Leu Glu Gly Pro Val 75 70 Gly Ala Thr Glu Arg Ile Val Leu Val Ser Gly Lys Glu Asp Pro Gly 90 85 Leu Glu Leu Ser Pro Ala Met Asp Ala Ser His Glu Ser Phe 105 (2) INFORMATION FOR SEQ ID NO:2913: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 391 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..391 (D) OTHER INFORMATION: / Ceres Seq. ID 1602209 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2913: gttcatcttt cctggcgcac agccagcccc cccacaggag cttctctgag gaagttgctg 60 cacttaaccg ctacttkggc ggcctgacaa tctggtggta atgcatatgt gattggagat 120 ccagcaagac ctggacagaa gtggcacgtc ttctacgcca ctgagtaccc agagcaacca 180 atgattaacc ttgagatgtg catgactggt ctggacaaga agaaagcttc tgtctttttc 240 aagactaatg ctgatgggaa cacaacatgt gccaaggaaa tgacaaagct ctctggcatc 300 tctgyaaatc atccccgaga tggagatctg cgatttcgac tttgaaccct gtggctaccc 360 atgaatgcga tccatggctc yttcattctc c (2) INFORMATION FOR SEQ ID NO:2914: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..54 (D) OTHER INFORMATION: / Ceres Seq. ID 1602210 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2914: Met Ile Asn Leu Glu Met Cys Met Thr Gly Leu Asp Lys Lys Ala 10 5 Ser Val Phe Phe Lys Thr Asn Ala Asp Gly Asn Thr Thr Cys Ala Lys

25

Glu Met Thr Lys Leu Ser Gly Ile Ser Xaa Asn His Pro Arg Asp Gly

Asp Leu Arg Phe Arg Leu 50

- (2) INFORMATION FOR SEQ ID NO:2915:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 49 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..49
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602211
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2915:

Met Cys Met Thr Gly Leu Asp Lys Lys Lys Ala Ser Val Phe Phe Lys 1 5 10 15

Thr Asn Ala Asp Gly Asn Thr Thr Cys Ala Lys Glu Met Thr Lys Leu 20 25 30

Ser Gly Ile Ser Xaa Asn His Pro Arg Asp Gly Asp Leu Arg Phe Arg 35 40

Leu

- (2) INFORMATION FOR SEQ ID NO:2916:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 47 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..47
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602212
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2916:

Met Thr Gly Leu Asp Lys Lys Ala Ser Val Phe Phe Lys Thr Asn 1 10 15

Ala Asp Gly Asn Thr Thr Cys Ala Lys Glu Met Thr Lys Leu Ser Gly 20 25 30

Ile Ser Xaa Asn His Pro Arg Asp Gly Asp Leu Arg Phe Arg Leu 35 40 45

- (2) INFORMATION FOR SEQ ID NO:2917:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 503 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..503
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602213
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2917:

(XI) Objection productivities and the second						
tgggcagctg	cgagcactgc	catctccatc	cacctgcgtt	ctgagcagta	catccattcc	60
attccqtccc	atcgatcggt	ccactggacg	atggcttccc	tcctcctgtt	cctgcgagcc	120
attotcatca	gtgccgatga	cgaggaactc	acgggcgcgg	acgagggacg	ggatgcggcg	180
gcgcgtgaac	ggcgaccgga	gaactgcgcg	ttcgggccgg	cggcggcgcg	cgacacggag	240
gaggaggagg	aggaggagga	gaacccaagc	aactggcctt	ctctgctgcc	ctcggtgtca	300
caattaggat	ctttccgata	tqtqqqacca	ctgttattct	tggtgctgtt	gttgtagcaa	360
tattaggaag	tcgttgcaat	gctgttactc	ttatggttct	aaatttggcc	gccactccaa	420
	cttgatcgtc					480
	tgacagccga					

- (2) INFORMATION FOR SEQ ID NO:2918:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..118
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602214
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2918:

Trp Ala Ala Ala Ser Thr Ala Ile Ser Ile His Leu Arg Ser Glu Gln  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Tyr Ile His Ser Ile Pro Ser His Arg Ser Val His Trp Thr Met Ala 20 25 30

Ser Leu Leu Phe Leu Arg Ala Ile Val Ile Ser Ala Asp Asp Glu 35 40 45

Glu Leu Thr Gly Ala Asp Glu Gly Arg Asp Ala Ala Ala Arg Glu Arg 50 55 60

Arg Pro Glu Asn Cys Ala Phe Gly Pro Ala Ala Ala Arg Asp Thr Glu 65 70 75 80

Glu Glu Glu Glu Glu Glu Asn Pro Ser Asn Trp Pro Ser Leu Leu 85 90 95

Pro Ser Val Ser Arg Leu Gly Ser Phe Arg Tyr Val Gly Pro Leu Leu 100 105 110

Phe Leu Val Leu Leu Leu 115

- (2) INFORMATION FOR SEQ ID NO:2919:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS:
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602215
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2919:

Gly Gln Leu Arg Ala Leu Pro Ser Pro Ser Thr Cys Val Leu Ser Ser 1 5 10 15

Thr Ser Ile Pro Phe Arg Pro Ile Asp Arg Ser Thr Gly Arg Trp Leu 20 25 30

Pro Ser Ser Cys Ser Cys Glu Pro Leu Ser Ser Val Pro Met Thr Arg 35 40 45

Asn Ser Arg Ala Arg Thr Arg Asp Gly Met Arg Arg Arg Val Asn Gly 50 55 60

Asp Arg Arg Thr Ala Arg Ser Gly Arg Arg Arg Arg Ala Thr Arg Arg 65 70 75 80

Arg Arg Arg Arg Arg Thr Gln Ala Thr Gly Leu Leu Cys Cys 85 90 95

Pro Arg Cys His Asp Trp Asp Leu Ser Asp Met Trp Asp His Cys Tyr
100 105 110

Ser Trp Cys Cys Cys Cys Ser Asn Val Gly Lys Ser Leu Gln Cys Cys 115 120 125

Tyr Ser Tyr Gly Ser Lys Phe Gly Arg His Ser Asn 130 135 140

- (2) INFORMATION FOR SEQ ID NO:2920:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 95 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..95
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2920:

Met Thr Arg Asn Ser Arg Ala Arg Thr Arg Asp Gly Met Arg Arg Arg 1 5 10 15

Val Asn Gly Asp Arg Arg Thr Ala Arg Ser Gly Arg Arg Arg Ala 20 25 30

Thr Arg Arg Arg Arg Arg Arg Arg Thr Gln Ala Thr Gly Leu 35 40 45

Leu Cys Cys Pro Arg Cys His Asp Trp Asp Leu Ser Asp Met Trp Asp 50 60

His Cys Tyr Ser Trp Cys Cys Cys Cys Ser Asn Val Gly Lys Ser Leu 70 75 80

Gln Cys Cys Tyr Ser Tyr Gly Ser Lys Phe Gly Arg His Ser Asn 85 90 95

- (2) INFORMATION FOR SEQ ID NO:2921:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 427 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..427
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602221
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2921:

aaacacgctc tcettetta aggacetggg cgccaacgtg ggcgtcattt cgggcctcat 60 caacgaggtc acgccgcgt gggtggtget cgccatgggc gccgccatga acctggcggg 120 ctacctcatg atctacctcg ccatcgacgg gcgcaccggc aggcccccg tctggctcat 180 gtgcatctac atctgcgtgg gcgccaactc ccagtccttc gccaacaccg gcgcgctcgt cacctgcgtc aagaacttcc cggagagccg cggcgtcgtg ctcggcctcc tcaagggctt cgtcggcctc aggcgccca tcttcacgca gctctacctc gccaatctacg gcgacgacgc 360 caagtcgctc gtgctgctca tcgcctgct ccccgcccc gtctcatcc tcttcgtcca 420 caccqtc

- (2) INFORMATION FOR SEQ ID NO:2922:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..142
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602222
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2922:

Lys His Ala Leu Leu Gln Gly Pro Gly Arg Gln Arg Gly Arg His

Phe Gly Pro His Gln Arg Gly His Ala Ala Val Gly Gly Ala Arg His 20 25 30

Gly Arg Arg His Glu Pro Gly Gly Leu Pro His Asp Leu Pro Arg His 35 40 45

Arg Arg Ala His Arg Gln Ala Pro Arg Leu Ala His Val His Leu His 50 55 60

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Client Docket No. 80146.003
Leu Arg Gly Arg Gln Leu Pro Val Leu Arg Gln His Arg Arg Ala Arg
                                    75
                  70
His Leu Arg Gln Glu Leu Pro Gly Glu Pro Arg Arg Arg Ala Arg Pro
                                90
             8.5
Pro Gln Gly Leu Arg Arg Pro Gln Arg Arg His Leu His Ala Ala Leu
                           105
          100
Pro Arg His Leu Arg Arg Arg Gln Val Ala Arg Ala His Arg
       115 120
                                          125
Leu Ala Pro Arg Arg Leu His Pro Leu Arg Pro His Arg
           135
   130
(2) INFORMATION FOR SEQ ID NO:2923:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 142 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
```

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..142
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602223
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2923:

Asn Thr Leu Ser Phe Phe Lys Asp Leu Gly Ala Asn Val Gly Val Ile 5 10

Ser Gly Leu Ile Asn Glu Val Thr Pro Pro Trp Val Val Leu Ala Met 25 20

Gly Ala Ala Met Asn Leu Ala Gly Tyr Leu Met Ile Tyr Leu Ala Ile 40 45

Asp Gly Arg Thr Gly Arg Pro Pro Val Trp Leu Met Cys Ile Tyr Ile 55 60

Cys Val Gly Ala Asn Ser Gln Ser Phe Ala Asn Thr Gly Ala Leu Val 75 70

Thr Cys Val Lys Asn Phe Pro Glu Ser Arg Gly Val Val Leu Gly Leu 90 85

Leu Lys Gly Phe Val Gly Leu Ser Gly Ala Ile Phe Thr Gln Leu Tyr 105 110 100

Leu Ala Ile Tyr Gly Asp Asp Ala Lys Ser Leu Val Leu Leu Ile Ala 115 120 125

Trp Leu Pro Ala Ala Val Ser Ile Leu Phe Val His Thr Val 135 140

- (2) INFORMATION FOR SEQ ID NO:2924:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 111 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..111
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602224
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2924:

Met Gly Ala Ala Met Asn Leu Ala Gly Tyr Leu Met Ile Tyr Leu Ala 10 5

Ile Asp Gly Arg Thr Gly Arg Pro Pro Val Trp Leu Met Cys Ile Tyr 30 25

Ile Cys Val Gly Ala Asn Ser Gln Ser Phe Ala Asn Thr Gly Ala Leu 40

Val Thr Cys Val Lys Asn Phe Pro Glu Ser Arg Gly Val Val Leu Gly 60 55 Leu Leu Lys Gly Phe Val Gly Leu Ser Gly Ala Ile Phe Thr Gln Leu Client Docket No. 80146.003 70 Tyr Leu Ala Ile Tyr Gly Asp Asp Ala Lys Ser Leu Val Leu Leu Ile 90 Ala Trp Leu Pro Ala Ala Val Ser Ile Leu Phe Val His Thr Val 105 100 (2) INFORMATION FOR SEQ ID NO:2925: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 550 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..550
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602229
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2925: actgttccac tccagtcggt cgaggagtag ggttctagcg cctatctggt ttctccctgc gccgccgccg ccgccgtgga caaccggagc gtagtgggag gggatgatgg agggaggtag 120 ccgcgcggat gggcggaatc cgaaccagct ccggccgttc acctgcaccg ggaacccgct 180 240 ccaccgcgcc cacggctccg cgcggtgggc gcagggcgac accgtcgtgc tggccgctgt 300 gtacgggccc aagtcgggaa cccggaaggg cgagaacccc gagaaggcct ccatcgaggt 360 cgtgtggaag cccaagaccg gccagatcgg aaggcaagag agggaatatg agatgacact caagaggacg ttgcagagca tctgcttgct cacagttcat cctaacacca ccacctctgt 420 cgtgcttcag gttgtgggtg atgatggttc tcttatgtca tgtgcaatta atgcttcttg 480 tgctgctctt gmatttgctg gaatccctat ggaaacatct cgctggtcgc gattagctgt 540 ggagtgatgg
- (2) INFORMATION FOR SEQ ID NO:2926:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..147
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602230
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2926: Met Met Glu Gly Gly Ser Arg Ala Asp Gly Arg Asn Pro Asn Gln Leu 10 5

Arg Pro Phe Thr Cys Thr Gly Asn Pro Leu His Arg Ala His Gly Ser 20 25

Ala Arg Trp Ala Gln Gly Asp Thr Val Val Leu Ala Ala Val Tyr Gly 40

Pro Lys Ser Gly Thr Arg Lys Gly Glu Asn Pro Glu Lys Ala Ser Ile 60 55

Glu Val Val Trp Lys Pro Lys Thr Gly Gln Ile Gly Arg Gln Glu Arg 75 70 Glu Tyr Glu Met Thr Leu Lys Arg Thr Leu Gln Ser Ile Cys Leu Leu

90 85

Thr Val His Pro Asn Thr Thr Thr Ser Val Val Leu Gln Val Val Gly 110 105 100

Asp Asp Gly Ser Leu Met Ser Cys Ala Ile Asn Ala Ser Cys Ala Ala 125 120 Leu Xaa Phe Ala Gly Ile Pro Met Glu Thr Ser Arg Trp Ser Arg Leu

135

140

130 Ala Val Glu

- (2) INFORMATION FOR SEQ ID NO:2927:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..146 (D) OTHER INFORMATION: / Ceres Seq. ID 1602231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2927: Met Glu Gly Gly Ser Arg Ala Asp Gly Arg Asn Pro Asn Gln Leu Arg 10 Pro Phe Thr Cys Thr Gly Asn Pro Leu His Arg Ala His Gly Ser Ala 30 25 20 Arg Trp Ala Gln Gly Asp Thr Val Val Leu Ala Ala Val Tyr Gly Pro 40 Lys Ser Gly Thr Arg Lys Gly Glu Asn Pro Glu Lys Ala Ser Ile Glu 55 Val Val Trp Lys Pro Lys Thr Gly Gln Ile Gly Arg Gln Glu Arg Glu 75 70 Tyr Glu Met Thr Leu Lys Arg Thr Leu Gln Ser Ile Cys Leu Leu Thr 90 85 Val His Pro Asn Thr Thr Ser Val Val Leu Gln Val Val Gly Asp 105 100 1.10 Asp Gly Ser Leu Met Ser Cys Ala Ile Asn Ala Ser Cys Ala Ala Leu 115 120 125 Xaa Phe Ala Gly Ile Pro Met Glu Thr Ser Arg Trp Ser Arg Leu Ala 140 135 Val Glu (2) INFORMATION FOR SEQ ID NO:2928: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..75 (D) OTHER INFORMATION: / Ceres Seq. ID 1602232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2928: Met Gly Gly Ile Arg Thr Ser Ser Gly Arg Ser Pro Ala Pro Gly Thr 10 1 5 Arg Ser Thr Ala Pro Thr Ala Pro Arg Gly Gly Arg Arg Ala Thr Pro 25 Ser Cys Trp Pro Leu Cys Thr Gly Pro Ser Arg Glu Pro Gly Arg Ala 40 Arg Thr Pro Arg Arg Pro Pro Ser Arg Ser Cys Gly Ser Pro Arg Pro 55 Ala Arg Ser Glu Gly Lys Arg Gly Asn Met Arg 70 (2) INFORMATION FOR SEQ ID NO:2929: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ix) FEATURE:
    - (A) NAME/KEY: -

(ii) MOLECULE TYPE: DNA (genomic)

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1602233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2929:

acatcctaat cgaaaaaccc atcgccacca ccaatcaatc catcacgtta gctgcacctg 60
cgcctctcct tgaggtcgcg cagccagcaa tggcgtgctc caaagcggtg ctgctcgccg 120
cgctcctagc cgtcgcagga gcgctctcct ccgctgcggt gtgggaggac tacgaccacc 180
acatgtacca caggtgctac aggtcctgca tgaggaagtg cgacgacgac gatgccgatg atgcattgaa gaatagcatc agccccgttg ccacctccgt gtcggatgat catgaccacg 300
accatgacga ccaccacgat gatcacgacc acgaccacga ccacaaccat gacgaccacc 360
acaatgatca tgaccac

- (2) INFORMATION FOR SEQ ID NO:2930:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..125
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2930:

Ile Leu Ile Glu Lys Pro Ile Ala Thr Thr Asn Gln Ser Ile Thr Leu
1 5 10 15

Ala Ala Pro Ala Pro Leu Leu Glu Val Ala Gln Pro Ala Met Ala Cys 20 25 30

Ser Lys Ala Val Leu Leu Ala Ala Leu Leu Ala Val Ala Gly Ala Leu 35 40 45

Ser Ser Ala Ala Val Trp Glu Asp Tyr Asp His His Met Tyr His Arg

Cys Tyr Arg Ser Cys Met Arg Lys Cys Asp Asp Asp Asp Ala Asp Asp 65 70 75 80

Ala Leu Lys Asn Ser Ile Ser Pro Val Ala Thr Ser Val Ser Asp Asp 85

His Asp His Asp His Asp Asp His Asp Asp His As

Asp His Asn His Asp Asp His His Asn Asp His Asp His 115 120 125

- (2) INFORMATION FOR SEQ ID NO:2931:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602235
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2931:

Met Ala Cys Ser Lys Ala Val Leu Leu Ala Ala Leu Leu Ala Val Ala 1 5 10 15

Gly Ala Leu Ser Ser Ala Ala Val Trp Glu Asp Tyr Asp His His Met 20 25 30

Tyr His Arg Cys Tyr Arg Ser Cys Met Arg Lys Cys Asp Asp Asp Asp 40

Ala Asp Asp Ala Leu Lys Asn Ser Ile Ser Pro Val Ala Thr Ser Val

Ser Asp Asp His Asp His Asp His Asp Asp His Asp Asp His Asp Asp 65 70 75 80

His Asp His Asp His Asn His Asp Asp His His Asn Asp His Asp His

Ti

41,5

453

M

H

90

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(2) INFORMATION FOR SEQ ID NO:2932:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 65 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..65
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602236
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2932:
Met Tyr His Arg Cys Tyr Arg Ser Cys Met Arg Lys Cys Asp Asp Asp
                                    10
Asp Ala Asp Asp Ala Leu Lys Asn Ser Ile Ser Pro Val Ala Thr Ser
                               25
           20
Val Ser Asp Asp His Asp His Asp His Asp Asp His His Asp Asp His
                            40
Asp His Asp His Asp His Asn His Asp Asp His His Asn Asp His Asp
                        55
His
65
(2) INFORMATION FOR SEQ ID NO:2933:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 475 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..475
          (D) OTHER INFORMATION: / Ceres Seq. ID 1602239
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2933:
aaatgtttga caaacacaaa gaatctaggc ggcggcatct ggctatccat actccaataa
ttattcctgt ttggtctcag gttcggatgg ttgaggatga tttaatgtat agcacttttc
                                                                       120
ttgaggtgta tgaaattaat tgtgcacggc ataatagaga agctgactcg cctattacaa
                                                                       180
ttttcaaaga gcagcttaat caagccgttt cagggcagct ctctcctgaa gcaattgtgg
                                                                       240
agctacgtct gcaagcatac aatgagatta caaaaaatat tgttaatgat aatattttct
                                                                       300
cccaatatat gcacaagatt ctgccaactg gcaactacct gtggaccttc aagaaacaat
                                                                       360
ttgcaatcca agtggctctc tcctgcttca tgtcgtatat gctgcagatt ggcggcaggg
ctcctaacaa aattctattt gctaaaaata ctgggaagat cttccagact gactt
(2) INFORMATION FOR SEQ ID NO:2934:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 157 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (ix) FEATURE:
           (A) NAME/KEY: peptide
           (B) LOCATION: 1..157
           (D) OTHER INFORMATION: / Ceres Seq. ID 1602240
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2934:
Met Phe Asp Lys His Lys Glu Ser Arg Arg Arg His Leu Ala Ile His
                                     10
Thr Pro Ile Ile Ile Pro Val Trp Ser Gln Val Arg Met Val Glu Asp
                                 25
             20
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Client Docket No. 80146.003
Asp Leu Met Tyr Ser Thr Phe Leu Glu Val Tyr Glu Ile Asn Cys Ala
                        4.0
Arg His Asn Arg Glu Ala Asp Ser Pro Ile Thr Ile Phe Lys Glu Gln
                   55
Leu Asn Gln Ala Val Ser Gly Gln Leu Ser Pro Glu Ala Ile Val Glu
                                  75
                 70
Leu Arg Leu Gln Ala Tyr Asn Glu Ile Thr Lys Asn Ile Val Asn Asp
                              90
Asn Ile Phe Ser Gln Tyr Met His Lys Ile Leu Pro Thr Gly Asn Tyr
                                             110
         100
                           105
Leu Trp Thr Phe Lys Lys Gln Phe Ala Ile Gln Val Ala Leu Ser Cys
    115 120
                                125
Phe Met Ser Tyr Met Leu Gln Ile Gly Gly Arg Ala Pro Asn Lys Ile
  130 135
                                     140
Leu Phe Ala Lys Asn Thr Gly Lys Ile Phe Gln Thr Asp
       150
(2) INFORMATION FOR SEQ ID NO:2935:
    (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..129
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602242
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2935:

Met Val Glu Asp Asp Leu Met Tyr Ser Thr Phe Leu Glu Val Tyr Glu 10 5

Ile Asn Cys Ala Arg His Asn Arg Glu Ala Asp Ser Pro Ile Thr Ile 25

Phe Lys Glu Gln Leu Asn Gln Ala Val Ser Gly Gln Leu Ser Pro Glu 4.5 40

Ala Ile Val Glu Leu Arg Leu Gln Ala Tyr Asn Glu Ile Thr Lys Asn 55 60

Ile Val Asn Asp Asn Ile Phe Ser Gln Tyr Met His Lys Ile Leu Pro 70 75

Thr Gly Asn Tyr Leu Trp Thr Phe Lys Lys Gln Phe Ala Ile Gln Val 90

Ala Leu Ser Cys Phe Met Ser Tyr Met Leu Gln Ile Gly Gly Arg Ala 110 100 105

Pro Asn Lys Ile Leu Phe Ala Lys Asn Thr Gly Lys Ile Phe Gln Thr 120 115

Asp

- (2) INFORMATION FOR SEQ ID NO:2936:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 406 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..406
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602253
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2936:

acggcccaac cccatccact cctttcctcc cacccgccag ccgtcacccg cgcgtgcagc cagetteeet getaceeegg egegeegeea geegagegga egeeggeeet geeeegeaeg ceggeaegeg geaegegeag ceagetgeee cacaegaege eggeegeeet egeaeteeee

60

accgcgctac ccggcagccc cgcgctaccc ggtcctcgct cggcgtcctt gattcccacc 240 gcacggcggc ccttcttctg ccaccgcaca ccgcgcagga gcactgccct tcgccccttg 300 tttagctgca gcaggagcgc cgcccagccg gccaccacca ccgcagcttg agagttgaga 360 cctgcagttg acgaccagag gccagagggc gttgctngcg ctgctt

(2) INFORMATION FOR SEQ ID NO:2937:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 116 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..116
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602254
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2937:

Thr Ala Gln Pro His Pro Leu Leu Ser Ser His Pro Pro Ala Val Thr

Arg Ala Cys Ser Gln Leu Pro Cys Tyr Pro Arg Ala Pro Pro Ala Glu 20 25 30

Arg Thr Pro Ala Leu Pro Arg Thr Pro Ala Arg Gly Thr Arg Ser Gln
35 40 45

Leu Pro His Thr Thr Pro Ala Ala Leu Ala Leu Pro Thr Ala Leu Pro

Gly Ser Pro Ala Leu Pro Gly Pro Arg Ser Ala Ser Leu Ile Pro Thr
70 75 80

Ala Arg Arg Pro Phe Phe Cys His Arg Thr Pro Arg Arg Ser Thr Ala 85 90 95

Leu Arg Pro Leu Phe Ser Cys Ser Arg Ser Ala Ala Gln Pro Ala Thr

Thr Thr Ala Ala

115

- (2) INFORMATION FOR SEQ ID NO:2938:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 76 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..76
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602255
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2938:

Arg Pro Asn Pro Ile His Ser Phe Pro Pro Thr Arg Gln Pro Ser Pro 1 5 10 15

Ala Arg Ala Ala Ser Phe Pro Ala Thr Pro Ala Arg Arg Gln Pro Ser

Gly Arg Arg Pro Cys Pro Ala Arg Arg His Ala Ala Arg Ala Ala Ser 35 40 45

Cys Pro Thr Arg Arg Arg Pro Pro Ser His Ser Pro Pro Arg Tyr Pro 50 55 60

Ala Ala Pro Arg Tyr Pro Val Leu Ala Arg Arg Pro 65 70 75

- (2) INFORMATION FOR SEQ ID NO:2939:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 100 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..100
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602256
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2939:
- Gly Pro Thr Pro Ser Thr Pro Phe Leu Pro Pro Ala Ser Arg His Pro 1 10 15
- Arg Val Gln Pro Ala Ser Leu Leu Pro Pro Arg Ala Ala Ser Arg Ala 20 25 30
- Asp Ala Gly Pro Ala Pro His Ala Gly Thr Arg His Ala Gln Pro Ala 35 40 45
- Ala Pro His Asp Ala Gly Arg Pro Arg Thr Pro His Arg Ala Thr Arg 50 55 60
- Gln Pro Arg Ala Thr Arg Ser Ser Leu Gly Val Leu Asp Ser His Arg 65 70 75 80
- Thr Ala Ala Leu Leu Pro Pro His Thr Ala Gln Glu His Cys Pro 85 90 95

Ser Pro Leu Val

- (2) INFORMATION FOR SEQ ID NO:2940:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 357 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..357
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2940:
- aaaaaactgc atcgaacacc aatggcattc ttgcattgaa ggaaccttcc ctccacctcc 60 accgcccgag agcgagggc cggacgggt tttggttggg catggctgcc ccggcgatgc 120 tccaagtggt gatcctcgcc gcggtcctcc ttctcccgtt cctcaagcgtg ccgggcgcg aggcacagac caagaagttc tgcctcacgc agttcgccat cgctagccag gcctgcgcca tcctgccacc caccagtcct gagcaccacc accatcatca cgatgacgag gacaatgacg aggacaacga tgaagatgaa gacgagg
- (2) INFORMATION FOR SEQ ID NO:2941:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..118
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602265
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2941:
- Lys Thr Ala Ser Asn Thr Asn Gly Ile Leu Ala Leu Lys Glu Pro Ser 1 10 15
- Leu His Leu His Arg Pro Arg Ala Ser Gly Arg Thr Gly Phe Trp Leu 20 25 30
- Gly Met Ala Ala Pro Ala Met Leu Gln Val Val Ile Leu Ala Ala Val 35 40 45
- Leu Leu Pro Phe Leu Ser Val Pro Gly Ala Glu Ala Gln Thr Lys 50 55
- Lys Phe Cys Leu Thr Gln Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile 65 70 75 80
- Leu Pro Pro Thr Ser Pro Glu His His His His His His Asp Asp Glu 85 90 95

Asp Asn Asp Glu Asp Asn Asp Glu Asp Glu Asp Glu Asp Glu Asp Asn 100 105 110

Asp Glu Asp Glu Asp Glu 115

- (2) INFORMATION FOR SEQ ID NO:2942:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..85
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602266
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2942:

Met Ala Ala Pro Ala Met Leu Gln Val Val Ile Leu Ala Ala Val Leu 1 5 10 15

Leu Leu Pro Phe Leu Ser Val Pro Gly Ala Glu Ala Gln Thr Lys Lys 20 25 30

Phe Cys Leu Thr Gln Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile Leu 35 40 45

Pro Pro Thr Ser Pro Glu His His His His His Asp Asp Glu Asp 50 55 60

Asn Asp Glu Asp Asn Asp Glu Asp Glu Asp Glu Asp Glu Asp Asn Asp 65 70 75 80

Glu Asp Glu Asp Glu

85

- (2) INFORMATION FOR SEQ ID NO:2943:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..80
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602267
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2943:

Met Leu Gln Val Val Ile Leu Ala Ala Val Leu Leu Pro Phe Leu 1 5 10 15

Ser Val Pro Gly Ala Glu Ala Gln Thr Lys Lys Phe Cys Leu Thr Gln 20 25 30

Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile Leu Pro Pro Thr Ser Pro

Glu His His His His His Asp Asp Glu Asp Asn Asp Glu Asp Asn 50 55 60

Asp Glu 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:2944:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -

- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2944: acacacteet tegeetegeg eeggeegteg tegeeteett ceaeegaaeg ateceteete 60 ctcctcctcc tcctcctcct cgcatcccac csgsrcccca cettctcctt aaagctacct 120 180 qmcatacccg gcggttgccg ccgccgcaat cgatcgaccg gaagagaaag agcagctagc tagctagcag atcggagcac ggcaacaagg cgatggggcg cggcaaggta cagctgaagc 240 ggatagagaa caagataaac cggcaggtga ccttctccaa gcgccggaac ggcctgctca 300 agaaggegea egagatetee gteetetgeg atgeegaggt egeegteate gtettetyee 360 ccaagggcaa gctctacgag tacgccaccg actcccgcat ggacaaaatt cttgaacgct 420 atgagcgata ttcctatgct gaaaaggctc ttatttcagc tgaatc
- (2) INFORMATION FOR SEQ ID NO:2945:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 60 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..60
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602285
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2945:

Thr His Ser Phe Ala Ser Arg Arg Pro Ser Ser Pro Pro Ser Thr Glu
1 5 10 15

Arg Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Ala Ser His Xaa Xaa 20 25 30

Pro Thr Phe Ser Leu Lys Leu Pro Xaa Ile Pro Gly Gly Cys Arg Arg 35 40 45

Arg Asn Arg Ser Thr Gly Arg Glu Arg Ala Ala Ser 50 55 60

- (2) INFORMATION FOR SEQ ID NO:2946:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 58 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..58
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602286
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2946:

Thr Leu Leu Arg Leu Ala Pro Ala Val Val Ala Ser Leu His Arg Thr
1 5 10 15

Ile Pro Pro Pro Pro Pro Pro Pro Pro Pro Arg Ile Pro Xaa Xaa Pro 20 25 30

His Leu Leu Leu Lys Ala Thr Xaa His Thr Arg Arg Leu Pro Pro Pro 35 40 45

Gln Ser Ile Asp Arg Lys Arg Lys Ser Ser 50 55

- (2) INFORMATION FOR SEQ ID NO:2947:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 84 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1602287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2947:

Met Gly Arg Gly Lys Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala 20 25 30

His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Val Ile Val Phe 35 40 45

Xaa Pro Lys Gly Lys Leu Tyr Glu Tyr Ala Thr Asp Ser Arg Met Asp 50 55 60

Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Lys Ala Leu 65 70 75 80

Ile Ser Ala Glu

- (2) INFORMATION FOR SEQ ID NO:2948:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..445
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602302
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2948:

- (2) INFORMATION FOR SEQ ID NO:2949:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 129 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..129
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602303
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2949:

Ser Gln Pro Ile Thr Phe Ala Ser Pro Phe Thr Leu Gln Ser Leu Ala
1 5 10 15

Arg Ser Arg Asn Arg Ala Arg Gln Leu Thr Asp Glu Glu Glu Ala Ser 20 25 30

Gln Ala Ala Ser Glu Ala Arg Glu Arg Arg Gly Arg Gly Asp Asp Gly 35 40 45

Ser Arg Asp Gly Asp Asn Asp Gly Pro Gly Val Arg Gly Asp Gly Ala 50 55 60

Pro Pro Gly Pro Ala Arg Arg Gln Arg Arg Gly Arg Gly Ala 65 70 75 80

Gly Ala Gly Arg Arg Gly Glu Glu Leu Val Leu Arg Leu Arg Gln Glu 85 90 95

Gly Leu Arg Arg Asp His Arg Pro Glu Ala Glu Ala Gly Ala Ser Gly 100 105 110

Arg Arg Gly Gly Gly Gly Gly Gly Pro Arg Arg Cys Cys

115 120 125

Pro

- (2) INFORMATION FOR SEQ ID NO:2950:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602304
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2950:

Met Ala Thr Thr Thr Asp Leu Gly Phe Glu Ala Thr Glu Leu Arg Leu
1 10 15

Gly Leu Pro Gly Gly Ser Gly Gly Gly Gly Gly Glu Leu Ala Leu 20 25 30

Gly Gly Glu Gly Arg Ser Ser Ser Ser Ala Ser Gly Lys Arg Gly Phe 35 40

Ala Glu Thr Ile Asp Leu Lys Leu Lys Leu Glu Pro Ala Ala Val Val 50 55 60

Glu Ala Glu Glu Glu Glu Glu Asp His Gly Val Ala Val Ala Leu Glu 65 70 75 80

Lys Glu Glu Glu Ala Gly Lys Met Lys Arg Ser Pro Ser Gln Ser Ser 85 90 95

Val

- (2) INFORMATION FOR SEQ ID NO:2951:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..472
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602305
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2951:

ggggtteteg accaatcact ccagtateca gtetetetet eggeteteet eteceegatt 60 teetteeea eeggetgtea gteteactee eeggeggeg getetetett teetegeett 120 eggeggegge gaegagettg agetegaget ggtteetegt atagaagaeg aeggeegggg 180 tatggagee atgaaegtag acaaeggegg eageggtgge ettgaeggeg agategaaea 240 getgatgeag tegeeggee tegeeggea agaggttaag geaetgtegg agaaggeeaa 300 ggagatattg atbgaggaaa geaaegttea geetgteaag agteeagtga eaatatgtgg 360 tgatataeat acttattat gggagattat gtagategtg getaetatte tg

- (2) INFORMATION FOR SEQ ID NO:2952:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 150 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..150
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602306
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2952:

```
Gly Phe Ser Thr Asn His Ser Ser Ile Gln Ser Leu Ser Arg Leu Ser
                               10
Ser Pro Arg Phe Pro Ser Pro Pro Ala Val Ser Leu Thr Pro Arg Ala
                                              30
                           25
      20
Arg Ala Leu Ser Phe Leu Ala Phe Ala Ala Gly Asp Glu Leu Glu Leu
                        40
Glu Leu Val Pro Arg Ile Glu Asp Asp Gly Arg Gly Met Glu Pro Met
                    55
Asn Val Asp Asn Gly Gly Ser Gly Gly Leu Asp Ala Gln Ile Glu Gln
                 70
                                  75
Leu Met Gln Cys Arg Pro Leu Ala Glu Gln Glu Val Lys Ala Leu Cys
                               90
             85
Glu Lys Ala Lys Glu Ile Leu Xaa Glu Glu Ser Asn Val Gln Pro Val
       100 105
Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe His Asp
    115 120 125
Leu Val Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro Asp Thr Ile Thr
  130 135
Tyr Leu Trp Glu Ile Met
     150
(2) INFORMATION FOR SEQ ID NO:2953:
   (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..90
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602307
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2953:

Met Glu Pro Met Asn Val Asp Asn Gly Gly Ser Gly Gly Leu Asp Ala
1 5 10 15

Gln Ile Glu Gln Leu Met Gln Cys Arg Pro Leu Ala Glu Gln Glu Val $20 \hspace{1cm} 25 \hspace{1cm} 30 \hspace{1cm}$ 

Lys Ala Leu Cys Glu Lys Ala Lys Glu Ile Leu Xaa Glu Glu Ser Asn 35 40 45

Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly
50 55 60

Gln Phe His Asp Leu Val Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro
65 70 75 80

Asp Thr Ile Thr Tyr Leu Trp Glu Ile Met 85 90

- (2) INFORMATION FOR SEQ ID NO:2954:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 87 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..87
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602308
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2954:

Met Asn Val Asp Asn Gly Gly Ser Gly Gly Leu Asp Ala Gln Ile Glu

1 10 15

Gln Leu Met Gln Cys Arg Pro Leu Ala Glu Gln Glu Val Lys Ala Leu 20 25 30

Cys Glu Lys Ala Lys Glu Ile Leu Xaa Glu Glu Ser Asn Val Gln Pro

60

300

360

420

40 35 Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe His 55 Asp Leu Val Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro Asp Thr Ile 75 70 Thr Tyr Leu Trp Glu Ile Met 85 (2) INFORMATION FOR SEQ ID NO:2955: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..454 (D) OTHER INFORMATION: / Ceres Seq. ID 1602309 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2955: ctataaataa ataccgccca ccaacatctg gtggtatcaa agaatctcct ctgtatctct ggcagccgca tcgtctcaat ctcagtcact cccggacacg cgcacgagcc accccgcacc 120 caactaacca acccatggac gcgggcggaa cgccgccgct gctgttcctc ctggccgcgg 180 cggccgccct gctgggcgcg gcgctcaggt ggctgctcct ggcctggcgg tcggcgga 240 ggacggggcg gctgccaccg ggcagcacgg ggctgccgct catcggggag acgctgcgcc tcatcgcggc gtacaagacg ccgaacccgg agccgttcat cgacgagcgc gtggcgcggc acggcagcgg ggtgttcacg acgcacgtgt tcggcgagcg caccgtgttc tccgcggacc eggeetteaa eegeetgete etggeegeeg aggg (2) INFORMATION FOR SEQ ID NO:2956: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..150 (D) OTHER INFORMATION: / Ceres Seq. ID 1602310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2956: Ile Asn Lys Tyr Arg Pro Pro Thr Ser Gly Gly Ile Lys Glu Ser Pro 10 Leu Tyr Leu Trp Gln Pro His Arg Leu Asn Leu Ser His Ser Arg Thr 30 20 25 Arg Ala Arg Ala Thr Pro His Pro Thr Asn Gln Pro Met Asp Ala Gly 40 Gly Thr Pro Pro Leu Leu Phe Leu Leu Ala Ala Ala Ala Leu Leu 60 55 Gly Ala Ala Leu Arg Trp Leu Leu Leu Ala Trp Arg Ser Ala Ala Arg 75 70 Thr Gly Arg Leu Pro Pro Gly Ser Thr Gly Leu Pro Leu Ile Gly Glu 90 8.5 Thr Leu Arg Leu Ile Ala Ala Tyr Lys Thr Pro Asn Pro Glu Pro Phe 105 110 100 Ile Asp Glu Arg Val Ala Arg His Gly Ser Gly Val Phe Thr His 125 120 Val Phe Gly Glu Arg Thr Val Phe Ser Ala Asp Pro Ala Phe Asn Arg 140 135 130 Leu Leu Leu Ala Ala Glu

150

(2) INFORMATION FOR SEQ ID NO:2957: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..106
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602311
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2957:

Met Asp Ala Gly Gly Thr Pro Pro Leu Leu Phe Leu Leu Ala Ala Ala 1 5 10 15

Ala Ala Leu Leu Gly Ala Ala Leu Arg Trp Leu Leu Leu Ala Trp Arg  $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$ 

Ser Ala Ala Arg Thr Gly Arg Leu Pro Pro Gly Ser Thr Gly Leu Pro 35 40 45

Leu Ile Gly Glu Thr Leu Arg Leu Ile Ala Ala Tyr Lys Thr Pro Asn 50 55 60

Pro Glu Pro Phe Ile Asp Glu Arg Val Ala Arg His Gly Ser Gly Val 65 70 75 80

Phe Thr Thr His Val Phe Gly Glu Arg Thr Val Phe Ser Ala Asp Pro 85 90 95

Ala Phe Asn Arg Leu Leu Leu Ala Ala Glu 100 105

- (2) INFORMATION FOR SEQ ID NO:2958:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 489 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: DNA (genomic)
    - (ix) FEATURE:
      - (A) NAME/KEY: -
      - (B) LOCATION: 1..489
      - (D) OTHER INFORMATION: / Ceres Seq. ID 1602320
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2958:

60 attttcattt accacacct getetegete ttgttgtgac ggtegatteg ettgtacaag tgaccaccet teegeteeet teteacetat agetageaac ettgagatee ageeaagate 120 cagccatgag ggagattete cacatecagg gtggacagtg eggcaaceag ateggtteca 180 agttctggga ggtcgtctgc gacgagcatg gtatcgaccc caccggacgc tatgtcgqca 240 cctccgacct ccagctcgag cgcgtcaatg tctactacaa cgaggcctca tgcggccgct 300 tegtgeegeg egeegtgete atggaeeteg ageeeggeae catggaeage gteegeaeeg 360 ggccgtacgg ccagatette cgccccgaca acttcgtett cggccagtet ggcgcggggn 420 aacaactggg ccaagggcca ctacacagag ggcgctgagc tcatcgactc tgtgcttgac 480 gtcgtgagg

- (2) INFORMATION FOR SEQ ID NO:2959:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 161 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..161
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602321
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2959:

Phe Ser Phe Thr Thr Pro Cys Ser Arg Ser Cys Cys Asp Gly Arg Phe 1 5 10 15

Ala Cys Thr Ser Asp His Pro Ser Ala Pro Phe Ser Pro Ile Ala Ser 20 25 30

Ser

Asn Leu Glu Ile Gln Pro Arg Ser Ser His Glu Gly Asp Ser Pro His 40 Pro Gly Trp Thr Val Arg Gln Pro Asp Arg Phe Gln Val Leu Gly Gly 60 55 Arg Leu Arg Arg Ala Trp Tyr Arg Pro His Arg Thr Leu Cys Arg His 70 Leu Arg Pro Pro Ala Arg Ala Arg Gln Cys Leu Leu Gln Arg Gly Leu 90 Met Arg Pro Leu Arg Ala Ala Arg Arg Ala His Gly Pro Arg Ala Arg 110 100 105 His His Gly Gln Arg Pro His Arg Ala Val Arg Pro Asp Leu Pro Pro 115 120 125 Arg Gln Leu Arg Leu Arg Pro Val Trp Arg Gly Xaa Thr Thr Gly Pro 130 135 140 Arg Ala Thr Thr Gln Arg Ala Leu Ser Ser Ser Thr Leu Cys Leu Thr 155 145 150

- (2) INFORMATION FOR SEQ ID NO:2960:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 110 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..110
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602322
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2960:

Met Arg Glu Ile Leu His Ile Gln Gly Gln Cys Gly Asn Gln Ile 1 5 10 15

Gly Ser Lys Phe Trp Glu Val Val Cys Asp Glu His Gly Ile Asp Pro 20 25 30

Thr Gly Arg Tyr Val Gly Thr Ser Asp Leu Gln Leu Glu Arg Val Asn 35 40 45

Val Tyr Tyr Asn Glu Ala Ser Cys Gly Arg Phe Val Pro Arg Ala Val 50 55 60

Leu Met Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Thr Gly Pro 65 70 75 80

Tyr Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly 85 90 95

Ala Gly Xaa Gln Leu Gly Gln Gly Pro Leu His Arg Gly Arg
100 105 110

- (2) INFORMATION FOR SEQ ID NO:2961:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..94
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602323
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2961:

Met Val Ser Thr Pro Pro Asp Ala Met Ser Ala Pro Pro Thr Ser Ser 1 10 15

Ser Ser Ala Ser Met Ser Thr Thr Thr Arg Pro His Ala Ala Ala Ser 20 25 30

Cys Arg Ala Pro Cys Ser Trp Thr Ser Ser Pro Ala Pro Trp Thr Ala

40Ser Ala Pro Gly Arg Thr Ala Arg Ser Ser Ala Pro Thr Thr Ser Ser 60 55 Ser Ala Ser Leu Ala Arg Xaa Asn Asn Trp Ala Lys Gly His Tyr Thr 75 70 Glu Gly Ala Glu Leu Ile Asp Ser Val Leu Asp Val Val Arg 85 90 (2) INFORMATION FOR SEQ ID NO:2962: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..486 (D) OTHER INFORMATION: / Ceres Seq. ID 1602324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2962: aagaatagcg aacaaacatc gagtacagtc ggctaggtaa tctggtggta cgacgactga 120 cgacgacatg gcggccacca gcagcaagtc gtcgtcgtcc tcgagctcgg cgcagcgggc agcagctgcc gccctgctcg tggcggtgtc cgtcctggtg gtgggcgcgg cggcggtgtg 180 cgacatgage aactagcagt teatgtegtg ecageeegeg geggeeaaga egaeggaeee 240 300 gccggccgcg ccgtcgcagg cgtgctgcga cgcgctggcg ggggcggacc tcaagtgcct gtgcggctac aagaactcgc cgtggatggg cgtctacaac atcgacccca agcgcgccat 360 ggagetteeg gecaagtgeg geetegeeac geegeeegae tgetageagt gtgetageea 420 agccaagcca agcaggaagg cccccgggca ttgctagctg tacgtgtctg tgtgtgcatc 480 tgcagc (2) INFORMATION FOR SEQ ID NO:2963: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..42 (D) OTHER INFORMATION: / Ceres Seq. ID 1602325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2963: Met Ala Ala Thr Ser Ser Lys Ser Ser Ser Ser Ser Ser Ser Ala Gln 5 10 1 Arg Ala Ala Ala Ala Leu Leu Val Ala Val Ser Val Leu Val Val 25 Gly Ala Ala Ala Val Cys Asp Met Ser Asn 35 (2) INFORMATION FOR SEQ ID NO:2964: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..67 (D) OTHER INFORMATION: / Ceres Seq. ID 1602326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2964: Met Ser Cys Gln Pro Ala Ala Ala Lys Thr Thr Asp Pro Pro Ala Ala 5 10

Pro Ser Gln Ala Cys Cys Asp Ala Leu Ala Gly Ala Asp Leu Lys Cys

60

120

180

240

300

360

Attorney Docket No. 2750-1237P Client Docket No. 80146.003 2.0 25 Leu Cys Gly Tyr Lys Asn Ser Pro Trp Met Gly Val Tyr Asn Ile Asp 40 45 Pro Lys Arg Ala Met Glu Leu Pro Ala Lys Cys Gly Leu Ala Thr Pro 50 Pro Asp Cys 65 (2) INFORMATION FOR SEQ ID NO:2965: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 478 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..478 (D) OTHER INFORMATION: / Ceres Seq. ID 1602330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2965: caaqcttaaa ccacaacqca aacaaccacc aaaqcaatcq aaaaqcaacc ctgcaagtgc aggcaaagag agggcgcgac caaacagatc caatccaatg gcgatggcac cgtccgcagc atgcqtcqtc tcgttccccg cccgcccggc ggcgtccacg gccgggcccc gcgccgccgc gggcgccggg gcggtccacg ctttcgcggg gtcggcggag ggcgccaagt ggtgggcgcc gctgctgggg tggtcgggga aggccgacta cctggaggcc ccggccccgg cgccggcggg ggcgcaggac gaggcgccgc ggaggcagtt cgtgggggtg atgacggagg agaaggcccg ggagctgcgg gcgcggatgg cgcagacgga gtccttccac gacgccatgt accactccgc

- (2) INFORMATION FOR SEQ ID NO:2966:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 149 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..149
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602331
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2966:
- Lys Leu Lys Pro Gln Arg Lys Gln Pro Pro Lys Gln Ser Lys Ser Asn 1 5 10 15

categorated edectedeac detecteda gggttggtge gegegeggee agetegee

- Pro Ala Ser Ala Gly Lys Glu Arg Ala Arg Pro Asn Arg Ser Asn Pro 20 25 30
- Met Ala Met Ala Pro Ser Ala Ala Cys Val Val Ser Phe Pro Ala Arg 35 40 45
- Pro Ala Ala Ser Thr Ala Gly Pro Arg Ala Ala Ala Gly Ala Gly Ala 50 55 60
- Val His Ala Phe Ala Gly Ser Ala Glu Gly Ala Lys Trp Trp Ala Pro 65 70 75 80
  Leu Leu Gly Trp Ser Gly Lys Ala Asp Tyr Leu Glu Ala Pro Ala Pro
- 85 90 95
  Ala Pro Ala Gly Ala Gln Asp Glu Ala Pro Arg Arg Gln Phe Val Gly
- 100 105 110 Val Met Thr Glu Glu Lys Ala Arg Glu Leu Arg Ala Arg Met Ala Gln
- 115 120 125
  Thr Glu Ser Phe His Asp Ala Met Tyr His Ser Ala Ile Ala Ser Arg
- Leu Ala Arg Ser Ser
- 145
- (2) INFORMATION FOR SEQ ID NO:2967:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..117
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602332
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2967:

Met Ala Met Ala Pro Ser Ala Ala Cys Val Val Ser Phe Pro Ala Arg 1 5 10 15

Pro Ala Ala Ser Thr Ala Gly Pro Arg Ala Ala Ala Gly Ala Gly Ala 20 25 30

Val His Ala Phe Ala Gly Ser Ala Glu Gly Ala Lys Trp Trp Ala Pro 35 40 45

Leu Leu Gly Trp Ser Gly Lys Ala Asp Tyr Leu Glu Ala Pro Ala Pro 50 55 60

Ala Pro Ala Gly Ala Gln Asp Glu Ala Pro Arg Arg Gln Phe Val Gly 65 70 75 80

Val Met Thr Glu Glu Lys Ala Arg Glu Leu Arg Ala Arg Met Ala Gln 85 90 95

Thr Glu Ser Phe His Asp Ala Met Tyr His Ser Ala Ile Ala Ser Arg  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 105$ 

Leu Ala Arg Ser Ser

115

- (2) INFORMATION FOR SEQ ID NO:2968:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 119 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..119
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602333
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2968:

Met Arg Arg Leu Val Pro Arg Pro Pro Gly Gly Val His Gly Arg Ala 1 5 10 15

Pro Arg Arg Gly Arg Arg Gly Gly Pro Arg Phe Arg Gly Val Gly 20 25 30

Gly Gly Arg Gln Val Val Gly Ala Ala Gly Val Val Gly Glu Gly 35 40 45

Arg Leu Pro Gly Gly Pro Gly Pro Gly Ala Gly Gly Ala Gly Arg 50 55 60

Gly Ala Ala Glu Ala Val Arg Gly Gly Asp Asp Gly Gly Glu Gly Pro 65 70 75 80 Gly Ala Ala Gly Ala Asp Gly Ala Asp Gly Val Leu Pro Arg Arg His

Val Pro Leu Arg His Arg Val Ala Pro Arg Thr Leu Leu Gly Leu
100 105 110

Val Arg Ala Arg Pro Ala Arg

- (2) INFORMATION FOR SEQ ID NO:2969:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 404 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)

360

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..404
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602334
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2969:

  agaaccgaaa ccaagcaacc caatccaaac cagacaagca aggaatccc cgatggctca 60

  tcgcgttctc ctcctctct ctctcgcgtc ggccgccgcg gttgcgccgc gtcgacgcgg 120

  aggacccgct gatccggcag gtggttcccg gtggagatga caacgatctg gagctgaacg 180

  cggagtccca cttcctgagc ttcgtgcagc ggttcggcaa gtcctacaag gacgccgacg 240

  agcacgcgta ccggctgtcc gttttcaagg ccaacctgcg ccgcgcgcc cggcaccagc 300
- tgctggaccc gtcggcggag cacggcgtca ctaagttctc cgacctcacg ccggcagagt tccgccggac ctacctcggc ctccgcaagt cccggcgcgc tctc
- (2) INFORMATION FOR SEQ ID NO:2970:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 134 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..134
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602335
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2970:
- Asn Arg Asn Gln Ala Thr Gln Ser Lys Pro Asp Lys Gln Gly Ile Pro 1 5 10 15
- Arg Trp Leu Ile Ala Phe Ser Ser Ser Ser Leu Ser Arg Arg Pro Pro 20 25 30
- Arg Leu Arg Arg Val Asp Ala Glu Asp Pro Leu Ile Arg Gln Val Val 35 40 45
- Pro Gly Gly Asp Asp Asn Asp Leu Glu Leu Asn Ala Glu Ser His Phe 50 55 60
- Leu Ser Phe Val Gln Arg Phe Gly Lys Ser Tyr Lys Asp Ala Asp Glu 65 70 75 80
- His Ala Tyr Arg Leu Ser Val Phe Lys Ala Asn Leu Arg Arg Ala Arg 85 90 95
- Arg His Gln Leu Leu Asp Pro Ser Ala Glu His Gly Val Thr Lys Phe 100 105 110
- Ser Asp Leu Thr Pro Ala Glu Phe Arg Arg Thr Tyr Leu Gly Leu Arg 115 120 125

Lys Ser Arg Arg Ala Leu

- (2) INFORMATION FOR SEQ ID NO:2971:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 483 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..483
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602346
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2971:

actcctgccc t	tcgtccaac	tcctccgttc	cccgttccct	cctctaccac	tggccccggc	60
accgcgggag c	geegaeege	ctgctcgtct	cgccgcagcc	cgtccctgag	ccggaaccct	120
ageggeegee a	ttgcccacg	cgccgcgcgc	ccgatggacg	gcgggggctc	cgggccggcg	180
cccaacgccg c	gcacaccgc	ggaagaggtc	ttccgcgact	acaaagcccg	ccgcgccggc	240
atgatcaagg c	actcaccac	cgatgtggag	aggttcttca	agctctgtga	ccccgaaaag	300
gagaacttgt g	cctctatgg	ctatcccgat	gagacatggg	aggttacctt	gccagctgag	360
gaagtgcccc c	agagatccc	tgaaccagca	ttaggaatca	actttgctag	ggatggcatg	420

aatgagaagg actggctggc gctagttgca gtccacagtg attccctggt tactatctgt 480

- (2) INFORMATION FOR SEQ ID NO:2972:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 161 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..161
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602347
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2972:

Thr Pro Ala Leu Arg Pro Thr Pro Pro Phe Pro Val Pro Ser Ser Thr 1 5 10 15

Thr Gly Pro Gly Thr Ala Gly Ala Pro Thr Ala Cys Ser Ser Arg Arg 20 25 30

Ser Pro Ser Leu Ser Arg Asn Pro Ser Gly Arg His Cys Pro Arg Ala 35 40 45

Ala Arg Pro Met Asp Gly Gly Gly Ser Gly Pro Ala Pro Asn Ala Ala 50 60

His Thr Ala Glu Glu Val Phe Arg Asp Tyr Lys Ala Arg Arg Ala Gly 65 70 75 80

Met Ile Lys Ala Leu Thr Thr Asp Val Glu Arg Phe Phe Lys Leu Cys 85 90 95

Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly Tyr Pro Asp Glu Thr 100 105 110

Trp Glu Val Thr Leu Pro Ala Glu Glu Val Pro Pro Glu Ile Pro Glu 115 120 125

Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp 130 135 140

Trp Leu Ala Leu Val Ala Val His Ser Asp Ser Leu Val Thr Ile Cys 145 150 155 160 Arg

(2) INFORMATION FOR SEQ ID NO:2973:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..110
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2973:

Met Asp Gly Gly Ser Gly Pro Ala Pro Asn Ala Ala His Thr Ala

1 5 10 15

Glu Glu Val Phe Arg Asp Tyr Lys Ala Arg Arg Ala Gly Met Ile Lys 20 25 30

Ala Leu Thr Thr Asp Val Glu Arg Phe Phe Lys Leu Cys Asp Pro Glu 35 40 45

Lys Glu Asn Leu Cys Leu Tyr Gly Tyr Pro Asp Glu Thr Trp Glu Val

Thr Leu Pro Ala Glu Glu Val Pro Pro Glu Ile Pro Glu Pro Ala Leu 65 70 75 80

Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp Trp Leu Ala 85 90 95

Leu Val Ala Val His Ser Asp Ser Leu Val Thr Ile Cys Arg

110 105 100 (2) INFORMATION FOR SEQ ID NO:2974: (i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 81 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..81 (D) OTHER INFORMATION: / Ceres Seq. ID 1602349 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2974: Met Ile Lys Ala Leu Thr Thr Asp Val Glu Arg Phe Phe Lys Leu Cys 10 5 Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly Tyr Pro Asp Glu Thr 25 20 Trp Glu Val Thr Leu Pro Ala Glu Glu Val Pro Pro Glu Ile Pro Glu 40 4.5 Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp 60 55 Trp Leu Ala Leu Val Ala Val His Ser Asp Ser Leu Val Thr Ile Cys 75 70 Arg (2) INFORMATION FOR SEQ ID NO:2975: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..484 (D) OTHER INFORMATION: / Ceres Seq. ID 1602360 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2975: acctegaaac ectagegeeg gegeeteeac ttegttttee teactetete etecagetea 60 gggtccggcg gcgaagggaa ggcaagatgt acaccgcgag gaagaagatc cagaaggaga 120 agggtcttga gccctccgag ttcgaggact ccgttgccca ggctttcttt gatctggaga 180 acgggaacca ggagctcaag agcgacctca aggacctgta catcaacaat gctatccaga 240 tggatgttac cgggagtagg aaggetgttg teatteacgt eccatacege etgegeaagg 300 ccttcaggaa gatccatgtc agactcgtca gggagctgga gaagaaattc agcggcaagg 360 atgtggtaat tgttgctaca cggaggattg tgaggccacc caagaagggt tcagctgttc 420 tgcgccctcg caccaggact ctgactgctg ttcacgatgg catcttggag gatgttgtct 480 accc (2) INFORMATION FOR SEQ ID NO:2976: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..160 (D) OTHER INFORMATION: / Ceres Seq. ID 1602361 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2976: Leu Glu Thr Leu Ala Pro Ala Pro Pro Leu Arg Phe Pro His Ser Leu

10

Leu Gln Leu Arq Val Arg Arg Arg Glu Gly Lys Met Tyr Thr Ala

Arg Lys Lys Ile Gln Lys Glu Lys Gly Leu Glu Pro Ser Glu Phe Glu 40 Asp Ser Val Ala Gln Ala Phe Phe Asp Leu Glu Asn Gly Asn Gln Glu 55 Leu Lys Ser Asp Leu Lys Asp Leu Tyr Ile Asn Asn Ala Ile Gln Met 75 70 Asp Val Thr Gly Ser Arg Lys Ala Val Val Ile His Val Pro Tyr Arg 90 8.5 Leu Arg Lys Ala Phe Arg Lys Ile His Val Arg Leu Val Arg Glu Leu 100 105 110 Glu Lys Lys Phe Ser Gly Lys Asp Val Val Ile Val Ala Thr Arg Arg 115 120 Ile Val Arg Pro Pro Lys Lys Gly Ser Ala Val Leu Arg Pro Arg Thr 130 135 140 Arg Thr Leu Thr Ala Val His Asp Gly Ile Leu Glu Asp Val Val Tyr 150 155

## (2) INFORMATION FOR SEQ ID NO:2977:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..132
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602362
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2977:

Met Tyr Thr Ala Arg Lys Lys Ile Gln Lys Glu Lys Gly Leu Glu Pro 1 10 15

Ser Glu Phe Glu Asp Ser Val Ala Gln Ala Phe Phe Asp Leu Glu Asn 20 25 30

Gly Asn Gln Glu Leu Lys Ser Asp Leu Lys Asp Leu Tyr Ile Asn Asn 35 40 45

Ala Ile Gln Met Asp Val Thr Gly Ser Arg Lys Ala Val Val Ile His 50 55 60

Val Pro Tyr Arg Leu Arg Lys Ala Phe Arg Lys Ile His Val Arg Leu 65 70 75 80

Val Arg Glu Leu Glu Lys Lys Phe Ser Gly Lys Asp Val Val Ile Val 85 90 95

Ala Thr Arg Arg Ile Val Arg Pro Pro Lys Lys Gly Ser Ala Val Leu 100 105 110

Arg Pro Arg Thr Arg Thr Leu Thr Ala Val His Asp Gly Ile Leu Glu
115 120 125

Asp Val Val Tyr

- (2) INFORMATION FOR SEQ ID NO:2978:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..81
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602363
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2978:

 Met
 Asp
 Val
 Thr
 Gly
 Ser
 Arg
 Lys
 Ala
 Val
 Val
 Ile
 His
 Val
 Pro
 Tyr

 Arg
 Leu
 Arg
 Lys
 Ala
 Phe
 Arg
 Lys
 Ile
 His
 Val
 Arg
 Leu
 Val
 Arg
 Glu

 Leu
 Glu
 Lys
 Ala
 Phe
 Ser
 Gly
 Lys
 Asp
 Val
 Ile
 Val
 Ala
 Thr
 Arg

 Arg
 Ile
 Val
 Arg
 Pro
 Pro
 Lys
 Lys
 Gly
 Ser
 Ala
 Val
 Leu
 Arg
 Pro
 Arg

 Thr
 Arg
 Thr
 Leu
 Thr
 Ala
 Val
 His
 Asp
 Gly
 Ser
 Ala
 Val
 Leu
 Arg
 Pro
 Arg

 Thr
 Arg
 Thr
 Ala
 Val
 His
 Asp
 Gly
 Ser
 Ala
 Val
 Leu
 Arg
 Pro
 Arg

 Thr
 Arg
 Thr
 Ala
 Val
 H

- (2) INFORMATION FOR SEQ ID NO:2979:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..498
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602364
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2979: 60 ategagecag tgcaaaceta geegacetet teteetegeg eegeegeege tgeegeegte gtcatgtcga agcgcgggag gggagggacg gcggggaaca agttccgcat gtcgctgggt 120 ctccccgtcg cagcgaccgt gaactgtgcg gacaacacag gcgccaagaa cctctacatc 180 atotocgtca agggcatcaa gggtaggctc aaccgcctgc cgtccgcctg cgtcggcgac 240 atggtcatgg ccaccgtcaa gaagggtaag cccgacctca ggaagaaggt catgcccgcc 300 gtcatcgtcc gccagcgcaa gctgtggcgc cgcaaggacg gagtctacat gtacttcgaa 360 gataatgctg gagtcattgt gaaccccaag ggcgagatga aaggatctgc tatcactgga 420 cctattggca aggagtgcgc tgacctttgg cctaggattg ctagtgcagc aaatgctatt gtctgatact actggttg
- (2) INFORMATION FOR SEQ ID NO:2980:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602365
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2980:
- Met Ser Lys Arg Gly Arg Gly Gly Thr Ala Gly Asn Lys Phe Arg Met 1 5 10 15
- Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr 20 25 30
- Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg 35 40 45
- Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr 50 55 60 Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val
- 65 70 75 80 Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr Met
- 85 90 95

  Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met
  100 105 110
- Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu 115 120 125

Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val 130 135 140

- (2) INFORMATION FOR SEQ ID NO: 2981:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..125
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602366
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2981:

Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn 1 5 10 15

Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly 20 25 30

Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala 35 40 45

Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala

50 55 60 Val Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr

65 70 75 80 Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu

85 90 95 Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp

Leu Trp Pro Arg lie Ala Ser Ala Ala Ash Ala lie va. 115 120

- (2) INFORMATION FOR SEQ ID NO:2982:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..81
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602367
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2982:

Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys

1 10 15

Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys
20 25 30

Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn 35 40 45

Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys 50 55 60

Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile 65 70 75 80 Val

- (2) INFORMATION FOR SEQ ID NO:2983:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 535 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..535
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602370
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2983: aattcgaacg acggagcacg acgcacgcag agccgcagag atccgtcaca ctgcaagttt 60 tgaaaactga actgtaagat ggcatcagca gagctttccc gtgaggaaaa tgtgtacatg 120 gcgaagctcg ccgagcaggc agagaggtac gaggaaatgg ttgagttcat ggagaaggta 180 gcgaaaactg ttgactcgga ggagctcact gtggaggagc gcaacctcct gtctgttgca 240 tacaagaacg tcattggagc ccgccgtgcc tcatggcgca tcatctcctc catcgagcag 300 aaggaggagg gtcgaggcaa tgaggaccgt gtaacactca tcaaggacta ccgtggcaag 360 attgaaactg agctcaccaa gatctgtgat ggcatcctca agcttctcga atctcacctt 420 480 qtqccqtctt ccaccqctcc cgagtccaag gtcttctatc tcaagatgaa gggtgactac tacagatacc tttgctgagt tcaagactgg agctgagaga aaggacgctg ctgag
- (2) INFORMATION FOR SEQ ID NO:2984:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 139 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..139
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602371
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2984:
- Met Ala Ser Ala Glu Leu Ser Arg Glu Glu As<br/>n Val Tyr Met Ala Lys 1 5 10 15
- Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Glu Phe Met Glu 20 25 30
- Lys Val Ala Lys Thr Val Asp Ser Glu Glu Leu Thr Val Glu Glu Arg 35 40 45
- Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala 50 55 60
- Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln Lys Glu Glu Gly Arg Gly 65 70 75 80
- Asn Glu Asp Arg Val Thr Leu Ile Lys Asp Tyr Arg Gly Lys Ile Glu 85 90 95
- Thr Glu Leu Thr Lys Ile Cys Asp Gly Ile Leu Lys Leu Leu Glu Ser
- His Leu Val Pro Ser Ser Thr Ala Pro Glu Ser Lys Val Phe Tyr Leu 115 120 125
- Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Cys 130
- (2) INFORMATION FOR SEQ ID NO:2985:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..126
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602372
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2985:
- Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Glu
  1 10 15
- Phe Met Glu Lys Val Ala Lys Thr Val Asp Ser Glu Glu Leu Thr Val 20 25 30
- Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala

35 40 Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln Lys Glu Glu 55 60 Gly Arg Gly Asn Glu Asp Arg Val Thr Leu Ile Lys Asp Tyr Arg Gly 75 70 Lys Ile Glu Thr Glu Leu Thr Lys Ile Cys Asp Gly Ile Leu Lys Leu 90 85 Leu Glu Ser His Leu Val Pro Ser Ser Thr Ala Pro Glu Ser Lys Val 100 105 Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Cys 115 120 (2) INFORMATION FOR SEQ ID NO:2986: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 amino acids (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..113
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602373
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2986:

Met Val Glu Phe Met Glu Lys Val Ala Lys Thr Val Asp Ser Glu Glu 1  $\phantom{0}$  5  $\phantom{0}$  10  $\phantom{0}$  15 Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val

Leu Thr Val Glu Glu Arg Ash heu heu sel Val Ard Tyr Lys Ash Val
20 25 30

Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln 35 40 45

Lys Glu Glu Gly Arg Gly Asn Glu Asp Arg Val Thr Leu Ile Lys Asp 50 55 60

Tyr Arg Gly Lys Ile Glu Thr Glu Leu Thr Lys Ile Cys Asp Gly Ile 65 70 75 80

Leu Lys Leu Leu Glu Ser His Leu Val Pro Ser Ser Thr Ala Pro Glu 85 90 95

Ser Lys Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu 100 105 110

Cys

- (2) INFORMATION FOR SEQ ID NO:2987:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 396 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..396
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602389
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2987:

ttgttcttga ctctggtgat ggtgtgagcc acactgtgcc catttacgga aggatatgcc 60 cttcctcatg ccattcttcg tttggatctt gctggtcggg acctcacaga ctccctcatg 120 aaaatcctga ctgagagggg ttactccttc acaacctctg ccgagcgaga aattgtaagg 180 gacatcaagg agaagctggs atatatagcc cttgactatg agcaagagtt ggaaactgcc 240 aagaacagct cctcagttga aaagagctat gagctacctg atggccaagt aatcaccatt 300 ggtgcagaa gattcagatg ccctgaggtc ctcttccagc catccatgat tggtatggag 360 gctgccggaa tccatgagac aacatacaat tcaatc

- (2) INFORMATION FOR SEQ ID NO:2988:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 93 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..93
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2988:

Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Ser Ala Glu 1 5 10 15

Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Ile Ala Leu 20 25 30

Asp Tyr Glu Glu Leu Glu Thr Ala Lys Asn Ser Ser Ser Val Glu 35 40 45

Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ala Glu 50 55 60

Arg Phe Arg Cys Pro Glu Val Leu Phe Gln Pro Ser Met Ile Gly Met 65 70 75 80

Glu Ala Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile 85 90

- (2) INFORMATION FOR SEQ ID NO:2989:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 459 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..459
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602391
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2989:

agaateteeg etetetgega ggcaacegga gecaatgtet etgaggtgge ttaegeegtg 60 ggcaaggaca egagaattgg ecceaagtte etgaacgeca gtgttgggtt eggtggetea 120 tgetteeaga aggacateet gaacetggtg tacatetgeg agtgcaaceg eetgeeegag 180 gtggecaact actggaagea ggtgateaag ateaacgact aceagaagag eeggttegtg 240 aacegegteg tggeeteea gtteaacace gtegeeggea agaagatege egteetegge teggeettea agaaagacac eggtgacace agggagacee eggeeattga egtetgeag 300 ggeetgetgg gegacaagge ecagateage atetaegace eccaggtgac ggaggaceag 420 atecageggg acetggega acetggeeat gaacaagtee gaetgggac

- (2) INFORMATION FOR SEQ ID NO:2990:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 153 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..153
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602392
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2990:

Arg Ile Ser Ala Leu Cys Glu Ala Thr Gly Ala Asn Val Ser Glu Val 1 5 10 15

Ala Tyr Ala Val Gly Lys Asp Thr Arg Ile Gly Pro Lys Phe Leu Asn 20 25 30

Ala Ser Val Gly Phe Gly Gly Ser Cys Phe Gln Lys Asp Ile Leu Asn 35 40 45

Leu Val Tyr Ile Cys Glu Cys Asn Gly Leu Pro Glu Val Ala Asn Tyr 50 55 60

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Trp Lys Gln Val Ile Lys Ile Asn Asp Tyr Gln Lys Ser Arg Phe Val
                    70
                                        75
Asn Arq Val Val Ala Ser Met Phe Asn Thr Val Ala Gly Lys Lys Ile
                85
                                    90
Ala Val Leu Gly Phe Ala Phe Lys Lys Asp Thr Gly Asp Thr Arg Glu
            100
                                105
                                                    110
Thr Pro Ala Ile Asp Val Cys Lys Gly Leu Leu Gly Asp Lys Ala Gln
                            120
                                                125
Ile Ser Ile Tyr Asp Pro Gln Val Thr Glu Asp Gln Ile Gln Arg Asp
                        135
                                            140
Leu Ala Met Asn Lys Phe Asp Trp Asp
145
                    150
(2) INFORMATION FOR SEQ ID NO:2991:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..475
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602394
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2991: agecteegee ecaceaacee ttgeeteece acaceteage ateaaceact egtetetttt 60 tetecquece quecquaque gaggaggaga ggggagcage gagategtge gegeeteega 120 qatctccacq aaqttgtggt aacatggggc tcaccttcac gaagctcttc agccggctct 180 240 tctccaagaa agagatgagg atccttatgg ttggtctcga tgcagctggt aagaccacca tectetacaa geteaagete ggagaaateg tgaccacate cetacaateg ggtttaatgt 300 ggagactgtt gaatacaaga acattagctt cactgtctgg gatgttggag gtcaggacaa 360 gatcaggcca ttgtggaggc actatttcca gaacacccaa ggccttatct ttgttgttga 420 tagcaatgac agagatcgtg tcgttgaagc aaaggatgag ctccacagga tgctg
- (2) INFORMATION FOR SEQ ID NO:2992:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..157
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602395
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2992:
- Pro Pro Pro His Gln Pro Leu Pro Pro His Thr Ser Ala Ser Thr Thr 5 10
- Arg Leu Phe Phe Ser Ala Pro Pro Glu Ala Glu Glu Glu Arg Gly Ala 25
- Ala Arg Ser Cys Ala Pro Pro Arg Ser Pro Arg Ser Cys Gly Asn Met 40 45
- Gly Leu Thr Phe Thr Lys Leu Phe Ser Arg Leu Phe Ser Lys Lys Glu 55 60
- Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile 7.0 75
- Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ser Leu Gln Ser 85 90
- Gly Leu Met Trp Arg Leu Leu Asn Thr Arg Thr Leu Ala Ser Leu Ser 105 110
- Gly Met Leu Glu Val Arg Thr Arg Ser Gly His Cys Gly Gly Thr Ile 120
- Ser Arg Thr Pro Lys Ala Leu Ser Leu Leu Ile Ala Met Thr Glu

(ix) FEATURE:

135 130 Ile Val Ser Leu Lys Gln Arg Met Ser Ser Thr Gly Cys 150 (2) INFORMATION FOR SEQ ID NO:2993: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..110 (D) OTHER INFORMATION: / Ceres Seq. ID 1602396 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2993: Met Gly Leu Thr Phe Thr Lys Leu Phe Ser Arg Leu Phe Ser Lys Lys 10 5 Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr 20 25 Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ser Leu Gln 35 40 Ser Gly Leu Met Trp Arg Leu Leu Asn Thr Arg Thr Leu Ala Ser Leu 50 55 Ser Gly Met Leu Glu Val Arg Thr Arg Ser Gly His Cys Gly Gly Thr 75 70 Ile Ser Arg Thr Pro Lys Ala Leu Ser Leu Leu Leu Ile Ala Met Thr 85 90 Glu Ile Val Ser Leu Lys Gln Arg Met Ser Ser Thr Gly Cys 100 105 (2) INFORMATION FOR SEQ ID NO:2994: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1602397 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2994: Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile 10 5 Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ser Leu Gln Ser 25 Gly Leu Met Trp Arg Leu Leu Asn Thr Arg Thr Leu Ala Ser Leu Ser 35 40 Gly Met Leu Glu Val Arg Thr Arg Ser Gly His Cys Gly Gly Thr Ile 55 60 Ser Arg Thr Pro Lys Ala Leu Ser Leu Leu Leu Ile Ala Met Thr Glu 70 75 Ile Val Ser Leu Lys Gln Arg Met Ser Ser Thr Gly Cys 85 (2) INFORMATION FOR SEQ ID NO:2995: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 448 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

- (A) NAME/KEY: -
- (B) LOCATION: 1..448
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2995:

atctcccata acggagaga acgaagaga cagaagcgaa gagcagcggc gcaaaggaaa 60 gggagccatg ctcgcctcgc cggcgctcgc cggcgccac tccttcgcgg cgtccgtgta 120 tggaaacatc ctcgtccct cgcctccgt ccccgcgccg gcacgtcgcg cggcgctgtc cgtcgtcgcc aaggtcaagg tggccacgcc ccaggacgac cgcatcgcc gccacgtccg 240 cctgcgcaag aaggtaagtg gcaccactga gaggccgagg ttgagtgtt tccgctcaaa caaacatctg tacgctcaag tcatcgacga cacaaagcaa tgtactctgg cttcagcttc 360 aaccatgcac aaatctctct ccaaggaatt tgaatactcg gctgggccaa cgatcgaaat 420 agcacaaaag atcggtgagg tgattgcc

- (2) INFORMATION FOR SEQ ID NO:2996:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..89
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602399
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2996:

Ile Ser His Asn Gly Glu Arg Arg Arg Glu Gln Lys Arg Arg Ala Ala

Ala Gln Arg Lys Gly Ser His Ala Arg Leu Ala Gly Ala Arg Arg Arg 20 25 30

Pro Leu Leu Arg Gly Val Arg Val Trp Lys His Pro Arg Pro Leu Ala 35 40 45

Ser Arg Pro Arg Ala Gly Thr Ser Arg Gly Ala Val Arg Arg Arg Gln 50 55 60

Gly Gln Gly Gly His Ala Pro Gly Arg Pro His Arg Pro Pro Arg Pro 65 70 75 80

Pro Ala Gln Glu Gly Lys Trp His His 85

- (2) INFORMATION FOR SEQ ID NO:2997:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 149 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..149
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602400
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2997:

Ser Pro Ile Thr Glu Arg Asp Glu Glu Ser Arg Ser Glu Glu Gln Arg 1 5 10 15

Arg Lys Gly Lys Gly Ala Met Leu Ala Ser Pro Ala Leu Ala Gly Ala 20 25 30

His Ser Phe Ala Ala Ser Val Tyr Gly Asn Ile Leu Val Pro Ser Pro  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Pro Val Pro Ala Pro Ala Arg Arg Ala Ala Leu Ser Val Val Ala Lys
50 60

Val Lys Val Ala Thr Pro Gln Asp Asp Arg Ile Ala Arg His Val Arg 65 70 75 80

Leu Arg Lys Lys Val Ser Gly Thr Thr Glu Arg Pro Arg Leu Ser Val 85 90 95

Phe Arg Ser Asn Lys His Leu Tyr Ala Gln Val Ile Asp Asp Thr Lys

110 105 100 Gln Cys Thr Leu Ala Ser Ala Ser Thr Met His Lys Ser Leu Ser Lys 120 125 Glu Phe Glu Tyr Ser Ala Gly Pro Thr Ile Glu Ile Ala Gln Lys Ile 140 135 Gly Glu Val Ile Ala 145 (2) INFORMATION FOR SEQ ID NO:2998: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..127 (D) OTHER INFORMATION: / Ceres Seq. ID 1602401 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2998: Met Leu Ala Ser Pro Ala Leu Ala Gly Ala His Ser Phe Ala Ala Ser 10 Val Tyr Gly Asn Ile Leu Val Pro Ser Pro Pro Val Pro Ala Pro Ala 25 2.0 Arg Arg Ala Ala Leu Ser Val Val Ala Lys Val Lys Val Ala Thr Pro 40 Gln Asp Asp Arg Ile Ala Arg His Val Arg Leu Arg Lys Lys Val Ser 60 55 Gly Thr Thr Glu Arg Pro Arg Leu Ser Val Phe Arg Ser Asn Lys His 75 70 Leu Tyr Ala Gln Val Ile Asp Asp Thr Lys Gln Cys Thr Leu Ala Ser 85 90 Ala Ser Thr Met His Lys Ser Leu Ser Lys Glu Phe Glu Tyr Ser Ala 105 110 Gly Pro Thr Ile Glu Ile Ala Gln Lys Ile Gly Glu Val Ile Ala 120 (2) INFORMATION FOR SEQ ID NO:2999: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..437 (D) OTHER INFORMATION: / Ceres Seq. ID 1602402 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2999: 60 agaaggaaca gattcatcga gacctcttct cctcgcgccg ccgcgctgcg ccgtcgtcat gtcgaagcgc gggaggggag ggacggcggg gaacaagttc cgcatgtcgc tgggtctccc 120 cgtcgcagcg accgtgaact gtgcggacaa cacaggcgcc aagaacctct acatcatctc 180 cgtcaagggc atcaagggta ggctcaaccg cctgccgtcc gcctgcgtcg gcgacatggt 240 catggccacc gtcaagaagg gtaagcccga cctcaggaag aaggtcatgc ccgccgtcat 300 cgtccgccag cgcaagctgt ggcgccgcaa ggacggagtc tacatgtact tcgaagataa 360 tgctggagtc attgtgaacc ccaagggcga gatgaaagga tctgctatca ctggacctat 420 tggcaaggag tgcgctg (2) INFORMATION FOR SEQ ID NO:3000: (i) SEQUENCE CHARACTERISTICS:

- - (A) LENGTH: 145 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
         (B) LOCATION: 1..145
         (D) OTHER INFORMATION: / Ceres Seq. ID 1602403
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3000:
Glu Gly Thr Asp Ser Ser Arg Pro Leu Leu Leu Ala Pro Pro Arg Cys
                               10
Ala Val Val Met Ser Lys Arg Gly Arg Gly Gly Thr Ala Gly Asn Lys
                           25
Phe Arg Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala
                        40
Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile
                  55
Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val
                70
Met Ala Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met
                        90
             8.5
Pro Ala Val Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly
                           105
         100
Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys
   115 120 125
Gly Glu Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys
130 135 140
Ala
145
(2) INFORMATION FOR SEQ ID NO:3001:
   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: peptide
   (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..126
        (D) OTHER INFORMATION: / Ceres Seq. ID 1602404
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3001:
Met Ser Lys Arg Gly Arg Gly Gly Thr Ala Gly Asn Lys Phe Arg Met
                            10
   5
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr
                           25
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg
    35 40
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr
  50 55
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val
                 70
                                75 80
Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr Met
                              90
            85
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met
         100 105
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala
      115 120
(2) INFORMATION FOR SEQ ID NO:3002:
    (i) SEQUENCE CHARACTERISTICS:
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(A) LENGTH: 111 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- Attorney Docket No. 2750-1237P Client Docket No. 80146.003 (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..111 (D) OTHER INFORMATION: / Ceres Seq. ID 1602405 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3002: Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly 20 25 Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala 40 Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala 55 Val Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr 70 Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu 85 90 Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala 100 105 (2) INFORMATION FOR SEQ ID NO:3003: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 501 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..501
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602411 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3003:
  - aacacgagta cacgaccacg agagactggt cggtctgcga ctgtctctga ccgctgaccg 60 cactetecte tgettetgte tttetetete teccetgtee eeettecaga ttteetecat 120 180 tegeggtttg cetetetgee tteetgeetg etteeeteee teegteagat eeeegetegg gttgccatgg cggaccagct caccgacgaa cagatcgccg agttcaagga ggccttcagc 240 300 ctcttcgaca aggacggcga cggctgcatc accaccaagg aacttggcac tgtgatgcgc tcattggggc agaaccctac tgaggctgag cttcaggaca tgatcaatga ggttgatgct 360 gatggcaatg gaaccatcga ctttcctgag tttctcaacc tgatggcacg caagatgaag 420 gacaccgact ctgaggagga gctcaaggag gccttccgtg tgttcgacaa ggaccagaac ggctcatctc cgctgctgag c

10

75

4.5

- (2) INFORMATION FOR SEQ ID NO:3004:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..97
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602412
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3004:
- Thr Arg Val His Asp His Glu Arg Leu Val Gly Leu Arg Leu Ser Leu 5 10
- Thr Ala Asp Arg Thr Leu Leu Cys Phe Cys Leu Ser Leu Ser Pro Leu 25
- Ser Pro Phe Gln Ile Ser Ser Ile Arg Gly Leu Pro Leu Cys Leu Pro
- Ala Cys Phe Pro Pro Ser Val Arg Ser Pro Leu Gly Leu Pro Trp Arg 55
- Thr Ser Ser Pro Thr Asn Arg Ser Pro Ser Ser Arg Arg Pro Ser Ala

70 75 65 Ser Ser Thr Arg Thr Ala Thr Ala Ala Ser Pro Pro Arg Asn Leu Ala 90 85 Leu (2) INFORMATION FOR SEQ ID NO:3005: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..105 (D) OTHER INFORMATION: / Ceres Seq. ID 1602413 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3005: Met Ala Asp Gln Leu Thr Asp Glu Gln Ile Ala Glu Phe Lys Glu Ala 10 5 Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu 20 25 Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu 40 45 Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile 55 60 Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr 70 75 Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp 90 85 Gln Asn Gly Ser Ser Pro Leu Leu Ser 100 (2) INFORMATION FOR SEQ ID NO:3006: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..69 (D) OTHER INFORMATION: / Ceres Seq. ID 1602414 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3006: Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met 5 10 Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu 25 Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu 40 45 Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Ser 55 60 Ser Pro Leu Leu Ser (2) INFORMATION FOR SEQ ID NO:3007: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602415
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3007:

actecgeege egetgettae egectatete gecaageace geegeateae egaaggtteg 60 caaagatggc ggtgccgctg ctgacgcaga agatcgtgaa gaagagggtc aagcagttca 120 agaggcccca tcttgaccgc tacaagtgcc ttaagccaag ctggcgcagg cccaagggta 180 240 togactoccg cgtgaggcgt aagttcaagg gatgcacctt gatgcccaac attggatatg 300 qctccqacaa qaaqaccaqq cactaccttc ccaacaagtt caaaaagttt gttgttcaca 360 atqtctccqa qctqqaqctq ctqctqatqc acaacaggac ctactgcgct gagatcgcc 420 acaacqtqtc cacccqcaaq cqcaaqtaqa ttgtcgagcg tgctgcgcaa atggacatcg tggtcaccaa caagettgee aggeteegea geeaagagga egagtgaaat gttgagtagt tttgattgtg ctctgctggt gttgaagatg t

- (2) INFORMATION FOR SEQ ID NO:3008:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..128
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602416
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3008:

Ser Ala Ala Ala Tyr Arg Leu Ser Arg Gln Ala Pro Pro His His 1 5 10 15

Arg Arg Phe Ala Lys Met Ala Val Pro Leu Leu Thr Gln Lys Ile Val 20 25 30

Lys Lys Arg Val Lys Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys 35 40 45

Cys Leu Lys Pro Ser Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val 50 55 60

Arg Arg Lys Phe Lys Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly 65 70 75 80

Ser Asp Lys Lys Thr Arg His Tyr Leu Pro Asn Lys Phe Lys Lys Phe 85 90 95 Val Val His Asn Val Ser Glu Leu Glu Leu Leu Met His Asn Arg

110 105 Arg Lys Arg Lys Arg Lys

Thr Tyr Cys Ala Glu Ile Ala His Asn Val Ser Thr Arg Lys 115 120 125

- (2) INFORMATION FOR SEQ ID NO:3009:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..107
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602417
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3009:

Met Ala Val Pro Leu Leu Thr Gln Lys Ile Val Lys Lys Arg Val Lys 1 5 10 15

Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys Cys Leu Lys Pro Ser 20 25 30

Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys 35 40 45

Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Lys Thr 50 55 60

Arg His Tyr Leu Pro Asn Lys Phe Lys Lys Phe Val Val His Asn Val 65 70 75 80

Ser Glu Leu Glu Leu Leu Leu Met His Asn Arg Thr Tyr Cys Ala Glu 85 90 95

Ile Ala His Asn Val Ser Thr Arg Lys Arg Lys 100 105

- (2) INFORMATION FOR SEQ ID NO:3010:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 489 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..489
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602422
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3010: 60 aactgcagac ttgtcggcac agccgtcgta atatatccat tcgatcgaag caatcgcgcc 120 ttgaacccta gctcccgccg ccaccccacg cctgcagcca tgccgcccaa gctcgacccg 180 tcqcaggtgg tggaggtgtt cgtccgtgtg accggcggcg aggtaggcgc ggcgtcttcg 240 ttgqccccca agatcgqtcc qctcgqtctt tctcccaaga agatcggaga ggacattgcc aaqqaqacqq ccaaqqactq qaaqqqcctc cgcgtcaccg ttaagctcac tgtccagaac 300 360 cgacaggccm saggtctccg tcgttccctc tgccgcggcg ctcgtcatca aggcgctcaa qqaqcccqaq aqqqaccqca aqaaqqtcaa qaacatcaga gcacagcggc aacatcagtc 420 tcqacqacqt catcqaqatt qccaqqacca tqaqqcccaq gtccatggcc aaggaaatgt 480 ccaactaca
- (2) INFORMATION FOR SEQ ID NO:3011:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 150 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..150
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602423
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3011:
- Asn Cys Arg Leu Val Gly Thr Ala Val Val Ile Tyr Pro Phe Asp Arg
  1 5 10 15
- Ser Asn Arg Ala Leu Asn Pro Ser Ser Arg Arg His Pro Thr Pro Ala 20 25 30
- Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val 35 40 45
- Arg Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu Ala Pro Lys 50 60
- Ile Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile Ala 65 70 75 80
- Lys Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys Leu 85 90 95
- Thr Val Gln Asn Arg Gln Ala Xaa Gly Leu Arg Arg Ser Leu Cys Arg
  100 105 110
- Gly Ala Arg His Gln Gly Ala Gln Gly Ala Arg Glu Gly Pro Gln Glu
  115 120 125
- Gly Gln Glu His Gln Ser Thr Ala Ala Thr Ser Val Ser Thr Thr Ser 130 135 140
- Ser Arg Leu Pro Gly Pro
- 145 150

- Page 1462 Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:3012: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..117 (D) OTHER INFORMATION: / Ceres Seq. ID 1602424 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3012: Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val Arg 10 Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu Ala Pro Lys Ile 30 20 25 Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile Ala Lys 40 45 Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys Leu Thr 55 60 Val Gln Asn Arg Gln Ala Xaa Gly Leu Arg Arg Ser Leu Cys Arg Gly 75 70 Ala Arg His Gln Gly Ala Gln Gly Ala Arg Glu Gly Pro Gln Glu Gly 90 85 Gln Glu His Gln Ser Thr Ala Ala Thr Ser Val Ser Thr Thr Ser Ser 110 100 105 Arg Leu Pro Gly Pro 115 (2) INFORMATION FOR SEQ ID NO:3013: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 502 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..502 (D) OTHER INFORMATION: / Ceres Seq. ID 1602425 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3013: aggatgaatc ggaagagaa atcctaccaa acctagctac caactcgatc gtcgtggtcg 60 120 acqaqtcqtq ctqqaqcqac ctcqaqttct qcqaqaaaac caggaactgg tactgctacg gcaaggeggt ggeggageag geggegtggg agaeggeeeg geggegggge gtggaeetgg 180 240 tagtagtaaa ccccatacta ataataaaccccatactaca agcaacaata aacaccaaca 300 tegegeacat ceteaagtae etggaegget eggeeegeac ettegeeaac geegtgeagg cgtacgtgga cgtgcgcgac gtggccgacg cgcacctccg cgtcttcgag agcccccqcg 360 cgtccggccg ccacctctgc gccgagcgcg tcctccaccg cgaggacgtc gtccgcatcc 420 tegecaaget etteeeegag taceeegtee cagecaggtg eteegaegag gtgaateege 480 ggaagcagcc gtacaagttc tc (2) INFORMATION FOR SEQ ID NO:3014: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 166 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear

  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..166
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602426
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3014:

```
Asp Glu Ser Glu Glu Arg Ile Leu Pro Asn Leu Ala Thr Asn Ser Ile
                                  10
Val Val Val Asp Glu Ser Cys Trp Ser Asp Leu Glu Phe Cys Glu Lys
                                                  30
           20
                               25
Thr Arg Asn Trp Tyr Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala
                           40
Trp Glu Thr Ala Arg Arg Gly Val Asp Leu Val Val Asn Pro
                                          60
                       55
Val Leu Val Val Gly Pro Leu Leu Gln Ala Thr Val Asn Ala Ser Ile
                   70
                                      75
Ala His Ile Leu Lys Tyr Leu Asp Gly Ser Ala Arg Thr Phe Ala Asn
               85
                                  90
Ala Val Gln Ala Tyr Val Asp Val Arg Asp Val Ala Asp Ala His Leu
                              105
          100
Arg Val Phe Glu Ser Pro Arg Ala Ser Gly Arg His Leu Cys Ala Glu
                          120
      115
                                              125
Arg Val Leu His Arg Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe
                     135
                            140
Pro Glu Tyr Pro Val Pro Ala Arg Cys Ser Asp Glu Val Asn Pro Arg
                   150
                                      155
Lys Gln Pro Tyr Lys Phe
```

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(2) INFORMATION FOR SEQ ID NO:3015:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 466 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..466
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602435
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3015:

  catcctaatc gaaaacacac accactccac agcagtagca agagggatag agcaaggcca 60
  cacacacaca cacaccaca ggctaggtta gccttttaat cgtcgtcgag aagcaagaag 120
  ggcgcgcacg caagcaggca agcaagaaga gagccgatcg accgaggct agcacgcgat 180
  ggcggaggtct tccaagatga tggtggcggc agctctgctg gccttggccc tggccgtgtc 240
  gaccgccgag gcgaggaaca tcaagaccac gacgacggar aagaaggacg acgcggtgt 300
  gcagccgcag accttcccc ccttcgaccg cctcggcgc ggcgctccc cggcgttcgg 360
  cggcctcccc ggcggcagca ttcctggcag cagcattccc gggttcagca tgcccggcag
- (2) INFORMATION FOR SEQ ID NO:3016:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids

cggcagcagc ctacccgggt acagcttgcc cggcagcggc agcatg

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..96
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602436
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3016:
- Met Ala Arg Ser Ser Lys Met Met Val Ala Ala Ala Leu Leu Ala Leu 1 5 10 15
- Ala Leu Ala Val Ser Thr Ala Glu Ala Arg Asn Ile Lys Thr Thr 20 25 30
- Thr Xaa Lys Lys Asp Asp Ala Val Val Gln Pro Gln Thr Phe Pro Pro 35 40 45
- Phe Asp Arg Leu Gly Gly Gly Ala Ser Pro Ala Phe Gly Gly Leu Pro

50 55 60

Gly Gly Ser Ile Pro Gly Ser Ser Ile Pro Gly Phe Ser Met Pro Gly 65 70 75 80

Ser Gly Ser Ser Leu Pro Gly Tyr Ser Leu Pro Gly Ser Gly Ser Met 85 90 95

- (2) INFORMATION FOR SEQ ID NO:3017:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 90 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..90
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602437
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3017:

Met Met Val Ala Ala Ala Leu Leu Ala Leu Ala Leu Ala Val Ser Thr 1 5 10 15

Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Xaa Lys Lys Asp Asp 20 25 30

Ala Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly 35 40 45

Gly Ala Ser Pro Ala Phe Gly Gly Leu Pro Gly Gly Ser Ile Pro Gly 50 55 60

Ser Ser Ile Pro Gly Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro 65 70 75 80

Gly Tyr Ser Leu Pro Gly Ser Gly Ser Met 85 90

- (2) INFORMATION FOR SEQ ID NO:3018:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..89
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602438
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3018:

Met Val Ala Ala Ala Leu Leu Ala Leu Ala Leu Ala Val Ser Thr Ala 1 5 10 15

Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Xaa Lys Lys Asp Asp Ala 20 25 30

Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly 35  $\phantom{-}40\phantom{+}45\phantom{+}$ 

Ala Ser Pro Ala Phe Gly Gly Leu Pro Gly Gly Ser Ile Pro Gly Ser 50 55 60

Ser Ile Pro Gly Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly 65 70 75 80

Tyr Ser Leu Pro Gly Ser Gly Ser Met 85

- (2) INFORMATION FOR SEQ ID NO:3019:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..356
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602439
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3019:

- (2) INFORMATION FOR SEQ ID NO:3020:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..118
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602440
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3020:

Asp Lys Gln Gln Arg Glu Lys Ala Ser Lys Ala Glu Ala Val Leu 20 25 30

Leu Val Gly Pro Ser Met Ala Pro Lys Arg Pro Val Ser Ala Ala Ala 35 40 45

Ala Ala Glu Gln Pro Arg Leu Arg Gly Val Arg Lys Arg Pro Trp Gly 50 60

Arg Tyr Ala Ala Glu Ile Arg Asp Pro Val Arg Lys Ala Arg Val Trp 65 70 75 80

Leu Gly Thr Phe Asp Thr Pro Glu Gln Ala Ala Arg Ala Tyr Asp Ala 85 90 95

Ala Ala Arg Lys Leu Arg Gly Pro Gly Ala Ala Thr Asn Tyr Pro Ala 100 105 110

Pro Glu Pro Thr Ala Glu 115

- (2) INFORMATION FOR SEQ ID NO:3021:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..118
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602441
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3021:

Ala Phe Pro Phe Pro Pro Val His Pro Ser Ser Glu Ala Pro Arg Gln
1 10 15

Thr Ser Ser Ser Glu Arg Lys Gln Ala Arg Gln Arg Gln Leu Cys Cys
20 25 30

Trp Ser Val Arg Pro Trp Arg Pro Arg Asp Gln Cys Arg Arg Arg Arg 40 45

Arg Arg Ser Ser Arg Gly Cys Ala Ala Cys Gly Ser Gly Arg Gly Ala 50 55 60

Gly Thr Arg Arg Arg Ser Ala Thr Arg Cys Gly Arg Arg Ala Cys Gly

Client Docket No. 80146.003 75 70 65 Trp Ala Pro Ser Thr Arg Arg Ser Arg Arg Arg Gly Arg Thr Thr Pro 90 85 Pro Arg Ala Ser Ser Ala Gly Pro Ala Pro Pro Pro Thr Thr Pro Pro 100 105 Arg Ser Arg Arg Arg Arg 115 (2) INFORMATION FOR SEQ ID NO:3022: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..118
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602442
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3022:

His Ser His Ser His Pro Ser Ile His Pro Pro Lys Leu Leu Gly Arg 10 5

Gln Ala Ala Arg Glu Ser Lys Gln Gly Arg Gly Ser Cys Val Ala 25 2.0

Gly Arg Ser Val His Gly Ala Gln Glu Thr Ser Val Gly Gly Gly 45 40

Gly Gly Ala Ala Glu Ala Ala Arg Arg Ala Glu Ala Ala Val Gly Pro 60 55

Val Arg Gly Gly Asp Pro Arg Pro Gly Ala Glu Gly Ala Arg Val Ala 75 70

Gly His Leu Arg His Ala Gly Ala Gly Gly Ala Gly Val Arg Arg Arg 90 85

Arg Ala Gln Ala Pro Arg Ala Arg Arg Arg His Gln Leu Pro Arg Pro 105 100

Gly Ala Asp Gly Gly Gly 115

- (2) INFORMATION FOR SEQ ID NO:3023:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..435
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602446
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3023:

attcaacaac totggcgagc agcagtgaac gtacttacgt cttcccccag ctagctagct 60 atctaccttg gtggtggcga ttggtatata gattaaacat ggcgcctcaa agcctggatc 120 tegggetgag teteggeetg ggegtggegg catteragee cagettetge caeceggeeg 180 gcaatgcggc ggcggagcgg gagaccagcc cgaccgcggc ggacgagagg gagcggaggt 240 gctcgcccgc cggcagcccg acgtcgagcg gcagcggcag cgggaagcgc gtcgcgacgg 300 agagategge eggeagegge ageggegaeg aggaegaega egggggeget egeaagaage 360 tgeggttgtc caaggaccag geegeegtge tegaggagtg etteaaagae geaccaeace 420 ctcactccga agcag

- (2) INFORMATION FOR SEQ ID NO:3024:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 144 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..144
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3024:

Ser Thr Thr Leu Ala Ser Ser Ser Glu Arg Thr Tyr Val Phe Pro Gln  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Leu Ala Ser Tyr Leu Pro Trp Trp Trp Arg Leu Val Tyr Arg Leu Asn
20 25 30

Met Ala Pro Gln Ser Leu Asp Leu Gly Leu Ser Leu Gly Leu Gly Val 35 40 45

Ala Ala Phe Gln Pro Ser Phe Cys His Pro Ala Gly Asn Ala Ala Ala 50 55 60

Glu Arg Glu Thr Ser Pro Thr Ala Ala Asp Glu Arg Glu Arg Cys
65 70 75 80

Ser Pro Ala Gly Ser Pro Thr Ser Ser Gly Ser Gly Ser Gly Lys Arg 85 90 95

Val Ala Thr Glu Arg Ser Ala Gly Ser Gly Ser Gly Asp Glu Asp Asp
100 105 110

Asp Gly Gly Ala Arg Lys Leu Arg Leu Ser Lys Asp Gln Ala Ala 115 120 125

Val Leu Glu Glu Cys Phe Lys Asp Ala Pro His Pro His Ser Glu Ala 130 135 140

- (2) INFORMATION FOR SEQ ID NO:3025:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..112
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602448
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3025:

Met Ala Pro Gln Ser Leu Asp Leu Gly Leu Ser Leu Gly Leu Gly Val 1 5 10 15

Ala Ala Phe Gln Pro Ser Phe Cys His Pro Ala Gly Asn Ala Ala Ala 20 25 30

Glu Arg Glu Thr Ser Pro Thr Ala Ala Asp Glu Arg Glu Arg Cys 35 40 45

Ser Pro Ala Gly Ser Pro Thr Ser Ser Gly Ser Gly Ser Gly Lys Arg 50 55

Val Ala Thr Glu Arg Ser Ala Gly Ser Gly Ser Gly Asp Glu Asp Asp 65 70 75 80

Asp Gly Gly Ala Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ala Ala 85 90 95

Val Leu Glu Glu Cys Phe Lys Asp Ala Pro His Pro His Ser Glu Ala 100 \$105\$

- (2) INFORMATION FOR SEQ ID NO: 3026:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 84 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602449
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3026:
- Ser Gly Gly Ala Arg Pro Pro Ala Ala Arg Arg Arg Ala Ala Ala Ala 20 25 30
- Ala Gly Ser Ala Ser Arg Arg Arg Arg Pro Ala Ala Ala Ala Ala 35 40 45
- Thr Arg Thr Thr Gly Ala Leu Ala Arg Ser Cys Gly Cys Pro Arg 50 55 60
- Thr Arg Pro Pro Cys Ser Arg Ser Ala Ser Lys Thr His His Thr Leu 70 75 80

Thr Pro Lys Gln

- (2) INFORMATION FOR SEQ ID NO:3027:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 390 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..390
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3027:

  atccaatacg cccaccagec accaccate etetetecet eccagtecca ggagegtge 60

  ctcactetee tegtegeate ecceetecte atettegeag egegggege ggeaatggeg 120

  atggeeteca ectacgegee gggeggagge gegegggege tegeggagg tagatgeagg 180

  gteegeggte eegegggget eaggegteete ggeeteetea aggeegeegg ecteeceege 240

  cecetegeee tegeetege eaggeggatg ageageeegg tegeggtgg egeaggetge 300

  gatgegegge gtegtegtee eegeggegg egeggeeege eaeggegeeg egetteatee 360
- agcacaagaa ggaggccttc tggttctacc (2) INFORMATION FOR SEQ ID NO:3028:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..130
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602451
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3028:
- Ile Gln Tyr Ala His Gln Pro Pro His Ile Leu Ser Pro Ser Gln Ser
  1 10 15
- Gln Glu Arg Gly Leu Thr Leu Leu Val Ala Ser Pro Leu Leu Ile Phe 20 25 30
- Ala Ala Arg Ala Ala Ala Met Ala Met Ala Ser Thr Tyr Ala Pro Gly 35 40 45
- Ala Gly Leu Gly Phe Leu Gly Pro Ser Lys Ala Ala Gly Leu Pro Arg
  65 70 75 80
- Pro Leu Ala Leu Ala Leu Ala Arg Arg Met Ser Ser Pro Val Ala Val 85 90 95 Gly Ala Gly Cys Asp Ala Arg Arg Arg Arg Pro Pro Arg Arg Gly

Client Docket No. 80146.003 105 Pro Pro Arg Arg Arg Ala Ser Ser Ser Thr Arg Arg Arg Pro Ser Gly 120 125 Ser Thr 130 (2) INFORMATION FOR SEQ ID NO:3029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..89 (D) OTHER INFORMATION: / Ceres Seq. ID 1602452 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3029: Ser Asn Thr Pro Thr Ser His His Thr Ser Ser Leu Pro Pro Ser Pro 10 Arg Ser Val Ala Ser Leu Ser Ser Ser His Pro Pro Ser Ser Ser Ser 25 Gln Arg Gly Arg Arg Gln Trp Arg Trp Pro Pro Pro Thr Arg Arg Ala 4.0 Glu Ala Arg Gly Arg Ser Arg Arg Val Asp Ala Gly Ser Ala Val Pro 55 Arg Gly Trp Ala Ser Ser Ala Pro Pro Arg Pro Pro Ala Ser Pro Ala 75 70 Pro Ser Pro Ser Pro Ser Pro Gly Gly 85 (2) INFORMATION FOR SEQ ID NO:3030: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..92 (D) OTHER INFORMATION: / Ceres Seq. ID 1602453 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3030: Met Ala Met Ala Ser Thr Tyr Ala Pro Gly Gly Ala Arg Ala Leu 10 5 Ala Gln Gly Arg Cys Arg Val Arg Gly Pro Ala Gly Leu Gly Phe Leu 20 25 Gly Pro Ser Lys Ala Ala Gly Leu Pro Arg Pro Leu Ala Leu Ala Leu 4.0 Ala Arg Arg Met Ser Ser Pro Val Ala Val Gly Ala Gly Cys Asp Ala 5.5 60 Arg Arg Arg Pro Pro Arg Arg Gly Pro Pro Arg Arg Ala 70 7.5 Ser Ser Ser Thr Arg Arg Pro Ser Gly Ser Thr

- 85 (2) INFORMATION FOR SEQ ID NO:3031:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 504 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..504
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3031:

aaaccgaaac aaacagtcac tcatcctctt tctgtctttc acccccgcgt tcacgccggc 60 ccaaacccca aatcgcacgc gtcatcccaa tcccaaccca attagtcaat tacgacacgc 120 ctgccgccgc acgccgcccg aaatccggag gggaagctcc tcgacgacgt agcggccagt 180 qqcaqctcqq acgatggcct cgtccaactc cgccgccccg gctcccgccg acgggggcga 240 300 egacetegae cageteeteg acagegeget egacgaette accaaceteg atetetetge ctctqccqcc cccaaaaqct ccqqcqaqqc atcqqqqtca ggatcqqqaq gcaaqqqqcc 360 aqtqaaqqqq ctqqqqctqq qqcttccqqa ccccaaqqcq ccqaaqcgqc gcqcgqggaa 420 480 qcaqccqccq ccqaqqqqcq cqtqcqcaaa qaggcqctcq aggagctgac gcgcgagacq cgggaggctg tgcgcggtct cgag

- (2) INFORMATION FOR SEQ ID NO:3032:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..120
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602455
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3032:

Thr Glu Thr Asn Ser His Ser Ser Ser Phe Cys Leu Ser Pro Pro Arg
1 5 10 15

Gln Leu Val Asn Tyr Asp Thr Pro Ala Ala Ala Arg Arg Pro Lys Ser 35 40 45

Gly Glu Ala Pro Arg Arg Ser Gly Gln Trp Gln Leu Gly Arg 50 55 60

Trp Pro Arg Pro Thr Pro Pro Pro Arg Leu Pro Pro Thr Gly Ala Thr 65 70 75 80

Thr Ser Thr Ser Ser Ser Thr Ala Arg Ser Thr Thr Ser Pro Thr Ser 85 90 95

Ile Ser Leu Pro Leu Pro Pro Pro Lys Ala Pro Ala Arg His Arg Gly 100 105 110

Gln Asp Arg Glu Ala Arg Gly Gln 115 120

- (2) INFORMATION FOR SEQ ID NO:3033:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 91 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..91
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602456
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3033:

Asp Leu Asp Gln Leu Leu Asp Ser Ala Leu Asp Asp Phe Thr Asn Leu 20 25 30

Asp Leu Ser Ala Ser Ala Ala Pro Lys Ser Ser Gly Glu Ala Ser Gly 35 40 45

Ser Gly Ser Gly Gly Lys Gly Pro Val Lys Gly Leu Gly Leu 50 55 60

Pro Asp Pro Lys Ala Pro Lys Arg Arg Ala Gly Lys Gln Pro Pro 7.0 Arg Gly Ala Cys Ala Lys Arg Arg Ser Arg Ser 85 (2) INFORMATION FOR SEQ ID NO:3034: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 519 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..519 (D) OTHER INFORMATION: / Ceres Seq. ID 1602457 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3034: gataagaaat ggtgagcagg caagcatgga gtggagtgct tttaaaatttg ggtgtcgctg tcgttgaaag cgatgggtgg ctagttttac agacagacag cagcacctgc tcctccgtct 120 ggactgactg actagtgact cagetecace caeateceee ttegtegtet teteceteee tgctagctga cctccaatcc acgataaggc aagataagct agctaggaag gcaagggatc cgatggacaa gtacgagccc gttcgcgaga tcggggcggg caacttcggg gtggccaagc tgatgaggaa caaggacacg agggagctgg tggccatgaa gttcatagag cgaggaaaca ggatcgacga gaacgtgttc cgcgagatcg tgaaccaccg ctccctccgc caccccaaca 420 tcatccggtt caaggaggtg gtgcctgack tcccacgcac cttgcgatcg tgatggagta cqctqcqqqc qqqqamsctq ttcgagcqca tctgcgacq (2) INFORMATION FOR SEQ ID NO:3035: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..76 (D) OTHER INFORMATION: / Ceres Seq. ID 1602458 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3035: Met Asp Lys Tyr Glu Pro Val Arg Glu Ile Gly Ala Gly Asn Phe Gly 5 1.0 Val Ala Lys Leu Met Arg Asn Lys Asp Thr Arg Glu Leu Val Ala Met 30 20 25 Lys Phe Ile Glu Arg Gly Asn Arg Ile Asp Glu Asn Val Phe Arg Glu 40 45 Ile Val Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe Lys 55 Glu Val Val Pro Asp Xaa Pro Arg Thr Leu Arg Ser 70 (2) INFORMATION FOR SEQ ID NO:3036: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..56

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3036:

(D) OTHER INFORMATION: / Ceres Seq. ID 1602459

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Met Arg Asn Lys Asp Thr Arg Glu Leu Val Ala Met Lys Phe Ile Glu

Client Docket No. 80146.003 Page 1472 Arg Gly Asn Arg Ile Asp Glu Asn Val Phe Arg Glu Ile Val Asn His 25 Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe Lys Glu Val Val Pro 35 40 Asp Xaa Pro Arg Thr Leu Arg Ser 55 (2) INFORMATION FOR SEQ ID NO:3037: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..45 (D) OTHER INFORMATION: / Ceres Seq. ID 1602460 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3037: Met Lys Phe Ile Glu Arg Gly Asn Arg Ile Asp Glu Asn Val Phe Arg 10 Glu Ile Val Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe 20 25 Lys Glu Val Val Pro Asp Xaa Pro Arg Thr Leu Arg Ser 40 35 (2) INFORMATION FOR SEQ ID NO:3038: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 496 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..496 (D) OTHER INFORMATION: / Ceres Seq. ID 1602461 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3038: 60 aaataagaaa ccatgggtct ggtgggatta tgtgactgat tttcacataa ggtgtccaat 120 qaaqqaqaaq aagtacaata aaaaatgtgc agaaactgtc atcaaatcac taggtctgga tqtqaaqaaq qtcqataaat gcatgggaga cccaaatgct gattctgacc acccgttact 180 240 taaaatqqaa caaqatqctc aqattgggaa aggttcaaga ggagatgtta ctatattgcc 300 tacacttqtt qtqaacaacc ggcaatatcg agggaagctt gagaggaaag ctgtcctcaa agctatttgt gctggttttg aggaaactac agaaccaaat gtttgcctga gtgatgatat 360 agagacaaat gagtgtctga atgacaacgg gggctgctgg caagacaaat ctgctaatgt 420 aacagcctgt agggacacct tccgtggtag agtgtgtgaa tgccccactt tcaatggcgt acaatttaaa ggcgat (2) INFORMATION FOR SEQ ID NO:3039: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1602462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3039:

Asn Lys Lys Pro Trp Val Trp Trp Asp Tyr Val Thr Asp Phe His Ile 5 10 Arg Cys Pro Met Lys Glu Lys Lys Tyr Asn Lys Lys Cys Ala Glu Thr 30 25 20

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Val Ile Lys Ser Leu Gly Leu Asp Val Lys Lys Val Asp Lys Cys Met 35 40 45
Gly Asp Pro Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu Gln
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Gly Asp Pro Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu Gln 50 55 60

Asp Ala Gln Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu Pro 65 70 75 80

Thr Leu Val Val Asn Asn Arg Gln Tyr Arg Gly Lys Leu Glu Arg Lys 85 90 95

Ala Val Leu Lys Ala Ile Cys Ala Gly Phe Glu Glu Thr Thr Glu Pro  $100 \,$   $105 \,$   $110 \,$ 

Asn Val Cys Leu Ser Asp Asp Ile Glu Thr Asn Glu Cys Leu Asn Asp 115 120 125

Asn Gly Gly Cys Trp Gln Asp Lys Ser Ala Asn Val Thr Ala Cys Arg 130 135 140

Asp Thr Phe Arg Gly Arg Val Cys Glu Cys Pro Thr Phe Asn Gly Val 145 150 155 160

Gln Phe Lys Gly Asp 165

- (2) INFORMATION FOR SEQ ID NO:3040:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..146
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602463
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3040:

Met Lys Glu Lys Lys Tyr Asn Lys Lys Cys Ala Glu Thr Val Ile Lys 1  $\phantom{0}$  5  $\phantom{0}$  10  $\phantom{0}$  15

Ser Leu Gly Leu Asp Val Lys Lys Val Asp Lys Cys Met Gly Asp Pro 20 25 30

Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu Gln Asp Ala Gln 35 40 45

Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu Pro Thr Leu Val
50 55 60

Val Asn Asn Arg Gln Tyr Arg Gly Lys Leu Glu Arg Lys Ala Val Leu
65 70 75 80

Lys Ala Ile Cys Ala Gly Phe Glu Glu Thr Thr Glu Pro Asn Val Cys
85
90
.95

Leu Ser Asp Asp Ile Glu Thr Asn Glu Cys Leu Asn Asp Asn Gly Gly
100 105 110

Cys Trp Gln Asp Lys Ser Ala Asn Val Thr Ala Cys Arg Asp Thr Phe 115 120 125

Arg Gly Arg Val Cys Glu Cys Pro Thr Phe Asn Gly Val Gln Phe Lys 130 135 140

Gly Asp

145

- (2) INFORMATION FOR SEQ ID NO:3041:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..118
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602464

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    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3041:
Met Gly Asp Pro Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu
                                  10
Gln Asp Ala Gln Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu
                                25
Pro Thr Leu Val Val Asn Asn Arg Gln Tyr Arg Gly Lys Leu Glu Arg
                                                45
Lys Ala Val Leu Lys Ala Ile Cys Ala Gly Phe Glu Glu Thr Thr Glu
                        55
Pro Asn Val Cys Leu Ser Asp Asp Ile Glu Thr Asn Glu Cys Leu Asn
                                        75
                    70
Asp Asn Gly Gly Cys Trp Gln Asp Lys Ser Ala Asn Val Thr Ala Cys
                                    90
Arg Asp Thr Phe Arg Gly Arg Val Cys Glu Cys Pro Thr Phe Asn Gly
                                105
            100
Val Gln Phe Lys Gly Asp
        115
(2) INFORMATION FOR SEQ ID NO:3042:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 487 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
          (A) NAME/KEY: -
          (B) LOCATION: 1..487
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(D) OTHER INFORMATION: / Ceres Seq. ID 1602476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3042: ataaaagctc ccctccatct ctcctcctca ctcccttctc cgccgccacg ctagagagga 60 agagcgcgcg gagagcgaga gcccgggaga aacagcggcc ggcggcaaaa tggtgcagcg 120 gctcacctac cggaagcgcc acagctacgc cacaaaatcc aatcagaccc gcgtggtcaa 180 gacccctggt gggaggcttg tgtaccagta caccaagaag cgcgcgagcg gaccgaaatg 240 cccggtcacc gggaagaaga tccaaggaat tccacacctg agacctgctg agtacaagag 300 gtccaggttg gcaaggaacc gcaggactgt gaaccgtcca tatggtggtg ttctgtctgg 360 420 taccgcagtg agagagaga tcatccgtgc ctttttggtc gaggagcaga agatcgtgaa gaaggttttg aagatccaaa aaaccaagga taaggcctcc aagaactagg cgatataggc 480 atcttcc

- (2) INFORMATION FOR SEQ ID NO:3043:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 92 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..92
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3043: Lys Ser Ser Pro Pro Ser Leu Leu Leu Thr Pro Phe Ser Ala Ala Thr 10 5 Leu Glu Arg Lys Ser Ala Arg Arg Ala Arg Ala Arg Glu Lys Gln Arg

25 20 Pro Ala Ala Lys Trp Cys Ser Gly Ser Pro Thr Gly Ser Ala Thr Ala 4.0

Thr Pro Gln Asn Pro Ile Arg Pro Ala Trp Ser Arg Pro Leu Val Gly 60 55

Gly Leu Cys Thr Ser Thr Pro Arg Ser Ala Arg Ala Asp Arg Asn Ala 70 75

Arg Ser Pro Gly Arg Arg Ser Lys Glu Phe His Thr

90 85 (2) INFORMATION FOR SEQ ID NO:3044: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..119 (D) OTHER INFORMATION: / Ceres Seq. ID 1602478 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3044: Met Val Gln Arg Leu Thr Tyr Arg Lys Arg His Ser Tyr Ala Thr Lys 10 5 Ser Asn Gln Thr Arg Val Val Lys Thr Pro Gly Gly Arg Leu Val Tyr 25 20 Gln Tyr Thr Lys Lys Arg Ala Ser Gly Pro Lys Cys Pro Val Thr Gly 40 Lys Lys Ile Gln Gly Ile Pro His Leu Arg Pro Ala Glu Tyr Lys Arg 60 50 55 Ser Arg Leu Ala Arg Asn Arg Arg Thr Val Asn Arg Pro Tyr Gly Gly 75 70 Val Leu Ser Gly Thr Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu 90 85 Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Ile Gln Lys Thr 105 Lys Asp Lys Ala Ser Lys Asn 115 (2) INFORMATION FOR SEQ ID NO:3045: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..252 (D) OTHER INFORMATION: / Ceres Seq. ID 1602479 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3045: 60 gcagagttgt tgattgcagg gaaaccgcca attggcaagg atgaagcttg tgaccgcctt cgttgtgctg ctcttttctc tcctccccga ctcgtccacc gcggaggact tcgatttctt 120 ctaccttgtc caacagtggc cgggctcgtt ctgcgacacg cggcagggtt gctgcttccc 180 ggacggcgcg ggcaagccgg aggcggcgtt cggcatccac gggctgtggc ccaactacgc 240 caagtgccgc gg (2) INFORMATION FOR SEQ ID NO:3046: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..84 (D) OTHER INFORMATION: / Ceres Seq. ID 1602480 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3046: Ala Glu Leu Leu Ile Ala Gly Lys Pro Pro Ile Gly Lys Asp Glu Ala 15 10 5 1 Cys Asp Arg Leu Arg Cys Ala Ala Leu Phe Ser Pro Pro Arg Leu Val

- (2) INFORMATION FOR SEQ ID NO:3047:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..70
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602481
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3047:

Met Lys Leu Val Thr Ala Phe Val Val Leu Leu Phe Ser Leu Leu Pro 1 5 10 15

Asp Ser Ser Thr Ala Glu Asp Phe Asp Phe Phe Tyr Leu Val Gln Gln 20 25 30

Trp Pro Gly Ser Phe Cys Asp Thr Arg Gln Gly Cys Cys Phe Pro Asp 35 40 45

Gly Ala Gly Lys Pro Glu Ala Ala Phe Gly Ile His Gly Leu Trp Pro 50 55 60

Asn Tyr Ala Lys Cys Arg 65 70

- (2) INFORMATION FOR SEQ ID NO:3048:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 460 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..460
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602482
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3048:

aaattgcct ggtatcatta agcctggtga gtgtaacaat tggaatcatg ccaggttaca 60 tccacaagcc tgggcgtatt gggatcgtat ctcgttctgg tactttgaca tatgaagcgg 120 tgtttcaaac aacagctgta ggattgggtc agtcaacttg tgtaggcatt ggtggtgacc cgttcaacgg ccacaaattt tgttgattgc cttgaaaagt tcgttaacga ccctcagaca 240 gaaggtattg ttctcattgg tgaaattgga ggtacggctg aggaggatgc tgcgacattc atcaggcaac gcaggccgtc gcatgggtca tgctggagct actcgtggca ggaggaaagg gtactgcca 360 ccgggccgtc gcatgggtca tgctggagct actcgtggca ggaggaaagg gtactgcca 420 ggacaaaatc aaggcactca gagaggcagg tgtaccgttg

- (2) INFORMATION FOR SEQ ID NO:3049:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1602483 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3049: Ile Ala Leu Val Ser Leu Ser Leu Val Ser Val Thr Ile Gly Ile Met 10 Pro Gly Tyr Ile His Lys Pro Gly Arg Ile Gly Ile Val Ser Arg Ser 25 20 Gly Thr Leu Thr Tyr Glu Ala Val Phe Gln Thr Thr Ala Val Gly Leu 40 Gly Gln Ser Thr Cys Val Gly Ile Gly Gly Asp Pro Phe Asn Gly His 50 55 Lys Phe Cys (2) INFORMATION FOR SEQ ID NO:3050: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1602484 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3050: Met Pro Gly Tyr Ile His Lys Pro Gly Arg Ile Gly Ile Val Ser Arg 10 5 Ser Gly Thr Leu Thr Tyr Glu Ala Val Phe Gln Thr Thr Ala Val Gly 25 Leu Gly Gln Ser Thr Cys Val Gly Ile Gly Gly Asp Pro Phe Asn Gly 40 35 His Lys Phe Cys 50 (2) INFORMATION FOR SEQ ID NO:3051: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..58 (D) OTHER INFORMATION: / Ceres Seq. ID 1602485 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3051: Met Leu Arg His Ser Ser Arg Lys Ala Lys His Lys Ser Leu Leu 10 5 His Ser Leu Leu Asp Leu Arg His Pro Arg Ala Val Ala Trp Val Met 30 25 Leu Glu Leu Leu Val Ala Gly Gly Lys Gly Thr Ala Gln Asp Lys Ile 4.0 Lys Ala Leu Arg Glu Ala Gly Val Pro Leu 5.5 (2) INFORMATION FOR SEQ ID NO:3052: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 489 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(ix) FEATURE:

- (B) LOCATION: 1..489
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3052:

**=', ~='&'-*''							
atataaaaat	cccggtaaaa	ttccccccc	acccccgacg	cgacgcctca	aatcgctccc	60	
tgcctctggt	cacctcgctt	ccgctcccgg	ctcccctccg	gccacccaga	catcgtccgt	120	
tcgctcgcca	agagacagga	ccggagacca	tggcggacca	gctcaccgac	gaccagatcg	180	
ccgagttcaa	ggaggccttc	agcctcttcg	acaaggacgg	cgacggttgc	atcacaacca	240	
aggagctcgg	aactgtcatg	cgatcactgg	gtcagaaccc	aaccgaggct	gagctccagg	300	
acatgatcaa	cgaggtcgat	gcggacggca	acggcaccat	cgacttcccg	gagttcctca	360	
acctcatggc	ccgcaagatg	aaggacaccg	actccgagga	ggagctcaag	gaggcgttca	420	
gggtgttcga	caaggaccag	aacggcttca	tctctgcggc	ggagctccgc	cacgtgatga	480	
ccaacctcq							

- (2) INFORMATION FOR SEQ ID NO:3053:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602487
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3053:

Tyr Lys Asn Pro Gly Lys Ile Pro Pro Pro Pro Pro Thr Arg Arg Leu
1 5 10 15

Lys Ser Leu Pro Ala Ser Gly His Leu Ala Ser Ala Pro Gly Ser Pro 20 25 30

Pro Ala Thr Gln Thr Ser Ser Val Arg Ser Pro Arg Asp Arg Thr Gly 35 40 45

Asp His Gly Gly Pro Ala His Arg Arg Pro Asp Arg Arg Val Gln Gly 50 55 60

Gly Leu Gln Pro Leu Arg Gln Gly Arg Arg Arg Leu His His Asn Gln 65 70 75 80

Gly Ala Arg Asn Cys His Ala Ile Thr Gly Ser Glu Pro Asn Arg Gly 85 90 95

- (2) INFORMATION FOR SEQ ID NO:3054:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 162 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..162
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602488
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3054:

Ile Lys Ile Pro Val Lys Phe Pro Pro His Pro Arg Arg Asp Ala Ser
1 5 10 15

Asn Arg Ser Leu Pro Leu Val Thr Ser Leu Pro Leu Pro Ala Pro Leu 20 25 30

Arg Pro Pro Arg His Arg Pro Phe Ala Arg Gln Glu Thr Gly Pro Glu 35 40 45

Thr Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu 50 55 60

Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys 65 70 75 80 Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala

| Solid | Color | Solid | Soli

- (2) INFORMATION FOR SEQ ID NO:3055:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..113
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3055:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala 1 5 10 15

Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu 20 25 30

Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu 35 40 45

Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile 50 55 60

Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr 65 70 75 80

Asp Ser Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp 85 90 95

Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn 100 105 110

Leu

- (2) INFORMATION FOR SEQ ID NO:3056:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..402
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602494
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3056:

aaccategea atteacaage aaagcaatea gageeaagea eccacegtee teetttettt 60 cettegaete ateaaageat gtettgetge ggeggeaaet gegggtgeae eteeggetge 120 aactgeggea geggatgegg eggetgeaag atgiteeetg aegtggagae egeegggete 180 gaggeggegg eeggetgee eccegeeaee aggegagege eggegggte 240 gaggeggeeg eeggeggg eggetgegae tgeaaeaeet geaaetgegg eaceagetge 300 ggetgeteet getgeagetg eacetgagee aecegegatg aegagaeae eaceeggeet 360 ecceceaeee ategtaetae aactatgtag eggegtetaa at

- (2) INFORMATION FOR SEQ ID NO:3057:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 108 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..108
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602495
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3057:

Asn His Arg Asn Ser Gln Ala Lys Gln Ser Glu Pro Ser Thr His Arg

1 10 15

Pro Pro Phe Pro Ser Thr His Gln Ser Met Ser Cys Cys Gly Gly 20 25 30

Asn Cys Ala Cys Thr Ser Gly Cys Asn Cys Gly Ser Gly Cys Gly Gly 35 40 45

Cys Lys Met Phe Pro Asp Val Glu Thr Ala Gly Val Gly Val Lys 50 55

Pro Thr Val Leu Ala Ala Pro Ala Thr Lys Ala Ser Ala Gly Gly Phe 65 70 75 80

Glu Ala Ala Glu Gly Gly Cys Asp Cys Asn Thr Cys Asn Cys 85 90 95

- (2) INFORMATION FOR SEQ ID NO:3058:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 62 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..62
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602496
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3058:

Thr Ile Ala Ile His Lys Gln Ser Asn Gln Ser Gln Ala Pro Thr Val 1 5 10 15

Leu Leu Ser Phe Leu Arg Leu Ile Lys Ala Cys Leu Ala Ala Ala Ala 20 25 30

Thr Ala Arg Ala Pro Pro Ala Ala Thr Ala Ala Ala Asp Ala Ala Ala 35 40 45

Ala Arg Cys Ser Leu Thr Trp Arg Pro Pro Ala Ser Ala Ala 50 55 60

- (2) INFORMATION FOR SEQ ID NO:3059:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..82
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602497
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

Met Ser Cys Cys Gly Gly Asn Cys Ala Cys Thr Ser Gly Cys Asn Cys 1  $\phantom{-}$  5  $\phantom{-}$  10  $\phantom{-}$  15

Gly Val Gly Gly Val Lys Pro Thr Val Leu Ala Ala Pro Ala Thr Lys 35 40 45

Ala Ser Ala Gly Gly Phe Glu Ala Ala Ala Glu Gly Gly Cys Asp 50 55 60

Cys Asn Thr Cys Asn Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys Ser 65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:3060:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 487 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:

Cys Asn

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602503
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3060:

aaagectegg ectetgetee eggeteecee aeggtaetee ageegetage etgegattee 60 gecagtaege caccaccae gageetggae tacegeege gecettegee gatatettea 120 geggegaaca gegecaeca gateeegee etgegatgga gteegtggtg aaccegaagg 180 catacceget ggetgatgeg eagetgaega tgggtateet egatateate eageaggeeg 240 ceaactaeaa acagettaag aagggagega atgaagege gaagaceetg aataggggea 300 tateggagtt tgtagtgatg geggegaea eagageetet egagateetg eteeaectee 360 eettgttage tgaggataag aacgtgeeat atgtgtttgt teeategaag eaagetettg 420 geegtgettg tggtgtgaea agaeeggtta ttgettgete agtgaecagt aatgagggta 480 geagetg

- (2) INFORMATION FOR SEQ ID NO:3061:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 161 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..161
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602504
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3061:

Ser Leu Gly Leu Cys Ser Arg Leu Pro His Gly Thr Pro Ala Ala Ser 1 5 10 15 Leu Arg Phe Arg Gln Tyr Ala Thr Thr Thr Glu Pro Gly Leu Pro Pro

20 25 30

Pro Pro Phe Ala Asp Ile Phe Ser Gly Glu Gln Arg Pro Pro Asp Pro 35 40 45

Ala Pro Ala Met Glu Ser Val Val Asn Pro Lys Ala Tyr Pro Leu Ala 50 55 60

Asp Ala Gln Leu Thr Met Gly Ile Leu Asp Ile Ile Gln Gln Ala Ala 65 70 75 80
Asn Tyr Lys Gln Leu Lys Lys Gly Ala Asn Glu Ala Thr Lys Thr Leu

85 90 95
Asn Arg Gly Ile Ser Glu Phe Val Val Met Ala Ala Asp Thr Glu Pro
100 105 110

Leu Glu Ile Leu Leu His Leu Pro Leu Leu Ala Glu Asp Lys Asn Val

Pro Tyr Val Phe Val Pro Ser Lys Gln Ala Leu Gly Arg Ala Cys Gly
130 135 140

Val Thr Arg Pro Val Ile Ala Cys Ser Val Thr Ser Asn Glu Gly Ser 145 150 155 160

Ser

- Client Docket No. 80146.003 (2) INFORMATION FOR SEQ ID NO:3062: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..110 (D) OTHER INFORMATION: / Ceres Seq. ID 1602505 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3062: Met Glu Ser Val Val Asn Pro Lys Ala Tyr Pro Leu Ala Asp Ala Gln 10 Leu Thr Met Gly Ile Leu Asp Ile Ile Gln Gln Ala Ala Asn Tyr Lys 20 25 30 Gln Leu Lys Lys Gly Ala Asn Glu Ala Thr Lys Thr Leu Asn Arg Gly 40 45 Ile Ser Glu Phe Val Val Met Ala Ala Asp Thr Glu Pro Leu Glu Ile 55 60 Leu Leu His Leu Pro Leu Leu Ala Glu Asp Lys Asn Val Pro Tyr Val 70 75 Phe Val Pro Ser Lys Gln Ala Leu Gly Arg Ala Cys Gly Val Thr Arg 90 85 Pro Val Ile Ala Cys Ser Val Thr Ser Asn Glu Gly Ser Ser 100 105 (2) INFORMATION FOR SEQ ID NO:3063: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..92 (D) OTHER INFORMATION: / Ceres Seq. ID 1602506 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3063: Met Gly Ile Leu Asp Ile Ile Gln Gln Ala Ala Asn Tyr Lys Gln Leu 10 5 Lys Lys Gly Ala Asn Glu Ala Thr Lys Thr Leu Asn Arg Gly Ile Ser 25 2.0 Glu Phe Val Val Met Ala Ala Asp Thr Glu Pro Leu Glu Ile Leu Leu 40 4.5 His Leu Pro Leu Leu Ala Glu Asp Lys Asn Val Pro Tyr Val Phe Val 60 55 Pro Ser Lys Gln Ala Leu Gly Arg Ala Cys Gly Val Thr Arg Pro Val 7.5 7.0 Ile Ala Cys Ser Val Thr Ser Asn Glu Gly Ser Ser 85 (2) INFORMATION FOR SEQ ID NO:3064: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 405 base pairs (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..405
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3064:									
actctccagt	ctccactagc	atcagtcgcc	gccgcctatc	ctcgagcacc	atttccatca	60			
				gcactccgcg		120			
				gctaaaggtg		180			
				gtggcggcaa		240			
				gcggcggagc		300			
				caaggccaan		360			
tagtacacaa	acctggactc	caaggactgg	gtcaggacct	gcgag					

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:3065:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..134
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602515
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3065:

Ser Pro Val Ser Thr Ser Ile Ser Arg Arg Leu Ser Ser Ser Thr 1 5 10 15

Ile Ser Ile Asn Ser Ile Arg Leu Trp Lys Leu Ala Tyr Xaa Asn Ser 20 25 30

Trp His Ser Ala Arg Ser Thr Thr Arg Cys Pro Pro Pro Ser Arg Ser 35 40 45

Gly Pro Arg Arg Trp Leu Lys Val Gly Val Pro Ala Val Arg Arg Gln 50 55 60

Xaa Arg Arg Leu Pro Leu Pro Arg Glu Trp Arg Gln Glu Glu Glu Trp 65 70 75 80

Val Thr Thr Arg Thr Arg Gln Gly Pro Arg Pro Arg Arg Ser 85 90 95

Xaa Arg Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu Ala Ala Ser 100 105 110

Pro Lys Ala Xaa Ala Ala Gly Leu Val Arg Gly Pro Gly Leu Gln Gly 115 120 125

Leu Gly Gln Asp Leu Arg 130

- (2) INFORMATION FOR SEQ ID NO: 3066:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..102
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602516
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3066:

Met Ala Leu Arg Ala Leu Asp Asn Thr Met Pro Ala Ala Val Glu Glu 1 5 10 15

Arg Pro Lys Lys Val Ala Lys Gly Gly Arg Pro Arg Arg Pro Pro Pro 20 25 30

Arg Xaa Pro Pro Pro Pro Pro Gly Val Ala Ala Arg Arg Met 35 40 45

Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala Ala Ala Glu 50 55 60

Xaa Ala Gly Gly Val His Leu Val Gly Gly Ala Gly Gly Gly Gln 65 70 75 80

Pro Gln Gly Gln Xaa Arg Gly Ala Gly Ala Arg Thr Trp Thr Pro Arg

Ala Pro Pro Arg

90 95 85 Thr Gly Ser Gly Pro Ala 100 (2) INFORMATION FOR SEQ ID NO:3067: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..93 (D) OTHER INFORMATION: / Ceres Seq. ID 1602517 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3067: Met Pro Ala Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Gly Gly 10 Arg Pro Arg Arg Pro Pro Pro Arg Xaa Pro Pro Pro Pro Pro Gly 25 20 Val Ala Ala Arg Arg Met Gly Asn Asp Glu Asn Ser Ala Pro Arg 40 45 Ala Thr Ala Ala Ala Ala Glu Xaa Ala Gly Gly Val His Leu Val Gly 55 Gly Ala Gly Gly Gly Gln Pro Gln Gly Gln Xaa Arg Gly Ala Gly 70 75 Ala Arg Thr Trp Thr Pro Arg Thr Gly Ser Gly Pro Ala 85 (2) INFORMATION FOR SEQ ID NO: 3068: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..158 (D) OTHER INFORMATION: / Ceres Seq. ID 1602518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3068: 60 attatccqaa qttccqaacc caaqccaagc cccagggtcc gaccgcagaa ccgacccaaa atgtcgcccg cctgctccat gctcaccacc gcgtcgctct cctccccgct cccagccccg 120 cgcctccgcg ccgccgccgc cttcgctccg ccgcgccg (2) INFORMATION FOR SEQ ID NO: 3069: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: peptide (B) LOCATION: 1..52 (D) OTHER INFORMATION: / Ceres Seq. ID 1602519 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3069: Ile Ile Arg Ser Ser Glu Pro Lys Pro Ser Pro Arg Val Arg Pro Gln 10 Asn Arg Pro Lys Met Ser Pro Ala Cys Ser Met Leu Thr Thr Ala Ser 25 20 Leu Ser Ser Pro Leu Pro Ala Pro Arg Leu Arg Ala Ala Ala Phe 40 35

Client Docket No. 80146.003 50 (2) INFORMATION FOR SEQ ID NO:3070: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..52
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602520
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3070:

Leu Ser Glu Val Pro Asn Pro Ser Gln Ala Pro Gly Ser Asp Arg Arg 10

Thr Asp Pro Lys Cys Arg Pro Pro Ala Pro Cys Ser Pro Pro Arg Arg 25

Ser Pro Pro Arg Ser Gln Pro Arg Ala Ser Ala Pro Pro Pro Ser 35 40

Leu Arg Arg Ala 50

- (2) INFORMATION FOR SEQ ID NO:3071:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 52 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..52
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602521
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3071:

Tyr Pro Lys Phe Arg Thr Gln Ala Lys Pro Gln Gly Pro Thr Ala Glu 10

Pro Thr Gln Asn Val Ala Arg Leu Leu His Ala His His Arg Val Ala 25

Leu Leu Pro Ala Pro Ser Pro Ala Pro Pro Arg Arg Arg Leu Arg 35 40

Ser Ala Ala Pro 50

- (2) INFORMATION FOR SEQ ID NO:3072:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 455 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..455

atctgtcagg aaaaccaacc gattggtgac tgttg

- (D) OTHER INFORMATION: / Ceres Seq. ID 1602530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3072:

tattqttttt agaggaccaa atggagctgc tgctggagtt ggtgctcaac actcacagtg 60 ttatgcagct tggtttgcac atgttccagg acttaaggtt ctcacaccat actcttcaga 120 180 agatgcccga ggcttgctta aagctgctat tagggatccc gatcctgtta ttttcttgga 240 aaatqaattq ctttatggag aatctttccc agtttctgct gaagtgcttg attctagttt ttgcctacca attggcaaag ctaagataga acgtgggggt aaagatgtta ccattactgc 300 gttctccaag atggttggct atgctctcca ggctgcagag atactgtcca aggaaggaat 360 cagtgctgag gtgatcaacc ttcgatcgat cagaccactt gataaagctg ctattaatgc 420

- (2) INFORMATION FOR SEQ ID NO:3073:

  (i) SEQUENCE CHARACTERISTICS:

  (A) LENGTH: 151 amino acids

  (B) TYPE: amino acid

  (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..151
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602531
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3073:

Ile Val Phe Arg Gly Pro Asn Gly Ala Ala Ala Gly Val Gly Ala Gln
1 5 10 15

His Ser Gln Cys Tyr Ala Ala Trp Phe Ala His Val Pro Gly Leu Lys 20 25 30

Val Leu Thr Pro Tyr Ser Ser Glu Asp Ala Arg Gly Leu Leu Lys Ala 35 40 45

Ala Ile Arg Asp Pro Asp Pro Val Ile Phe Leu Glu Asn Glu Leu Leu 50 55 60

Tyr Gly Glu Ser Phe Pro Val Ser Ala Glu Val Leu Asp Ser Ser Phe 65 70 75 80

Cys Leu Pro Ile Gly Lys Ala Lys Ile Glu Arg Gly Gly Lys Asp Val 85 90 95

Thr Ile Thr Ala Phe Ser Lys Met Val Gly Tyr Ala Leu Gln Ala Ala 100 105 110

Glu Ile Leu Ser Lys Glu Gly Ile Ser Ala Glu Val Ile Asn Leu Arg 115 120 125

Ser Ile Arg Pro Leu Asp Lys Ala Ala Ile Asn Ala Ser Val Arg Lys 130 135 140

Thr Asn Arg Leu Val Thr Val 145 150

- (2) INFORMATION FOR SEQ ID NO:3074:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..88
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1602532
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3074:

Leu Phe Leu Glu Asp Gln Met Glu Leu Leu Leu Glu Leu Val Leu Asn 1 5 10 15

Thr His Ser Val Met Gln Leu Gly Leu His Met Phe Gln Asp Leu Arg
20 25 30

Phe Ser His His Thr Leu Gln Lys Met Pro Glu Ala Cys Leu Lys Leu 35 40 45

Leu Leu Gly Ile Pro Ile Leu Leu Phe Ser Trp Lys Met Asn Cys Phe 50 55 60

Met Glu Asn Leu Ser Gln Phe Leu Leu Lys Cys Leu Ile Leu Val Phe 65 70 75 80

Ala Tyr Gln Leu Ala Lys Leu Arg 85

- (2) INFORMATION FOR SEQ ID NO:3075:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..82
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3075:
- Met Glu Leu Leu Glu Leu Val Leu Asn Thr His Ser Val Met Gln 1 5 10 15
- Leu Gly Leu His Met Phe Gln Asp Leu Arg Phe Ser His His Thr Leu 20 25 30
- Gln Lys Met Pro Glu Ala Cys Leu Lys Leu Leu Gly Ile Pro Ile 35 40 45
- Leu Leu Phe Ser Trp Lys Met Asn Cys Phe Met Glu Asn Leu Ser Gln 50 55 60
- Phe Leu Leu Lys Cys Leu Ile Leu Val Phe Ala Tyr Gln Leu Ala Lys 65 70 75 80

Leu Arg

13 . ts 19

## POWER OF ATTORNEY

CERES, INC. 3007 Malibu Canyon Road Malibu, CA 90265

I, Richard Hamilton, Chief Financial Officer of CERES, INC. of 3007 Malibu Canyon Road, Malibu, California 90265, grant Power of Attorney and authority to empower the following attorneys to act on behalf of CERES, INC. for executing Verified Statements (Declarations) Claiming Small Entity Status to be submitted to the U.S. Patent and Trademark Office in connection with the filing of provisional or regular patent applications on behalf of CERES, INC.

Raymond C. Stewart (Reg. No. 21,066)
Joseph A. Kolasch (Reg. No. 22,463)
Leonard R. Svensson (Reg. No. 30,330)
Gerald M. Murphy, Jr. (Reg. No. 28,977)
Mark J. Nuell (Reg. No. 36,623)

This Power of Attorney is to remain in full force and effect until terminated by an official of CERES, INC.

By Richard Hamilton

Date 9/34/98

1.3 . ha 1.7

## IN THE U.S. PATENT AND TRADEMARK OFFICE

## INFORMATION SHEET

Applicant:

Nickolai ALEXANDROV and Vyacheslav BROVER

Appl. No.:

NEW

Filed:

October 13, 2000

For:

SEQUENCE-DETERMINED DNA FRAGMENTS AND

CORRESPONDING

POLYPEPTIDES **ENCODED** 

THEREBY

Priority Claimed:

2750-0578P 60/159,331 October 14, 1999

Send Correspondence to:

BIRCH, STEWART, KOLASCH & BIRCH, LLP or CUSTOMER NO. 2292

P.O. Box 747

Falls Church, VA 22040-0747

(703) 205-8000

The above information is submitted to advise the U.S.P.T.O.

of all relevant facts in connection with the present application.

A timely executed Declaration in accordance with 37 C.F.R. § 1.64 will follow.

Respectfully submitted,

BIRCH, STEWART, KOLASCH & BIRCH, LLP

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RCS/CAV 2750-1237P